



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07H 21/02, 2/04, C12N 5/00, 5/10, 15/00, 15/09, 15/11, 15/31		A1	(11) International Publication Number: WO 98/58943
			(43) International Publication Date: 30 December 1998 (30.12.98)
(21) International Application Number: PCT/US98/12764		(US). SMITH, Hamilton, O. [US/US]; 8222 Carrbridge Circle, Towson, MD 21204 (US).	
(22) International Filing Date: 18 June 1998 (18.06.98)		(74) Agents: HOOVER, Kenley, K. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).	
(30) Priority Data: 60/050,359 20 June 1997 (20.06.97) US 60/053,377 22 July 1997 (22.07.97) US 60/053,344 22 July 1997 (22.07.97) US 60/057,483 3 September 1997 (03.09.97) US		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(71) Applicants (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). MEDIMMUNE, INC. [US/US]; 35 West Watkins Mill Road, Gaithersburg, MD 20878 (US).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(72) Inventors; and (75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; 11915 Glen Mill Road, Potomac, MD 20854 (US). WHITE, Owen, R. [US/US]; 886 Quince Orchard Boulevard #202, Gaithersburg, MD 20878 (US). CLAYTON, Rebecca [US/US]; 6706 B. Polor Avenue, Takoma Park, MD 20912 (US). DOUGHERTY, Brian, A. [US/US]; 10 Rosemary Lane, Killingworth, CT 06419 (US). LATHIGRA, Raju [IN/US]; 19051 Steeple Place, Germantown, MD 20874			
(54) Title: BORRELIA BURGDORFERI POLYNUCLEOTIDES AND SEQUENCES			
(57) Abstract <p>The present invention provides polynucleotide sequences of the genome of <i>Borrelia burgdorferi</i>, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

***Borrelia burgdorferi* Polynucleotides and Sequences**

5

Field of the Invention

The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Borrelia burgdorferi*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation, polypeptide production, assays and pharmaceutical development, among others.

Statement as to Rights to Inventions Made Under Federally-Sponsored Research and Development

15

Part of the work performed during development of this invention utilized U.S. Government funds. The U.S. Government may have certain rights in the invention - DE-FC02-95ER61962; DE-FC02-95ER61963; and NAGW 2554.

20

Background of the Invention

Spirochetes are a family of motile, unicellular, spiral-shaped bacteria which share a number of structural characteristics. Three genera of the spirochetes are pathogenic in humans: (a) *Treponema*, which includes the pathogens that cause syphilis (*T. pallidum*), yaws (*T. pertenue*), and pinta (*T. carateum*); (b) *Borrelia*, which includes the pathogens that cause epidemic and endemic relapsing fever and Lyme disease; and (c) *Leptospira*, which includes a wide variety of small spirochetes that cause mild to serious systemic human illness (Koff, A. B. and Rosen, T. *J. Am. Acad. Dermatol.* **29**:519-535 (1993)).

Lyme borreliosis, more commonly known as Lyme disease, is presently the most common human disease in the United States transmitted by an arthropod vector. Centers for Disease Control, Morbid. Mortal. Weekly Rep. 44:590-591 (1995). Further, infection of household pets, such as dogs, is a considerable problem. The causative agent of this affliction is the spirochete *Borrelia burgdorferi*, which is generally transmitted to mammalian hosts by feeding ticks. Barbour, A. and Fish, D. *Science* 260:1610-1616 (1993). Once the bacteria pass through the skin they disseminate and produce a variety of clinical manifestations. Diagnosis of this disease is often made serologically by the identification of antiborreliacal antibodies. Hilton, E. et al., *J. Clin. Microbiol.* 35:774-776 (1997).

35

While initial symptoms often include a rash at the infection point, Lyme disease is a multisystemic disorder that may include arthritic, carditic, and neurological manifestations. While antibiotics are currently used to treat active cases of Lyme disease, *B. burgdorferi* appears to be able to persist even after prolonged antibiotic treatment. Further, *B. burgdorferi* can persist for years in a mammalian host even in the presence of an active immune response. Straubinger, R. et al., J. Clin. Microbiol. 35:111-116 (1997); Steere, A., N. Engl. J. Med. 321:586-596 (1989).

Animal models have proven useful for studying the progression of Lyme disease, methods for preventing this disease, and immunological responses to antigenic challenges with *B. burgdorferi* proteins. Garcia-Monoco, J. et al., J. Infect. Dis. 175:1243-1245 (1997). Using a canine model, Starubinger, R. et al., Infect. Immun. 65:1273-1285 (1977), demonstrated that *B. burgdorferi* migrates into joints and induces up-regulation of interleukin-8 in synovial membranes. Similarly, *B. burgdorferi* induction of interleukin-8 production has been demonstrated in cultured human endothelial cells. Burns, M. et al., Infect. Immun. 65:1217-1222 (1997).

Antigenic heterogeneity has been postulated as a mechanism used by *B. burgdorferi* for evasion of host immune responses. Schwan, T. et al., Can. J. Microbiol. 37:450-454 (1991). In support of this mechanism, antigenic variation has been described with other pathogenic bacteria. Hagbloom, P. et al., Nature 315:156-158 (1985). Further, cassette type genetic recombination of genes encoding *B. burgdorferi* surface proteins has been shown to decrease the antigenicity of these organisms to antibodies generated against strains which have not undergone the same recombination. Zhang, J. et al., Cell 89:275-285 (1997).

A number of different types of Lyme disease vaccines have been tested and shown to induce immunological responses. Whole-cell *B. burgdorferi* vaccines have been shown to induce both immunological responses and protective immunity in several animal models. Reviewed in Wormser, G., Clin. Infect. Dis. 21:1267-1274 (1995). For example, dogs inoculated with a chemically inactivated whole-cell vaccine primarily develop antibodies to outer surface membrane proteins of the administered organism. Further, passive immunity has been also demonstrated in animals using *B. burgdorferi* specific antisera. Similarly, passive immunity is conferred human by the administration of sera obtained from Lyme disease patients.

While whole-cell Lyme disease vaccines confer protective immunity in animal models, use of such vaccines presents the risk that responsive antibodies will be generated which cross react with human antigens. Reviewed in Wormser, G., supra. This problem is at least partly the result of the production of *B. burgdorferi* specific antibodies which cross-react with hepatocytes and both muscle and nerve cells. *B. burgdorferi* heat shock proteins and the 41-kd flagellin subunit are believed to contain the antigens against which these cross-reactive antibodies are generated.

It is clear that the etiology of diseases mediated or exacerbated by *B. burgdorferi* genes, and that characterizing the genes and their patterns of expression would add dramatically to our

understanding of the organism and its host interactions. Knowledge of *B. burgdorferi* genes and genomic organization would dramatically improve understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *B. burgdorferi* would provide reagents for, among other things, detecting, characterizing and controlling *B. burgdorferi* infections. There is a need therefore to characterize the genome of *B. burgdorferi* and for polynucleotides and sequences of this organism.

SUMMARY OF THE INVENTION

The present invention is based on the sequencing of fragments of the *Borrelia burgdorferi* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-155.

The present invention provides the complete nucleotide sequence of the *Borrelia burgdorferi* chromosome and 154 contigs representing the majority of the sequence of the *B. burgdorferi* extrachromosomal elements, all of which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS: 1-155.

The present invention further provides nucleotide sequences which are at least 95%, 96%, 97%, 98%, and 99%, identical to the nucleotide sequences of SEQ ID NOS:1-155, ORF IDs and corresponding ORFs.

The nucleotide sequences of SEQ ID NOS:1-155, ORF ID or ORF within, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to said nucleotide sequence may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Borrelia burgdorferi* genome.

Another embodiment of the present invention is directed to fragments of the *Borrelia burgdorferi* genome having particular structural or functional attributes. Such fragments of the *Borrelia burgdorferi* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression

modulating fragments or EMFs, and fragments which can be used to diagnose the presence of *Borrelia burgdorferi* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORF IDs and ORFs in fragments of the *Borrelia burgdorferi* genome disclosed in Tables 1-6, and the EMFs found 5' prime of the initiation codon, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Borrelia burgdorferi* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Borrelia burgdorferi* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Borrelia burgdorferi* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Borrelia burgdorferi* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such

methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b) determining whether the agent binds to said protein.

The present genomic sequences of *Borrelia burgdorferi* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Borrelia burgdorferi* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Borrelia burgdorferi* researchers and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

DESCRIPTION OF THE FIGURES

FIGURE 1 is a block diagram of a computer system (102) that can be used to implement computer-based systems of present invention.

FIGURE 2 is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Borrelia burgdorferi* genome of the present invention. Both Macintosh and Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth*

Annual Hawaii International Conference on System Sciences, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Borrelia burgdorferi* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL database. The resulting sequence file is processed to trim portions of the sequences with a high rate ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research (TIGR) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is loaded into the database with the lassie program. Identification of open reading frames (ORFs) is accomplished by processing contigs with zorf. The ORFs are searched against *B. burgdorferi* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990). Results of the ORF determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-6.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention is based on the sequencing of fragments of the *Borrelia burgdorferi* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS: 1-155. (As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.) SEQ ID NOS:1-155

In addition, the present invention provides the nucleotide sequences of SEQ ID NOS: 1-155, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-155" refers to any portion of the SEQ ID NOS: 1-155 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Borrelia burgdorferi* open reading frames (ORFs) represented by ORF IDs, expression modulating fragments (EMFs) and diagnostic fragments (DFs) which can be used to diagnose the presence of *Borrelia burgdorferi* in sample. A non-limiting identification of preferred representative portions are provided in Tables 1-6 as ORF IDs. As discussed in detail below, the information provided in SEQ ID NOS:1-155 and in Tables 1-6 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled in the art to clone and sequence all "representative fragments" of interest, including ORFs encoding a large variety of *Borrelia burgdorferi* proteins.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1-6 (ORF IDs) and SEQ ID NOS:1-155, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in SEQ ID NOS:1-155 is position 1 (therefore, the sequence positions for each ORF ID is determined by the numbering of the SEQ ID comprising the ORF ID). That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of SEQ ID NOS:1-155 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of SEQ ID NOS:1-155 wherein the contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire ORF ID or SEQ ID NO., minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Tables 1-6 (ORF IDs) and SEQ ID NOS:1-155. The preferred sizes are, of course, meant to exemplify not limit the present invention as all size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, of each ORF ID and SEQ ID NO., are included in the invention.

The present invention also provides for the exclusion of any fragment, specified by 5' and 3' base positions or by size in nucleotide bases as described above for any ORF ID or SEQ ID NOS:1-155. Any number of fragments of nucleotide sequences in ORF IDs or SEQ ID NOS:1-155, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

While the presently disclosed sequences of SEQ ID NOS: 1-155 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances, further investigation of a fragment or sequence of the invention may reveal a nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS: 1-155. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS: 1-155 and Tables 1-6 has been made available), resolving a rare sequencing error in SEQ ID NOS: 1-155 will be well within the skill

of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS: 1-155 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS: 1-155.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are provided below, for instance. A wide variety of *Borrelia burgdorferi* strains that can be used to prepare *B. burgdorferi* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *B. burgdorferi* strain that provided the DNA of the present Sequence Listing, has been deposited with the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, as Deposit No. 202012, on 8 August 1997. The ATCC Deposit is provided merely as a convenience to those of skill in the art. Reference to the deposit is not a waiver of any rights of the inventors or their assignees in the present subject matter.

The nucleotide sequences of the genomes from different strains of *Borrelia burgdorferi* differ somewhat. However, the nucleotide sequences of the genomes of all *Borrelia burgdorferi* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS: 1-155 and the ORF IDs within. Nearly all will be at least 99% identical and the great majority will be 99.9% identical.

The present application is further directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in SEQ ID NOS: 1-155 and the ORF IDs within. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *B. burgdorferi* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *B. burgdorferi* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *B. burgdorferi* activity include, *inter alia*, isolating a *B. burgdorferi* gene or allelic variants thereof from a DNA library, and detecting *B. burgdorferi* mRNA expression from

biological or environmental samples, suspected of containing *B. burgdorferi* by Northern Blot, PCR, or similar analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in SEQ ID NOS: 1-155, the ORF IDs, and the ORF within each ORF ID, which do, in fact, encode a polypeptide having *B. burgdorferi* protein activity. By "a polypeptide having *B. burgdorferi* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *B. burgdorferi* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in SEQ ID NOS: 1-155, the ORF IDs, and the ORF within each ORF ID, will encode a polypeptide having *B. burgdorferi* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *B. burgdorferi* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 1, 2, 4, and 5 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genres, species, or strains listed in Tables 1, 2, 4, and 5.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *B. burgdorferi* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in SEQ ID NOS: 1-155, an ORF ID, or the ORF within each ORF ID, or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. *See* Brutlag et al. (1990) *Comp. App. Biosci.* 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the

subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

COMPUTER RELATED EMBODIMENTS

5 The nucleotide sequences provided in SEQ ID NOS: 1-155, including ORF IDs and corresponding ORFs, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 96%, 97%, 98% or 99%, and most preferably at least 99.9% identical to said nucleotide sequences may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule;
10 which contains a nucleotide sequence of the present invention, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of the present invention. Such a manufacture provides a large portion of the *Borrelia burgdorferi* genome and parts thereof (e.g., a *Borrelia burgdorferi* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using
15 means not directly applicable to examining the *Borrelia burgdorferi* genome or a subset thereof as it exists in nature or in purified form.

 In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are
20 not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a
25 nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

 As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for
30 recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

 A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen
35 to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase,

Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of the present invention (e.g. SEQ ID NOS: 1-155), a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 96%, 97%, 98%, 99% and most preferably at least 99.9% identical to a sequence of the present invention (e.g. SEQ ID NOS: 1-155) enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Borrelia burgdorferi* genome which contain homology to ORFs or proteins from both *Borrelia burgdorferi* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Borrelia burgdorferi* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Borrelia burgdorferi* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of

commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for
5 conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random
10 occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a
15 three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Borrelia burgdorferi* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such
20 presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Borrelia burgdorferi* genome. In the present examples, implementing software which implement the BLAST and BLAZE
30 algorithms, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990), is used to identify open reading frames within the *Borrelia burgdorferi* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard
35 drive 112 and a removable medium storage device 114. The removable medium storage device

114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing and processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Borrelia burgdorferi* genome. The fragments of the *Borrelia burgdorferi* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Borrelia burgdorferi* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Borrelia burgdorferi* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS: 1-155, to representative fragments thereof as described above including ORF IDs and ORFs, to polynucleotides at least 95%, preferably at least 96%, 97%, 98%, or 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Borrelia burgdorferi* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate a *Borrelia burgdorferi* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-6 can then be generated using nucleotide sequence information provided in SEQ ID NOS: 1-155. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from the lambda DNA library or *Borrelia burgdorferi* genomic DNA. Thus, given the availability of SEQ ID NOS: 1-

155, the information in Tables 1-6, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-155 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of the present invention.

5 The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA. For purposes of numbering and reference to polynucleotide and polypeptide sequences the entire sequence of each sequence of SEQ ID NOS:1-155 is included with the first nucleotide being position 1. Therefore, for reference purposes the numbering used in the present invention is that provided in
10 the sequence listing for SEQ ID NOS:1-155.

 As used herein, an open reading frame (ORF), means a series of nucleotide triplets coding for amino acid residues without any termination codons and is a sequence translatable into protein. Further, unless specified, the term "ORF" for each ORF ID is defined by the termination codon at the 3' end and the 5' most methionine codon, at the 5' end, in frame with said 3'
15 termination codon. Unless specified, the term "ORF" also refers to a particular polypeptide sequence defined by the ORF polynucleotide sequence, wherein the N-terminus is defined by the 5' most methionine codon in frame with the termination codon at the 3' end of the ORF ID and the C-terminus is defined by the last codon before the said 3' termination codon. As used herein, an ORF ID represents a sequence without any internal termination codons flanked by termination
20 codons.

 Tables 1-6 list ORF IDs in the *Borrelia burgdorferi* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those
25 discussed herein, to generate more inclusive, more restrictive, or more selective lists.

 The *B. burgdorferi* genome consists of one large linear chromosome containing approximately two thirds of its genetic material and multiple extrachromosomal elements (approximately 15) containing the remaining one third of its genetic material. SEQ ID NO:1 (Contig ID 1) is the complete sequence of the large linear *B. burgdorferi* chromosome. SEQ ID
30 NOS:2-155 (Contig ID 2-155 respectively) are fragments (contigs) of the extrachromosomal elements. Tables 1-3 below relate only to SEQ ID NO:1. Tables 4-6 relate to the extrachromosomal elements (SEQ ID NOS:2-155).

 Table 1 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that cover a continuous region of at least 50 bases are 95% or more identical (by
35 BLAST analysis using default parameters) to a nucleotide sequence available through GenBank in July, 1997.

 Table 2 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in July, 1997.

Table 3 sets out ORF IDs in the *Borrelia burgdorferi* chromosome of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in July, 1997.

5 Table 4 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in July, 1997.

10 Table 5 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in July, 1997.

Table 6 sets out ORF IDs in the *Borrelia burgdorferi* extrachromosomal element contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in July, 1997.

15 In each table, the first and second columns identify the ORF ID by, respectively, contig number and ORF ID number within the contig; the third column indicates the first nucleotide of the ORF ID, counting from the 5' end of the contig strand; and the fourth column indicates the last nucleotide of the ORF ID, counting from the 5' end of the contig strand.

20 In Tables 1, 2, 4 and 5, column five, lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the database accession numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column seven provides the BLAST identity score from the comparison of the ORF ID and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis.

25 The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were
30 "similar" (*i.e.*, possessed similar biochemical characteristics). As is known in the art, substitution of one amino acid for a "similar" amino acid is a conservative substitution. Generally, proteins are highly tolerant of conservative substitutions. Many programs for analysis of nucleotide or amino acid sequence similarity, such as fasta and BLAST specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1, 2, 4 and 5
35 herein enumerate the percent identity and similarity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Borrelia burgdorferi* genome other than those listed in Tables 1-6, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Borrelia burgdorferi* genome by their proximity to the ORFs provided in Tables 1-6. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken from any one of the ORFs of Tables 1-6 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Borrelia burgdorferi* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below. A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host is examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Borrelia burgdorferi* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Borrelia burgdorferi* genome, such as by using well-known computer analysis software, and by generating and testing probes or

amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-155, ORF IDs and ORFs within, a representative fragment thereof, or a nucleotide sequence at least 99% and preferably 99.9% identical to SEQ ID NOS: 1-155, ORF IDs and ORFs within, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands).

Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Borrelia burgdorferi* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORF IDs and ORFs of the *Borrelia burgdorferi* genome disclosed in Tables 1-6, and the EMFs found 5' to the ORF IDs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Borrelia burgdorferi*. Especially preferred in this regard are ORF IDs and ORFs such as those of Tables 3 and 6, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Borrelia burgdorferi*. Also particularly preferred are ORF IDs and ORFs that can be used to distinguish between strains of *Borrelia burgdorferi*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano,

J. Neurochem. 56:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention.

5 Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Borrelia burgdorferi* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORF IDs or ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF ID or ORF. For vectors
10 comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF ID or ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention.

The following vectors are provided by way of example. Useful bacterial vectors include
15 phagescript, PsiX174, pBluescript SK, pBS KS, pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pDR540, pRIT5 (available from Pharmacia); pQE vectors (available from Promega). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

20 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK223-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of
25 the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing any one of the isolated fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such
30 as a yeast cell, or a procaryotic cell, such as a bacterial cell.

A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation, which are described in, for instance, Davis, L. *et al.*,
35 BASIC METHODS IN MOLECULAR BIOLOGY (1986).

A host cell containing one of the fragments of the *Borrelia burgdorferi* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

5 The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORF IDs depicted in Tables 2, 3, 5 and 6, and ORFs within, which encode proteins.

10 A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

15 In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

20 The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

30 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of the *B. burgdorferi* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in the art of protein purification.

35 The invention further provides for isolated *B. burgdorferi* polypeptides comprising an amino acid sequence selected from the group including: (a) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence from the first methionine codon to the termination codon of each sequence listed in SEQ ID NOS:1-155, wherein said termination codon is at the end of each SEQ ID NO: and said first methionine is the

first methionine in frame with said termination codon; and (b) the amino acid sequence of a full-length *B. burgdorferi* polypeptide having the complete amino acid sequence in (a) excepting the N-terminal methionine.

5 The polypeptides of the present invention also include polypeptides having an amino acid sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a) and (b) above.

The present invention is further directed to polynucleotides encoding portions or fragments of the amino acid sequences described herein as well as to portions or fragments of the isolated amino acid sequences described herein. Fragments include portions of the amino acid sequences described herein at least 5 contiguous amino acid in length and selected from any two
10 integers, one of which representing an N-terminal position and another representing a C-terminal position. The initiation codon of the ORFs of the present invention is position 1. The initiation codon (position 1) for purposes of the present invention is the first methionine codon of each ORF ID which is in frame with the termination codon at the end of each said sequence. Every
15 combination of a N-terminal and C-terminal position that a fragment at least 5 contiguous amino acid residues in length could occupy, on any given ORF is included in the invention, i.e., from initiation codon up to the termination codon. "At least" means a fragment may be 5 contiguous amino acid residues in length or any integer between 5 and the number of residues in an ORF, minus 1. Therefore, included in the invention are contiguous fragments specified by any N-
20 terminal and C-terminal positions of amino acid sequence set forth in SEQ ID NOS:1-155 or Tables 1-6 wherein the contiguous fragment is any integer between 5 and the number of residues in an ORF minus 1.

Further, the invention includes polypeptides comprising fragments specified by size, in amino acid residues, rather than by N-terminal and C-terminal positions. The invention includes
25 any fragment size, in contiguous amino acid residues, selected from integers between 5 and the number of residues in an ORF, minus 1. Preferred sizes of contiguous polypeptide fragments include about 5 amino acid residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100 amino acid residues, about 200 amino acid residues, about 300 amino acid residues, and
30 about 400 amino acid residues. The preferred sizes are, of course, meant to exemplify, not limit, the present invention as all size fragments representing any integer between 5 and the number of residues in a full length sequence minus 1 are included in the invention. The present invention also provides for the exclusion of any fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments
35 specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

Further polypeptides of the present invention include polypeptides which have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

5 A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *B. burgdorferi* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *B.*
10 *burgdorferi* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide
15 sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the
20 reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to the ORF amino acid sequences encoded by the sequences of SEQ
25 ID NOS:1-155, as described hererin, can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and
30 subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is
35 shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject

sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is
5 determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the
10 purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10
15 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C-termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
20 This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected. No other manual
25 corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present
30 invention that do not have *B. burgdorferi* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *B. burgdorferi* protein
35 expression or as agonists and antagonists capable of enhancing or inhibiting *B. burgdorferi* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *B. burgdorferi* protein binding proteins which are also candidate agonists and antagonists according to the present invention. *See, e.g.,* Fields et al. (1989) Nature 340:245-246.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Borrelia burgdorferi* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to

produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3- phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli*, *B. subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available from Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney

fibroblasts, described in Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. Particularly preferred in this regard are conservative substitutions, known to those of skill in the art. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence (e.g., removal of leader sequence(s)) should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Borrelia burgdorferi*, of the fragments of the *Borrelia burgdorferi* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Borrelia burgdorferi* is defined as a homolog of a fragment of the *Borrelia burgdorferi* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Borrelia burgdorferi* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 95% or more homology. Among especially

preferred homologs those with 96, 97%, 98%, 99% or more homology are particularly preferred. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

5 Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS: 1-155 or from a nucleotide sequence at least 95%, particularly at least 96%, 97%, 98% or 99%, especially at least 99.5% identical to a sequence of SEQ ID NOS: 1-155 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well
10 known and have been described in great detail in many publications such as, for example, Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS: 1-155 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-155, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC
15 and 50% formamide, and washing at 50- 65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

20 When using DNA probes derived from SEQ ID NOS:1-155, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS: 1-155 , for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences having regions which are greater than 90%
25 homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

30 Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Borrelia burgdorferi*.

ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

35 Each ORF of the ORF IDs provided in Tables 1, 2, 4 and 5 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide. Such identifications permit one skilled in the art to use the *Borrelia burgdorferi* ORFs in a manner similar to the known type

of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESIS, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Borrelia burgdorferi* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-6 and SEQ ID NOS:1-155.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*, *Symbiosis* 21:79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series* 389:93 (1989).

The metabolism of sugars is an important aspect of the primary metabolism of *Borrelia burgdorferi*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters* 1:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for example, in Bigelis *et al.*, beginning on page 357 in *GENE MANIPULATIONS AND FUNGI*; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in Owusu *et al.*, *Biochem. et Biophysica. Acta.* 872:83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, *Starch* 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, *Acid Proteases Structure Function and Biology*, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, *Industrial Enzymes*, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, *Report Industrial Enzymes by 1990*, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London* 310:227 (1985) and Poserke, *Journal of the American Oil Chemist Society* 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton,

Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo-selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein.

B. burgdorferi protein-specific antibodies for use in the present invention can be raised against the intact *B. burgdorferi* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *B. burgdorferi* polypeptide or fragment thereof is prepared and purified to render it substantially free

of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.*, Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *B. burgdorferi* polypeptide-binding fragments, chimeric, and humanized antibodies can be produced through the application of recombinant DNA technology or through synthetic chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide antigen of the present invention may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, *B. burgdorferi* polypeptide-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the *B. burgdorferi* polypeptide-specific antibody can be blocked by the *B. burgdorferi* polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to the *B. burgdorferi* polypeptide-specific antibody and can be used to immunize an animal to induce formation of further *B. burgdorferi* polypeptide-specific antibodies.

Antibodies and fragments thereof of the present invention may be described by the portion of a polypeptide of the present invention recognized or specifically bound by the antibody. Antibody binding fragments of a polypeptide of the present invention may be described or specified in the same manner as for polypeptide fragments discussed above, i.e., by N-terminal and C-terminal positions or by size in contiguous amino acid residues. Any number of antibody binding fragments, of a polypeptide of the present invention, specified by N-terminal and C-terminal positions or by size in amino acid residues, as described above, may also be excluded from the present invention. Therefore, the present invention includes antibodies that specifically bind a particularly described fragment of a polypeptide of the present invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Borrelia* other than *B. burgdorferi* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Borrelia*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Borrelia*, are included in the present invention.

3. Epitope-Bearing Portions

In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *B. burgdorferi* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, e.g., Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002. Amino acid residues comprising antigenic epitopes may be determined by algorithms such as the Jameson-Wolf analysis or similar algorithms or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, e.g., Sutcliffe, et al., (1983) Science 219:660-666. Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. See, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. See Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids)

can bind and displace the larger peptides in immunoprecipitation assays. *See, e.g.,* Wilson, et al., (1984) Cell 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

5 Antigenic epitope-bearing peptides and polypeptides of the invention designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides comprising a larger portion of an amino acid sequence of a polypeptide
10 of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.,* the
15 sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

 The epitope-bearing peptides and polypeptides of the present invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid
20 sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing
25 single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides
30 are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. 82:5131-5135 at 5134.

 Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies
35 according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*;; Wilson, et al., *supra*;; and Bittle, et al. (1985) J. Gen. Virol. 66:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such

as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989), describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is

hereby incorporated herein by reference.

As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Traunecker et al. (1988) Nature 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *B. burgdorferi* polypeptide or fragment thereof alone. See Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *B. burgdorferi* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

4. Diagnostic Assays and Kits

The present invention further relates to methods for assaying *Borrelia* infection in an animal by detecting the expression of genes encoding *Borrelia* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Borrelia*-specific antibodies, nucleic acids, or proteins. Analysis of nucleic acid specific to *Borrelia* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, *e.g.*, Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Borrelia* has already been made, the present invention is useful for monitoring progression or regression of the disease state whereby patients exhibiting enhanced *Borrelia* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Borrelia* polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Borrelia* polypeptides or nucleic acids. Methods for obtaining biological samples such as tissue are well known in the art.

The present invention is useful for detecting diseases related to *Borrelia* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Borrelia* polypeptides having sufficient homology to the nucleic acid sequences identified in SEQ ID NOS:1-155 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium phosphate buffer. A *B. burgdorferi* polynucleotide sequence shown in SEQ ID NOS:1-155 labeled according to any appropriate method (such as the ³²P-multiprimered DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *B. burgdorferi* DNA sequence of the present invention is used as a template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (i.e., mRNA encoding *Borrelia* polypeptides).

Levels of mRNA encoding *Borrelia* polypeptides are assayed, for e.g., using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers. Alternatively, rather than labeling the primers, a labeled dNTP can be included in the PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate

bands (corresponding to the mRNA encoding the *Borrelia* polypeptides of the present invention) are quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY

5 MANUAL (C.W. Dieffenbach et al. eds., Cold Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or *Borrelia* species including *B. burgdorferi* using bio chip technology. The present invention includes both high density chip arrays (>1000 oligonucleotides per cm²) and low density chip arrays (<1000 oligonucleotides per cm²). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect *Borrelia* species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other *Borrelia* infection. The bio chips of the present invention may comprise polynucleotide sequences of other pathogens

10 including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *B. burgdorferi* or other *Borrelia* infections and to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip

15 technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in the same manner as for the fragments, i.e. by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to

20 detect *Borrelia* species, including *B. burgdorferi*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681, 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

30 Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *B. burgdorferi* or other *Borrelia* species and infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions,

35 mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect *Borrelia* species, including *B. burgdorferi*, using biosensors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Borrelia* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Borrelia* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Borrelia* polypeptides for Western-blot or dot/slot assay. *See, e.g.*, Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Borrelia* polypeptide can be accomplished using an isolated *Borrelia* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Borrelia* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Borrelia* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and quantify a *Borrelia* polypeptide. The amount of a *Borrelia* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Borrelia* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Borrelia* polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group, which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable

labels include radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Borrelia* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include malate dehydrogenase, *Borrelia* nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}To , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Ci , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In addition, this radionuclide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977) Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *B. burgdorferi* infection. Such a kit may include an isolated *B. burgdorferi* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*B. burgdorferi* antibody. Such a kit also includes means for detecting the

binding of said antibody to the antigen. In specific embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

5 In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *B. burgdorferi* antigen can be detected by binding of the reporter labeled antibody to the anti-*B. burgdorferi* polypeptide antibody.

10 In a related aspect, the invention includes a method of detecting *B. burgdorferi* infection in a subject. This detection method includes reacting a body fluid, preferably serum, from the subject with an isolated *B. burgdorferi* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of
15 reporter-labeled antibody.

The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a
20 free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect *Borrelia* species including *B. burgdorferi* using bio chip and biosensor
25 technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize *Borrelia* species, including *B. burgdorferi*. Bio chip and biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect *Borrelia* species, including *B. burgdorferi* or specific polypeptides of the present invention. Bio chips or
30 biosensors comprising polypeptides or antibodies of the present invention may be used to detect *Borrelia* species, including *B. burgdorferi*, in biological and environmental samples and to diagnose an animal, including humans, with an *B. burgdorferi* or other *Borrelia* infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

35 The bio chips of the present invention may further comprise polypeptide sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal

polypeptide sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *B. burgdorferi* or other *Borrelia* infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention may be specified in the same manner as for the fragments, i.e., by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect *Borrelia* species, including *B. burgdorferi*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos. and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

5. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Borrelia burgdorferi* fragment and contigs herein described.

In general, such methods comprise steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Borrelia burgdorferi* genome; and
- (b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in *Synthetic*

Peptides, A User's Guide, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry* 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

6. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be used to modulate the growth or pathogenicity of *Borrelia burgdorferi*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth pathogenicity of *Borrelia burgdorferi* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or

rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

5 As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

10 The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight
15 and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another
20 molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980)
25 cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity,
30 susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously,
35 intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16th Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by

a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

7. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present disclosure.

ILLUSTRATIVE EXAMPLES

LIBRARIES AND SEQUENCING

1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics* 2:231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability, P_0 , that any given base in a sequence of size L , in nucleotides, is not sequenced after a certain amount, n , in nucleotides, of random sequence has been determined can be calculated by the equation $P_0 = e^{-m}$, where m is L/n , the fold coverage. For instance, for a genome of 2.8 Mb, $m=1$ when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point, $P_0 = e^{-1} = 0.37$. The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence L has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size L , in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length, G , is determined by the equation $G = Le^{-m}$, and the average gap size, g , follows the equation, $g = L/n$. Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

Borrelia burgdorferi DNA is prepared by phenol extraction. A mixture containing 200 μ g DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 μ l TE buffer.

To create blunt-ends, a 100 μ l aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 μ l BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 μ l TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the DNA. DNA is ethanol precipitated and redissolved in 20 μ l of TE buffer for ligation to vector.

A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50 μ l) contains 2 μ g of DNA fragments, 2 μ g pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr.

5 The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20 μ l TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, etc. The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20 μ l TE. The v+I DNA then is

10 blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50 μ l) containing the v+I linears, 500 μ M each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20 μ l TE. The final ligation to produce circles is carried out in a 50 μ l reaction containing 5 μ l of v+I linears and 5 units of T4 ligase at

15 14°C overnight. After 10 min. at 70°C the following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

Since deviation from randomness can arise from propagation the DNA in the host, *E. coli*

20 host cells deficient in all recombination and restriction functions (A. Greener, *Strategies 3 (1):5* (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

Plating is carried out as follows. A 100 μ l aliquot of Epicurian Coli SURE II

25 Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 μ l aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1 μ l aliquot of the final ligation is added to the cells and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and placed back on ice for 2 min. The outgrowth period in liquid culture is

30 eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with

35 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgCl₂ (1 M), and 1 ml MgSO₄/100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10 μ l aliquot of transformation.

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science* 252:1651 (1991); Adams *et al.*, *Nature* 355:632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from two *Borrelia burgdorferi* lambda genomic libraries. An amplified library is constructed in the vector Lambda GEM-12 (Promega) and an unamplified library is constructed in Lambda DASH II (Stratagene). In particular, for the unamplified lambda library, *Borrelia burgdorferi* DNA (> 100 kb) is partially digested in a reaction mixture (200 μ l) containing 50 μ g DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and electrophoresed on a 0.5% low melting agarose gel at 2V/cm for 7 hours. Fragments from 15 to 25 kb are excised and recovered in a final volume of 6 μ l. One μ l of fragments is used with 1 μ l of DASHII vector (Stratagene) in the recommended ligation reaction. One μ l of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage are plated directly without amplification from the packaging mixture (after dilution with 500 μ l of recommended SM buffer and chloroform treatment). Yield is about 2.5×10^3 pfu/ μ l. The amplified library is prepared essentially as above except the lambda GEM-12 vector is used. After packaging, about 3.5×10^4 pfu are plated on the restrictive NM539 host. The lysate is harvested in 2 ml of SM buffer and stored frozen in 7% dimethylsulfoxide. The phage titer is approximately 1×10^9 pfu/ml.

Liquid lysates (100 μ l) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature* 368:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and SP6 primers are used to sequence the ends of the inserts from the Lambda GEM-12 library and T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed

by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.*, Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

4. Protocol for Automated Cycle Sequencing

The sequencing is carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (*i.e.*, one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

INFORMATICS

1. Data Management

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi-user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

2. Assembly

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than 104 fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods*

in *Enzymology* 164:765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library). The process resulted in 155 contigs as represented by SEQ ID NOs:1-155.

3. Identifying Genes

The predicted coding regions of the *Borrelia burgdorferi* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all nucleotide sequences from GenBank (July, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity (using default parameters). Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

ILLUSTRATIVE APPLICATIONS

1. Production of an Antibody to a *Borrelia burgdorferi* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.*, *Basic Methods in Molecular Biology*, Elsevier, New York. Section 21-2 (1989).

3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological

samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of pneumococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.

4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Borrelia burgdorferi* genome, such as those of Tables 1-6 and SEQ ID NOS: 1-155 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

5. Isolation of a Selected DNA Clone From *B. burgdorferi*

Three approaches are used to isolate a *B. burgdorferi* clone comprising a polynucleotide of the present invention from any *B. burgdorferi* genomic DNA library. The *B. burgdorferi* strain B31PU has been deposited as a convenient source for obtaining a *B. burgdorferi* strain although a wide variety of strains *B. burgdorferi* strains can be used which are known in the art.

B. burgdorferi genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear). A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlaid with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *B. burgdorferi* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The

oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. *MOLECULAR CLONING: A LABORATORY MANUAL* (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY* (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. *MOLECULAR CLONING: A LABORATORY MANUAL* (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY* (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of SEQ ID NOS:1-155 are synthesized and used to amplify the desired DNA by PCR using a *B. burgdorferi* genomic DNA prep as a template. PCR is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Finally, overlapping oligos of the DNA sequences of SEQ ID NOS:1-155 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

6(a). Expression and Purification *Borrelia* polypeptides in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression of some of the polypeptide fragments of the present invention. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6

X His tag") covalently linked to the carboxyl terminus of that polypeptide.

The DNA sequence encoding the desired portion of a *B. burgdorferi* protein of the present invention is amplified from *B. burgdorferi* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *B. burgdorferi* polynucleotide shown in SEQ ID NOS:1-155. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *B. burgdorferi* polynucleotide sequence in SEQ ID NOS:1-155. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form. The 3' primer has a sequence containing an appropriate restriction site followed by nucleotides complementary to the 3' end of the polypeptide coding sequence of SEQ ID NOS:1-155, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *B. burgdorferi* DNA fragment and the vector pQE60 are digested with restriction enzymes which recognize the sites in the primers and the digested DNAs are then ligated together. The *B. burgdorferi* DNA is inserted into the restricted pQE60 vector in a manner which places the *B. burgdorferi* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kan^r"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing a *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

The cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell

debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity are purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, 5 QIAGEN, Inc., *supra*). Briefly the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *B. burgdorferi* polypeptide is eluted with 6 M guanidine-HCl, pH 5.

10 The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 15 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

The polypeptide of the present invention are also prepared using a non-denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture is 20 resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm is approximately 10-20 O.D./ml. The suspension is then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The 25 cells are lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample is then centrifuged at 15,000 RPM for 30 minutes at 4°C. The supernatant is passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction is collected.

30 The pre-cleared flow-through is applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant is loaded onto the column in Lysis Buffer A at 4°C, the column is first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the 35 column is washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein is eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations are used: 3 volumes of 75 mM Imidazole, 3 volumes of

150 mM Imidazole, 5 volumes of 500 mM Imidazole. The fractions containing the purified protein are analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein is then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein is stored at 4°C or frozen at -80°.

- 5 The following alternative method may be used to purify *B. burgdorferi* expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm

- 10 (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- 15 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- 25 Following high speed centrifugation (30,000 x g) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

- 30 To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-
35 PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4

volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

6(b). Alternative Expression and Purification Borrelia polypeptides in E. coli

The vector pQE10 is alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag")) covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of SEQ ID NOS:1-155 were amplified using PCR oligonucleotide primers from genomic *B. burgdorferi* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain its reading frame with that of *B. burgdorferi* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences of SEQ ID NOS:1-155 encoding amino acid sequences may also be cloned and expressed as fusion proteins by a protocol similar to that described directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

5 The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

10 6(c). Alternative Expression and Purification of *Borrelia* polypeptides in *E. coli*

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

15 The DNA sequence encoding the desired portion of the *B. burgdorferi* amino acid sequence is amplified from an *B. burgdorferi* genomic DNA prep the deposited DNA clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *B. burgdorferi* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

20 For cloning a *B. burgdorferi* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

25 The amplified *B. burgdorferi* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs are then ligated together. Insertion of the *B. burgdorferi* DNA into the restricted pQE60 vector places the *B. burgdorferi* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

30 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kan^r"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for expressing *B. burgdorferi* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on

LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *B. burgdorferi* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *B. burgdorferi* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *B. burgdorferi* polypeptide. The purified protein is stored at 4°C or frozen at -80°C.

The following alternative method may be used to purify *B. burgdorferi* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *B. burgdorferi* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 x g) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded *B. burgdorferi* polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the *B. burgdorferi* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *B. burgdorferi* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *B. burgdorferi* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

6(d). Cloning and Expression of *B. burgdorferi* in Other Bacteria

B. burgdorferi polypeptides can also be produced in: *B. burgdorferi* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods Chang et al., U.S. Patent No. 4,952,508.

7. Cloning and Expression in COS Cells

A *B. burgdorferi* expression plasmid is made by cloning a portion of the DNA encoding a

B. burgdorferi polypeptide into the expression vector pDNAI/Amp or pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

A DNA fragment encoding a *B. burgdorferi* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *B. burgdorferi* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of *B. burgdorferi* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* DNA, a stop codon, and a convenient restriction site.

The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis or other means for the presence of the fragment encoding the *B. burgdorferi* polypeptide

For expression of a recombinant *B. burgdorferi* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *B. burgdorferi* by the vector.

Expression of the *B. burgdorferi*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are

precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression product of the expected size is seen in the cell lysate, which is not seen in negative controls.

8. Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *B. burgdorferi* polypeptide in this example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. See, e.g., Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rouse Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell 41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718. Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *B. burgdorferi* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from

a 1% agarose gel. The DNA sequence encoding the *B. burgdorferi* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *B. burgdorferi* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *B. burgdorferi* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for transfection. Five μ g of the expression plasmid pC4 is cotransfected with 0.5 μ g of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100-200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the invention, in addition to those shown and described herein and will become apparant to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

TABLE 1. Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident
1	92	100363	100184	gil500722	similar to entire extracellular domain of glycine receptors [Caenorhabditis elegans]	100	66
1	537	513231	513608	gil47453	ribosomal protein S12 [Streptococcus pneumoniae]	92	85
1	283	272186	270849	gil1001376	ATP-dependent protease ATPase subunit [Synechocystis sp.]	89	75
1	847	798835	799131	gil467373	ribosomal protein S18 [Bacillus subtilis]	86	69
1	78	91504	91235	gil1573896	ribosomal protein L27 (rpL27) [Haemophilus influenzae]	85	70
1	732	687538	686753	gil1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	84	65
1	788	739513	739232	gil142459	initiation factor 1 [Bacillus subtilis]	84	68
1	960	901448	901780	gnlPIDle243769	ORF YGL149w [Saccharomyces cerevisiae]	84	68
1	760	717009	715843	gil623028	orf 361; translated orf similarity to SW: RFL_SALTY peptide chain release factor 1 of Salmonella typhimurium [Coxiella burnetii]	83	60
1	115	115536	115312	gil695315	NADH dehydrogenase subunit [Digitalis grandiflora]	82	58
1	184	178954	176918	bbs157690	EF-G=elongation factor G [Thermotoga maritima, Peptide, 682 aa] [Thermotoga maritima]	82	63
1	447	425980	425453	gil143804	Ndk [Bacillus subtilis]	82	56
1	201	194702	194103	gil530438	arabinose transport protein [Mycoplasma capricolum]	81	53
1	477	446671	445589	gil882454	fructose 1,6-bisphosphate aldolase [Escherichia coli]	81	61
1	601	569453	568650	gil349227	transmembrane protein [Escherichia coli]	81	56
1	887	838084	837224	gil1237019	Srb [Bacillus subtilis]	81	52
1	889	840561	839497	gil154276	peptide chain release factor 2 [Salmonella typhimurium]	81	65
1	896	846681	845440	gil1377823	aminopeptidase [Bacillus subtilis]	81	60
1	60	71604	68890	gil1619909	DNA mismatch repair protein [Thermotoga maritima]	80	59
1	354	348744	349157	gil1765976	chemotaxis protein CheY [Treponema pallidum]	80	42
1	423	409238	408855	gnlPIDle211829	50S ribosomal protein L14 [Odontella sinensis]	80	61
1	426	410130	409711	gil1652420	50S ribosomal protein L16 [Synechocystis sp.]	80	59
1	507	482736	482936	gil515924	glucosyltransferase [Saccharomyces cerevisiae]	80	40
1	534	505081	505467	pirIA02771IR	ribosomal protein L7/L12 - Micrococcus luteus	80	67

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

					7MCML				
1	597	567506	566532	gil580899	OppF gene product [Bacillus subtilis]			80	59
1	6	11241	9994	gnlPIDle242614	arginine deiminase [Clostridium perfringens]			79	62
1	478	447926	446835	gnlPIDle288124	glucose epimerase [Bacillus thuringiensis]			79	66
1	804	758549	757704	gil455176	glucosamine-6-phosphate deaminase protein [Escherichia coli]			79	60
1	25	31595	31894	gil1017809	similar to dihydropyridine-sensitive I-type, skeletal muscle calcium channel alpha-1 subunit (SP:CIC1_RABIT, P07293) [Caenorhabditis elegans]			78	57
1	134	134667	134323	gil159199	cecropin D [Hyalophora cecropia]			78	50
1	230	215177	216028	gnlPIDle265537	DnaJ-homologue [Thermus aquaticus thermophilus]			78	59
1	531	503406	503849	gil587583	ribosomal protein L11 [Thermus aquaticus thermophilus]			78	58
1	867	817849	819579	gil912449	Na+ -ATPase alpha subunit [Enterococcus hirae]			78	60
1	127	127383	127745	gil537364	heat shock protein 60 (GroEL) like protein [Porphyromonas gingivalis]			77	60
1	190	182991	182251	gil1235682	mevalonate pyrophosphate decarboxylase [Homo sapiens]			77	51
1	225	213158	212388	gil651340	Phosphoglycerate mutase 1 [Escherichia coli]			77	59
1	284	272770	272165	gil1001349	ATP-dependent protease ClpP [Synechocystis sp.]			77	62
1	324	318280	314789	gil1573746	DNA polymerase III, alpha chain (dnaE) [Haemophilus influenzae]			77	58
1	555	530150	531370	gil143795	transfer RNA-Tyr synthetase [Bacillus subtilis]			77	52
1	770	722470	722892	gil1653602	hypothetical protein [Synechocystis sp.]			77	54
1	833	790115	790909	gnlPIDle248886	unknown [Mycobacterium tuberculosis]			77	56
1	52	62205	61918	gnlPIDle118966	ribosomal protein S15 [Thermus aquaticus thermophilus]			76	60
1	144	141975	141736	bbs177721	KHS toxin, killer heat sensitive toxin=KHS [Saccharomyces cerevisiae, Peptide, 708 aa] [Saccharomyces cerevisiae]			76	38
1	293	280702	280529	gil1146275	VP2 protein [Bluetongue virus 9]			76	47
1	323	314795	314199	gil1651915	hypothetical protein [Synechocystis sp.]			76	48
1	362	356749	355508	gil633147	ribose-phosphate pyrophosphokinase [Bacillus caldolyticus]			76	44

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	410	403332	402922	gil606232	30S ribosomal subunit protein S11 [Escherichia coli]	76	52
1	411	403754	403341	gil1652405	30S ribosomal protein S13 [Synechocystis sp.]	76	55
1	454	431743	431003	gil1016012	neural cell adhesion protein BIG-2 precursor [Rattus norvegicus]	76	61
1	710	670457	671569	gil467376	unknown [Bacillus subtilis]	76	58
1	873	824849	826675	gil1303804	YqeQ [Bacillus subtilis]	76	52
1	942	886017	886751	gil1183839	unknown [Pseudomonas aeruginosa]	76	54
1	5	9956	8943	gil1552842	OTCase [Escherichia coli]	75	62
1	51	61909	59735	gil1184680	polynucleotide phosphorylase [Bacillus subtilis]	75	54
1	55	66283	63620	gil39954	IF2 (aa 1-741) [Bacillus stearothermophilus]	75	53
1	83	93454	94410	gnlPIDle289138	similar to flagellar hook-basal body proteins [Bacillus subtilis]	75	46
1	88	97435	98283	gil687583	RpoS [Yersinia enterocolitica]	75	47
1	245	229112	230158	gil1574806	spermidine/putrescine transport ATP-binding protein (potA) [Haemophilus influenzae]	75	55
1	264	251076	250801	gil1763634	alpha1A-voltage-dependent calcium channel [Homo sapiens]	75	60
1	297	285723	284461	gil556886	serine hydroxymethyltransferase [Bacillus subtilis]	75	58
1	375	367682	366903	gil467372	3'-exo-deoxyribonuclease [Bacillus subtilis]	75	62
1	385	378055	377114	gil45986	NAD synthetase [Rhodobacter capsulatus]	75	55
1	416	406437	405925	gil1044981	ribosomal protein S5 [Bacillus subtilis]	75	56
1	418	407390	406812	gil600032	L6 ribosomal protein [Streptomyces coelicolor]	75	53
1	424	409520	409251	gil44218	ribosomal protein S17 (AA 1-85) [Mycoplasma capricolum]	75	58
1	530	502806	503366	gil396321	nusG [Escherichia coli]	75	56
1	548	523428	522904	gil1573470	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	75	55
1	575	546579	548393	pirC30010IC30010	hypothetical ORF-6 protein - Sauroleishmania tarentolae mitochondrion (SGC6)	75	50
1	906	854433	855215	gil511148	hemolysin [Serpulina hyodysenteriae]	75	56
1	68	85054	83102	gil467458	cell division protein [Bacillus subtilis]	74	57
1	162	158608	157502	gil531460	Mbl protein [Bacillus subtilis]	74	49
1	177	172327	171950	pirA45434IA45434	ribosomal protein L19 - Bacillus stearothermophilus	74	54
1	475	443773	445203	gil396501	aspartyl-tRNA synthetase [Thermus aquaticus thermophilus]	74	52

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	549	524561	523374	gil1020317	S-adenosylmethionine synthetase [Staphylococcus aureus]	74	57
1	595	565672	564347	gil460259	enolase [Bacillus subtilis]	74	58
1	720	681529	680489	gil1651962	hypothetical protein [Synechocystis sp.]	74	49
1	745	702297	701173	gil289287	UDP-glucose pyrophosphorylase [Bacillus subtilis]	74	50
1	13	20409	17551	gil1652531	excinuclease ABC subunit A [Synechocystis sp.]	73	56
1	98	103790	104947	gil514330	sensor kinase [Bacillus subtilis]	73	49
1	188	182064	181102	gil887601	Erg8p [Saccharomyces cerevisiae]	73	43
1	314	303616	302786	gil473817	'ORF' [Escherichia coli]	73	53
1	366	358916	361078	gnl1PIDle245791	ORF YLR069c [Saccharomyces cerevisiae]	73	51
1	444	424047	423181	gil1574704	hypothetical [Haemophilus influenzae]	73	51
1	556	531372	533672	gil511145	hemolysin [Serpulina hyodysenteriae]	73	52
1	576	548257	548045	gil406135	glycoprotein 120 [Simian immunodeficiency virus]	73	53
1	598	568379	567504	gil143607	sporulation protein [Bacillus subtilis]	73	55
1	604	572375	570729	bbs1161785	60 kDa antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	73	53
1	674	634175	633648	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	73	47
1	692	654267	651727	gnl1PIDle268456	unknown [Mycobacterium tuberculosis]	73	54
1	719	679186	680499	gil500705	Similar to Seryl-tRNA synthetase [Saccharomyces cerevisiae]	73	56
1	725	682189	682899	gnl1PIDle243681	ORF YGR248w [Saccharomyces cerevisiae]	73	63
1	895	845455	844964	gil1652288	hypothetical protein [Synechocystis sp.]	73	50
1	16	24242	26497	gil511145	hemolysin [Serpulina hyodysenteriae]	72	53
1	99	104935	106305	gil619917	NtrC/NifA-like protein regulator [Escherichia coli]	72	54
1	133	134036	135055	gil556881	Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis]	72	51
1	270	256925	260308	gil467444	transcription-repair coupling factor [Bacillus subtilis]	72	49
1	280	267529	268221	gil1573812	ribosomal protein S4 (rpS4) [Haemophilus influenzae]	72	51
1	282	270922	268472	gil402504	lon protease [Bacillus brevis]	72	51
1	325	319544	318363	gil48362	haemolysin releasing protein (AA 1-548) [Vibrio cholerae]	72	41
1	328	322678	321053	gil1591801	CTP synthase [Methanococcus jannaschii]	72	42

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	348	341460	341182	gil145687	ptsH protein [Escherichia coli]		72	55
1	405	399941	399096	gil1045937	M. genitalium predicted coding region MG246 [Mycoplasma genitalium]		72	53
1	420	408009	407779	gil580930	S14 protein (AA 1-61) [Bacillus subtilis]		72	55
1	593	563383	563850	gil1574283	ribosomal protein L13 (rpL13) [Haemophilus influenzae]		72	54
1	682	641030	643399	gil1574437	sporulation protein (spoIIIE) [Haemophilus influenzae]		72	51
1	754	710160	710750	gil460080	D-alanine:D-alanine ligase-related protein [Enterococcus faecalis]		72	47
1	767	721422	721640	gil868029	large ribosomal subunit protein L35 [Buchnera aphidicola]		72	48
1	860	811923	810511	gil1001357	asparaginyl-tRNA synthetase [Synecocystis sp.]		72	54
1	14	22434	20407	gil1737482	UvrB [Helicobacter pylori]		71	52
1	72	87471	87674	gil1016781	beta-b protein [Barley stripe mosaic virus]		71	42
1	289	278760	278239	gil534842	ORF9 [Rhizobium meliloti]		71	43
1	307	298685	296736	gil1652099	long-chain-fatty-acid CoA ligase [Synecocystis sp.]		71	48
1	321	313551	312130	gil1732243	RecG [Treponema pallidum]		71	52
1	522	494911	496383	gil459009	similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]		71	48
1	554	528795	530156	pirS58522IS58522	glycyl-tRNA synthetase - Thermus thermophilus		71	54
1	582	553725	552271	gil285623	pyruvate kinase [Bacillus stearothermophilus]		71	52
1	684	644626	643661	gil217121	ORF1 [Synecococcus elongatus]		71	52
1	723	681731	681561	gil44228	secretion protein SecY (AA 1-482) [Mycoplasma capricolum]		71	42
1	856	806939	807700	gil216341	ORF for methionine amino peptidase [Bacillus subtilis]		71	53
1	947	890096	890665	gil147485	queA [Escherichia coli]		71	56
1	28	38112	40613	gil1439562	Cdc28p [Schizosaccharomyces pombe]		70	53
1	36	45750	44806	gil290494	o287 [Escherichia coli]		70	32
1	84	94408	95220	gil47677	figG protein product (AA 1-260) [Salmonella typhimurium]		70	50
1	128	127889	128569	gil1574387	H. influenzae predicted coding region HI1534 [Haemophilus influenzae]		70	58
1	468	441049	441330	gil1673757	(AE000012) Mycoplasma pneumoniae, phosphocarrier protein HPr; similar to GenBank Accession Number A49683, from M. capricolum [Mycoplasma pneumoniae]		70	41
1	532	503834	504529	spIQ06797IRU1_BACSU	50S RIBOSOMAL PROTEIN L1 (BL1).		70	48

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	594	563858	564280	gil606169	30S ribosomal subunit protein S9 [Escherichia coli]	70	56
1	622	591070	591606	gil153906	CheW protein [Salmonella typhimurium]	70	48
1	703	664161	662611	gnlPIDle283919	glycerol kinase [Sulfolobus solfataricus]	70	60
1	726	682886	682659	gil836815	cdc4 gene product which is essential for initiation of DNA replication in yeast [Saccharomyces cerevisiae]	70	35
1	766	720854	721417	gil436165	Dsg [Myxococcus xanthus]	70	47
1	768	721649	722008	gnlPIDle254981	ribosomal protein L20 [Bacillus subtilis]	70	48
1	965	904395	905465	gil1100074	tryptophanyl-tRNA synthetase [Clostridium longisporum]	70	47
1	87	96986	97336	gil160092	asparagine-rich protein [Plasmodium falciparum]	69	46
1	110	112658	113602	gil1001733	ABC transporter [Synechocystis sp.]	69	46
1	181	174037	173762	pinC47154IC47154	ribosomal protein S16 - Bacillus subtilis	69	52
1	233	219872	218076	gil1001493	protein-export membrane protein SecD [Synechocystis sp.]	69	47
1	234	220245	219922	gil1402532	ORF11 [Enterococcus faecalis]	69	32
1	373	366148	363977	gil1574200	hypothetical [Haemophilus influenzae]	69	48
1	419	407781	407371	gil498771	ribosomal S8 protein [Thermus aquaticus thermophilus]	69	46
1	517	489315	491207	gil151932	fructose enzyme II [Rhodobacter capsulatus]	69	42
1	600	568891	568388	gil143606	sporulation protein [Bacillus subtilis]	69	44
1	733	689098	687536	gil1303856	YqgI [Bacillus subtilis]	69	46
1	874	826778	827746	pinS08183IS08183	L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus psychrosaccharolyticus	69	50
1	894	844392	844547	gil1592324	M. jannaschii predicted coding region MJ1172 [Methanococcus jannaschii]	69	53
1	934	879725	879237	gil153566	ORF (19K protein) [Enterococcus faecalis]	69	42
1	49	57779	57976	gil809583	unknown [Saccharomyces cerevisiae]	68	36
1	107	110374	111513	gnlPIDle255943	M04B2.4 [Caenorhabditis elegans]	68	48
1	132	133978	133148	gil1001663	rare lipoprotein A [Synechocystis sp.]	68	53
1	142	141239	142642	gnlPIDle233874	hypothetical protein [Bacillus subtilis]	68	45
1	148	145381	144005	gil558574	pyrophosphate--fructose-6-phosphate 1-phosphotransferase	68	48

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

[illegible]

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	111	113572	114333	gil1001529	hypothetical protein [Synecocystis sp.]	67	36
1	170	166286	165876	gil567036	CapE [Staphylococcus aureus]	67	35
1	202	195499	194651	gil1674275	(AE000056) Mycoplasma pneumoniae, hypothetical ABC transporter (yjcW) homolog; similar to Swiss-Prot Accession Number P32721, from E. coli [Mycoplasma pneumoniae]	67	41
1	206	197487	197098	gil1653841	P protein [Synecocystis sp.]	67	35
1	271	260292	261551	gil349834	acetate kinase [Methanosarcina thermophila]	67	44
1	313	302731	301643	gnlPIDe249981	phosphotransacetylase [Thermoanaerobacterium thermosaccharolyticum]	67	51
1	422	408897	408535	pirA02819IR5BS24	ribosomal protein L24 - Bacillus stearothermophilus	67	49
1	480	450326	448689	gil1574032	hypothetical [Haemophilus influenzae]	67	42
1	529	502315	502509	gil1001264	50S ribosomal protein L33 [Synecocystis sp.]	67	56
1	588	559618	561111	gil1224069	amidase [Moraxella catarrhalis]	67	51
1	683	643676	643437	gil710340	ribosomal protein S21 [Myxococcus xanthus]	67	49
1	698	658454	659500	gil460955	TagE [Vibrio cholerae]	67	38
1	700	660039	660536	gil467420	unknown [Bacillus subtilis]	67	42
1	729	684089	685888	gnlPIDe267607	alanyl-tRNA synthetase [Thermus aquaticus thermophilus]	67	51
1	835	791754	792341	gnlPIDe248763	unknown [Mycobacterium tuberculosis]	67	46
1	857	807722	809191	gil1526428	GsrA protein [Yersinia enterocolitica]	67	46
1	868	819577	820905	gil1590954	ATP synthase, subunit B [Methanococcus jannaschii]	67	53
1	74	88393	88028	gil1572979	hypothetical [Haemophilus influenzae]	66	43
1	91	99152	100252	gil561690	sialoglycoprotease [Pasteurella haemolytica]	66	44
1	123	121472	120783	gil1652843	endonuclease III [Synecocystis sp.]	66	42
1	149	146362	145379	gil1216385	orf304 gene product [Treponema pallidum]	66	43
1	185	179585	179001	gil1574811	neutrophil activating protein (napA) [Haemophilus influenzae]	66	49
1	275	265075	265584	gil401785	cytidine deaminase [Mycoplasma pirum]	66	41
1	330	324514	323696	gil1574641	ribonucleotide transport ATP-binding protein (mkl) [Haemophilus influenzae]	66	41
1	335	327265	326888	gil1510670	cheY gene product [Rhodobacter sphaeroides]	66	44
1	355	349142	349603	gil499382	Flis [Bacillus subtilis]	66	28

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	358	351051	350827	gil1546788	tar-1 [Trichostrongylus colubriformis]	66	55
1	404	399121	398324	gil296626	hemolysin [Serpulina hyodysenteriae]	66	53
1	491	461335	460550	gil45713	P.putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, uncl and uncB [Pseudomonas putida]	66	41
1	513	486046	485159	gil153903	methytransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium]	66	42
1	552	526495	527316	gil340613	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	66	40
1	611	579933	581069	gil886130	putative pectinesterase [Medicago sativa]	66	33
1	627	595395	596288	gilPIDle263931	OrfD [Streptococcus pneumoniae]	66	47
1	772	723788	723522	gil1762342	could accelerate degradation of certain transcripts [Bacillus subtilis]	66	47
1	816	770251	770060	gil393266	glycerol ester hydrolase [Staphylococcus aureus]	66	33
1	841	795927	795208	gil662880	novel hemolytic factor [Bacillus cereus]	66	46
1	882	835002	834262	gil862629	similar to the ATP-binding transport protein family [Buchnera aphidicola]	66	40
1	73	87915	87619	gil39656	spoVG gene product [Bacillus megaterium]	65	40
1	97	103039	102803	gil532272	phosphatidylserine decarboxylase [Bacillus subtilis]	65	39
1	106	110281	109649	gil1377852	ClpP [Yersinia enterocolitica]	65	42
1	159	156186	154372	gil1572977	penicillin-binding protein 2 (pbp2) [Haemophilus influenzae]	65	41
1	172	168084	169325	gil146238	poly(A) polymerase [Bacillus subtilis]	65	38
1	268	255918	253819	gil829194	bacterial cell wall hydrolase [Enterococcus faecalis]	65	43
1	353	348568	346553	gil1574651	DNA ligase (lig) [Haemophilus influenzae]	65	45
1	696	657577	655781	gil1651216	Pz-peptidase [Bacillus licheniformis]	65	47
1	741	695297	693456	gil1575784	DNA mismatch repair protein [Aquifex pyrophilus]	65	45
1	846	798339	798827	gil1001362	single-stranded DNA-binding protein [Synecocystis sp.]	65	45
1	932	876643	878559	gil508471	gyrase A [Helicobacter pylori]	65	40
1	936	881238	882224	gil1652260	leader peptidase I [Synecocystis sp.]	65	40
1	961	902331	901519	gil1256146	YbbQ [Bacillus subtilis]	65	48
1	963	903280	904407	gil1573307	hypothetical [Haemophilus influenzae]	65	41
1	37	47101	45683	gil556014	UDP-N-acetyl muramate-alanine ligase [Bacillus subtilis]	64	46

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	61	72211	71642	gil1041785	rhoptry protein [Plasmodium yoelii]	64	41
1	130	131969	129336	gil1574225	valyl-tRNA synthetase (valS) [Haemophilus influenzae]	64	43
1	156	152924	151140	gil43066	threonyl-tRNA synthetase (thrS; EC 6.1.1.3) [Escherichia coli]	64	43
1	174	170326	170033	gil1652390	acyl carrier protein [Synecocystis sp.]	64	48
1	175	171105	170545	gil1573650	lipopolysaccharide core biosynthesis protein (kdtB) [Haemophilus influenzae]	64	45
1	178	173033	172293	gil1046163	tRNA (guanine-N1)-methyltransferase [Mycoplasma genitalium]	64	47
1	180	173764	173513	gnlPIDe2488	unknown [Mycobacterium tuberculosis]	64	34
			93				
1	207	197654	197436	gil11665	ORF2136 [Marchantia polymorpha]	64	47
1	217	206795	205761	gil1652866	N-acetylmuramoyl-L-alanine amidase [Synecocystis sp.]	64	30
1	244	228146	229036	gil1046160	hypothetical protein (GB:U00021_5) [Mycoplasma genitalium]	64	33
1	246	230149	230967	gil147336	transmembrane protein [Escherichia coli]	64	36
1	267	253160	253723	gil467430	unknown [Bacillus subtilis]	64	52
1	340	333349	332783	gil145520	cheW peptide [Escherichia coli]	64	42
1	384	376509	375565	gil1653737	monophosphatase [Synecocystis sp.]	64	44
1	449	428137	426437	gil467409	DNA polymerase III subunit [Bacillus subtilis]	64	41
1	510	484558	483998	pirA00547IX	protein-glutamate methyltransferase (EC 3.1.1.61) - Salmonella typhimurium	64	45
1	603	570416	569451	gil1574678	dipeptide transport system permease protein (dppB) [Haemophilus influenzae]	64	44
1	679	637996	640224	gil1001335	soluble lytic transglycosylase [Synecocystis sp.]	64	42
1	753	709637	710194	gnlPIDe2833	unknown [Mycobacterium tuberculosis]	64	42
			60				
1	817	771784	771969	gnlPIDe2503	W04B2.3 [Caenorhabditis elegans]	64	41
			07				
1	839	793892	795211	gil1573939	hypothetical [Haemophilus influenzae]	64	38
1	861	811972	812853	gil396314	glutamate synthase [Escherichia coli]	64	38
1	870	821501	823339	gil472918	v-type Na-ATPase [Enterococcus hirae]	64	42
1	901	850668	851615	gil581088	methionyl-tRNA formyltransferase [Escherichia coli]	64	38
1	904	853492	853884	gil992960	thioredoxin [Arabidopsis thaliana]	64	41
1	24	34314	31444	gil42914	SbcC (AA 1-1048) [Escherichia coli]	63	45

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	77	91198	90194	gill1652022	GTP-binding protein [Synechocystis sp.]	63	45
1	209	198041	197862	gill1665	ORF2136 [Marchantia polymorpha]	63	42
1	227	214639	213956	gill1652349	oxygen independent coprophosphorylase III oxidase [Synechocystis sp.]	63	41
1	232	218116	217193	gill1573204	protein-export membrane protein (secF) [Haemophilus influenzae]	63	36
1	247	230965	231762	spP451691PO TC_HAEIN	SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC.	63	36
1	272	262171	261614	gill1780755	DJ-1 protein [Homo sapiens]	63	46
1	290	279964	278735	gill143439	DD-carboxypeptidase [Bacillus subtilis]	63	41
1	333	326012	325818	gill293954	mating type a-1 protein [Neurospora crassa]	63	42
1	508	484000	482759	gill1041116	TRAB [Plasmodium falciparum]	63	34
1	553	527314	528801	spP151891SY IE_RHIME	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE) (GLURS).	63	48
1	569	542317	543747	gill1652577	carboxyl-terminal protease [Synechocystis sp.]	63	49
1	620	590442	589360	gill1098641	Bts1p [Saccharomyces cerevisiae]	63	43
1	701	660784	660623	gill1339938	EC 1.1.99.5 [Mus musculus]	63	47
1	702	662231	660735	gill763191	glycerol 3 phosphate dehydrogenase [Saccharomyces cerevisiae]	63	37
1	704	664938	664159	gill142997	glycerol uptake facilitator [Bacillus subtilis]	63	45
1	746	702035	702631	gill41497	ORF 4 (AA 1-198); 20 kD [Escherichia coli]	63	36
1	748	705645	704671	gill436158	putative integral membrane protease required for high frequency lysogenization by bacteriophage lambda [Escherichia coli]	63	33
1	749	706431	705643	gill507734	HfIK [Vibrio parahaemolyticus]	63	28
1	756	715040	713019	gill407881	stringent response-like protein [Streptococcus equisimilis]	63	40
1	825	780572	783289	gill746399	transcription elongation factor [Escherichia coli]	63	43
1	853	803786	804832	gill155055	basic membrane protein precursor [Treponema pallidum]	63	36
1	4	8945	7467	gill1573583	H. influenzae predicted coding region HI0594 [Haemophilus influenzae]	62	38
1	42	50587	51786	gill1573978	pantothenate metabolism flavoprotein (dfp) [Haemophilus influenzae]	62	41
1	57	67740	66271	gill49316	ORF2 gene product [Bacillus subtilis]	62	36
1	64	78979	79767	gill1001473	hypothetical protein [Synechocystis sp.]	62	48
1	80	92123	91806	gnlPID1e2118 48	50S ribosomal protein L21 [Odontella sinensis]	62	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	101	107458	106793	gil1652679	hypothetical protein [Synecocystis sp.]	62	34
1	102	107464	107883	gil15893	predicted 12.5Kd protein [Mycobacteriophage 15]	62	44
1	226	213238	213969	gil1001678	ribose 5-phosphate isomerase [Synecocystis sp.]	62	39
1	266	251889	253175	gil529118	similar to APE1/LAP4, vacuolar aminopeptidase [Saccharomyces cerevisiae]	62	42
1	299	288749	287274	gil289284	cysteinyI-tRNA synthetase [Bacillus subtilis]	62	46
1	357	349982	352714	gil1633576	similar to proofreading 3'-5' exonuclease and polymerase [Treponema pallidum]	62	41
1	443	423190	422495	gil12380	putative orfW gene product [Clostridium acetobutylicum]	62	32
1	489	458740	459582	gil40031	spoIJ93 gene product [Bacillus subtilis]	62	36
1	511	485147	484494	gil145524	cheB peptide [Escherichia coli]	62	28
1	518	491201	492322	gil146722	phosphomannose isomerase [Escherichia coli]	62	45
1	685	646727	644598	gil1574144	single-stranded-DNA-specific exonuclease (recJ) [Haemophilus influenzae]	62	40
1	695	655800	655063	gil1477770	unknown [Helicobacter pylori]	62	37
1	758	715668	714979	gil1574130	protoporphyrinogen oxidase (hemK) [Haemophilus influenzae]	62	36
1	762	718374	719198	gil1652444	hypothetical protein [Synecocystis sp.]	62	40
1	837	792941	793891	gil1652668	phosphatidate cytidyltransferase [Synecocystis sp.]	62	41
1	917	862498	862737	gil440851	collagenase [Clostridium perfringens]	62	29
1	46	55889	54726	gil498141	tRNA guanine transglycosylase [Zymomonas mobilis]	61	35
1	81	92710	92174	gil726305	adenine phosphoribosyltransferase form I [Triticum aestivum]	61	45
1	100	106820	106557	gil460955	TagE [Vibrio cholerae]	61	45
1	109	111699	112664	gil1001126	hypothetical protein [Synecocystis sp.]	61	48
1	157	154445	153051	gil143657	endospore forming protein [Bacillus subtilis]	61	40
1	193	185315	184227	gil148409	gene not found in Erwinia uredovora crt gene cluster; ORF6 [Erwinia herbicola]	61	42
1	223	209790	210668	spiP37214IER A_STRMU	GTP-BINDING PROTEIN ERA HOMOLOG.	61	37
1	273	262392	264062	gil438455	possible N-terminal signal sequence; mature protein may be membrane-anchored and start at Cys-17. 17.5% identity over 354-aa overlap with Candida pelliculosa beta-glucosidase.; putative [Bacillus subtilis]	61	37
1	277	265982	265581	gil1513240	ORFveg110 [Dictyostelium discoideum]	61	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	301	291935	289686	gil1354776	MCP-1 [Treponema pallidum]		61	43
1	322	314201	313338	gil1732243	RecG [Treponema pallidum]		61	37
1	380	371430	372392	gil973332	OrfC [Bacillus subtilis]		61	38
1	408	401874	401479	gil147716	ribosomal protein L17 [Escherichia coli]		61	44
1	413	404277	404444	gil1185286	ORF [Sulfolobus shibatae]		61	47
1	415	405927	405616	pirA02827/R	ribosomal protein L30 - Bacillus stearothermophilus		61	31
			5BS3F					
1	417	406848	406435	pirB29102/R	ribosomal protein L18 - Bacillus stearothermophilus		61	44
			5BS8F					
1	441	421784	421224	gil153045	prolipoprotein signal peptidase [Staphylococcus aureus]		61	29
1	467	440722	441042	gil173128	ubiquitin-specific processing protease [Saccharomyces cerevisiae]		61	32
1	613	582695	581547	gil1303756	YqbP [Bacillus subtilis]		61	38
1	615	584397	585476	gil551522	TpN38(b) [Treponema pallidum]		61	26
1	673	632123	633622	gil143999	dnaK homologue [Borrelia burgdorferi]		61	41
1	675	634207	635469	gil1653709	lipoprotein NlpD [Synechocystis sp.]		61	50
1	743	699438	698647	gil1303863	YqgP [Bacillus subtilis]		61	45
1	897	847575	846688	gil1573586	hydrolase (GB:Z33006_1) [Haemophilus influenzae]		61	43
1	938	882836	883282	gil1303831	YqfM [Bacillus subtilis]		61	36
1	7	10415	10627	gnlPIDle2119	T24A11.1 [Caenorhabditis elegans]		60	45
			90					
1	23	31428	30475	gil1303865	YqgR [Bacillus subtilis]		60	45
1	35	44812	44267	gil1591369	cytidylate kinase [Methanococcus jannaschii]		60	49
1	198	192994	192053	gil1045801	hypothetical protein (SP:P32720) [Mycoplasma genitalium]		60	33
1	347	341167	339440	gil602680	phosphocarrier protein (enzyme I) [Mycoplasma capricolum]		60	37
1	369	361817	362233	gil1372995	OrfH [Borrelia burgdorferi]		60	37
1	409	402924	401872	gil142463	RNA polymerase alpha-core-subunit [Bacillus subtilis]		60	40
1	438	420142	418793	gnlPIDle2768	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacillus subtilis]		60	40
			30					
1	566	540696	539698	gil1573923	prolipoprotein diacylglycerol transferase (lgt) [Haemophilus influenzae]		60	57
1	587	559368	559655	gil1335805	CD45 homolog [Heterodontus francisci]		60	26
1	589	561098	562558	gil1653395	PET112 [Synechocystis sp.]		60	37

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	736	690957	690076	gil1001260	hypothetical protein [Synecocystis sp.]	60	47
1	738	691078	691659	gil1399829	elongation factor P [Synecococcus PCC7942]	60	34
1	750	707879	706626	gil1573060	hypothetical [Haemophilus influenzae]	60	33
1	784	734589	735635	gil1164996	mxnC gene product [Methylobacterium extorquens]	60	26
1	829	785899	786567	gil1046033	cytidylate kinase [Mycoplasma genitalium]	60	38
1	862	812835	813773	gil1574569	hypothetical [Haemophilus influenzae]	60	36
1	863	813727	816105	gnlPIDle255093	hypothetical protein [Bacillus subtilis]	60	38
1	878	831250	829943	gil1742766	NifS protein. [Escherichia coli]	60	34
1	929	872578	874110	gil1002666	unknown [Schistosoma mansoni]	60	30
1	937	882211	882861	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	60	40
1	54	63629	63234	gil580902	ORF6 gene product [Bacillus subtilis]	59	38
1	96	102744	103802	gil467409	DNA polymerase III subunit [Bacillus subtilis]	59	40
1	120	118925	119914	gil1574678	dipeptide transport system permease protein (dppB) [Haemophilus influenzae]	59	33
1	140	139567	141174	gil42377	phosphoglucose isomerase (AA 1-549) [Escherichia coli]	59	42
1	195	186577	187659	gil1573129	hypothetical [Haemophilus influenzae]	59	41
1	259	242174	245713	gil1574781	exodeoxyribonuclease V (recB) [Haemophilus influenzae]	59	38
1	288	278281	276257	pirD64084ID64084	rep helicase, single-stranded DNA-dependent ATPase (rep) homolog - Haemophilus influenzae (strain Rd KW20)	59	36
1	291	280005	281525	gil882504	ORF_f560 [Escherichia coli]	59	34
1	306	294923	296707	gil487937	Similar to arginyl-tRNA synthetase (E. coli) [Saccharomyces cerevisiae]	59	35
1	332	325664	324564	gil466753	alternate gene name yibD [Escherichia coli]	59	39
1	414	405646	405179	gil216338	ORF for L15 ribosomal protein [Bacillus subtilis]	59	40
1	465	439470	440759	gil39269	sigma factor (nirA) (AA 1-502) [Azotobacter vinelandii]	59	35
1	492	462064	461411	pirA30191IA30191	hypothetical protein L - Bacillus subtilis (fragment)	59	39
1	495	462955	463752	gil467425	unknown [Bacillus subtilis]	59	38
1	503	480078	481016	gil1651878	regulatory components of sensory transduction system [Synecocystis sp.]	59	38
1	523	497621	496395	gil143002	proton glutamate symport protein [Bacillus caldotenax]	59	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	941	885060	886019	gil1685110	thermophilus]	tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus	59	36
1	40	50348	48951	gil1574003	pantothenate permease (panF)	[Haemophilus influenzae]	58	38
1	76	90160	89534	gil1303791	YqeJ	[Bacillus subtilis]	58	32
1	116	115845	115654	gnlPIDle275892	T06E6.f	[Caenorhabditis elegans]	58	37
1	179	173515	173009	gil1573163	hypothetical	[Haemophilus influenzae]	58	37
1	197	191904	189634	gil1066850	putative	[Rhodobacter capsulatus]	58	37
1	229	215111	214563	gil1573441	oxygen-independent coproporphyrinogen III oxidase (hemN)	[Haemophilus influenzae]	58	34
1	257	238952	241873	gil1041785	rhostry protein	[Plasmodium yoelii]	58	30
1	440	421010	420792	gil1674178	(AE000047) Mycoplasma pneumoniae, MG246 homolog, from	M. genitalium [Mycoplasma pneumoniae]	58	37
1	557	533653	534750	gil974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase	[Bacillus subtilis]	58	41
1	586	557259	559370	gil153062	helicase	[Staphylococcus aureus]	58	41
1	623	591542	592435	gil1653618	hypothetical protein	[Synechocystis sp.]	58	35
1	728	683208	684104	gil790935	flg	[Treponema denticola]	58	31
1	796	750629	749508	gil1574412	alanine racemase, biosynthetic (alr)	[Haemophilus influenzae]	58	29
1	823	778475	778723	gil1209836	minus strand repeat motif-containing gene	[Borrelia burgdorferi]	58	22
1	830	786540	788225	gil1574150	ribosomal protein S1 (rpS1)	[Haemophilus influenzae]	58	34
1	842	796255	796019	gnlPIDle243474	ORF YGR089w	[Saccharomyces cerevisiae]	58	35
1	883	834332	834520	gil1575792	low Mr GTP-binding protein Rab32	[Homo sapiens]	58	43
1	905	853953	854435	gil1303823	YqfG	[Bacillus subtilis]	58	34
1	919	863594	862875	gil1256625	putative	[Bacillus subtilis]	58	34
1	921	865297	864725	gil1054584	putative protein highly homologous to E. coli RNase HII	[Magnetospirillum sp.]	58	42
1	196	189636	187702	gil496484	tlpC gene product	[Bacillus subtilis]	57	32
1	262	249142	248192	gil46605	lacC polypeptide (AA 1-310)	[Staphylococcus aureus]	57	41
1	311	300776	301660	gil467431	high level kasamycin resistance	[Bacillus subtilis]	57	35
1	365	358725	358495	gil396943	early protein	[Human papillomavirus type 19]	57	38
1	386	378249	378025	gil45986	NAD synthetase	[Rhodobacter capsulatus]	57	32

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	399	394690	394247	gil1592085	M. jannaschii predicted coding region MJ1437 [Methanococcus jannaschii]	57	31
1	402	397512	396193	gil1732241	GTP-binding protein [Treponema pallidum]	57	36
1	533	504504	505022	gil786163	Ribosomal Protein L10 [Bacillus subtilis]	57	29
1	735	689992	689096	gil1303855	YqgH [Bacillus subtilis]	57	30
1	794	745857	747644	gil11665	ORF2136 [Marchantia polymorpha]	57	33
1	814	768735	771866	gil1573914	acridine resistance protein (acrB) [Haemophilus influenzae]	57	31
1	821	776835	778244	gil1591660	histidyl-tRNA synthetase [Methanococcus jannaschii]	57	36
1	834	790907	791752	gil1518661	elongation factor Ts [Chlamydia trachomatis]	57	36
1	836	792328	793038	gil1573941	hypothetical [Haemophilus influenzae]	57	36
1	848	799086	799670	gil537044	50S ribosomal subunit protein L9 [Escherichia coli]	57	39
1	849	799668	801041	gil1001271	replicative DNA helicase [Synechocystis sp.]	57	33
1	851	802510	803742	pirA640921A 64092	acetyl coenzyme A acetyltransferase (thiolase) (fadA) homolog - Haemophilus influenzae (strain Rd KW20)	57	43
1	855	805240	806952	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	57	36
1	922	865347	867809	gil1237015	ORF4 [Bacillus subtilis]	57	38
1	12	17611	14156	pirB305651B 30565	phospholipase C (EC 3.1.4.3) precursor - Clostridium bifermentans	56	28
1	26	35530	34277	gil1657594	exonuclease SbcD [Escherichia coli]	56	39
1	59	68915	68271	gil148876	probable com101A gene [Haemophilus influenzae]	56	26
1	79	91821	91480	gil1139633	large tegument protein [Human herpesvirus 7]	56	30
1	112	113768	113571	gnlIP12469 33	ORF YPL216w [Saccharomyces cerevisiae]	56	35
1	147	142606	143988	gil642030	NADH oxidase [Serpulina hyodysenteriae]	56	36
1	153	148561	149100	gil1499018	M. jannaschii predicted coding region MJ0240 [Methanococcus jannaschii]	56	29
1	169	165431	164388	gil1573431	aminodeoxychorismate lyase (pabC) [Haemophilus influenzae]	56	41
1	183	176655	175432	gil143841	xylose repressor [Bacillus subtilis]	56	38
1	312	301170	300922	gnlIP12202 40	red alga1 chloroplast [Plasmodium falciparum]	56	36
1	317	308362	306992	gil1574691	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD) [Haemophilus influenzae]	56	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	448	426477	426133	gil467410	unknown [Bacillus subtilis]	56	28
1	456	432628	434457	gil142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	56	34
1	460	438178	437312	gil882453	ORF_f286; alternate name yggB; orf4 of X14436 [Escherichia coli]	56	31
1	469	441309	443438	gil148316	NaH-antiporter protein [Enterococcus hirae]	56	32
1	608	574772	574951	gil1019630	NADH dehydrogenase subunit 2 [Paramecium aurelia]	56	37
1	699	659498	660055	gil1372995	OrfH [Borrelia burgdorferi]	56	24
1	757	713509	713712	gil861327	F31D5.5 gene product [Caenorhabditis elegans]	56	40
1	791	741305	742837	gil1651873	4-alpha-glucanotransferase [Synechocystis sp.]	56	43
1	822	779478	778291	gil1500309	M. jannaschii predicted coding region MJ1428 [Methanococcus jannaschii]	56	28
1	967	907556	908932	gil1749528	similar to Saccharomyces cerevisiae probable UTP-glucose-1-phosphate uridylyltransferase, SWISS-PROT Accession Number P32861 [Schizosaccharomyces pombe]	56	37
1	39	48953	48048	gil1045895	hypothetical protein (SP:P23851) [Mycoplasma genitalium]	55	41
1	131	132989	131967	gil1574007	nitrogen fixation nifR3 protein (nifR3) (PIR:S49971) [Haemophilus influenzae]	55	39
1	152	148506	147148	gil1653100	Na+ -ATPase subunit J [Synechocystis sp.]	55	31
1	359	352690	353313	gil1213334	OrfX; hypothetical 22.5 KD protein downstream of type IV prepilin leader peptidase gene; Method: conceptual translation supplied by author [Vibrio vulnificus]	55	33
1	361	355510	354140	gil882698	L-fucose kinase [Escherichia coli]	55	44
1	515	488398	487652	gil397486	endonuclease G [Bos taurus]	55	33
1	551	526427	525285	gil558266	orf gene product [Wolinella succinogenes]	55	30
1	570	543745	544482	gil1303811	YqeU [Bacillus subtilis]	55	33
1	579	551201	551494	gil290487	50S ribosomal subunit protein L28 [Escherichia coli]	55	37
1	584	555359	556063	gil1592301	M. jannaschii predicted coding region MJ0687 [Methanococcus jannaschii]	55	32
1	706	665310	665936	gil403984	deoxyguanosine kinase/deoxyadenosine kinase(I) subunit [Lactobacillus acidophilus]	55	38
1	771	722876	723538	gil1736440	O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease). [Escherichia coli]	55	39
1	786	736537	737187	gil1589778	SPINDLY [Arabidopsis thaliana]	55	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	810	765243	766130	gil984805	glycine betaine-binding protein precursor [Bacillus subtilis]	55	35
1	871	823341	823790	gil1590959	ATP synthase, subunit K [Methanococcus jannaschii]	55	34
1	898	847660	849462	gil1517942	aminopeptidase P [Sus scrofa]	55	46
1	924	867811	868236	gil1142660	POM1 [Plasmodium chabaudi chabaudi]	55	41
1	927	870905	870039	gil534839	CheR [Rhizobium meliloti]	55	32
1	964	904091	903900	gil312694	ARS-binding factor 1 [Kluyveromyces marxianus]	55	50
1	33	44068	43124	gil146860	delta-2-isopentenyl pyrophosphate transferase [Escherichia coli]	54	31
1	63	79094	74679	gil415736	Orf635 gene product [Euglena gracilis]	54	37
1	192	184282	182969	gil151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii]	54	35
1	200	194105	192951	gil1045800	ribose transport system permease protein [Mycoplasma genitalium]	54	29
1	224	210749	212320	gil1591243	M. jannaschii predicted coding region MJ0539 [Methanococcus jannaschii]	54	45
1	256	237491	238954	gnlPIDle2450	unknown [Mycobacterium tuberculosis]	54	34
1	260	245698	247542	gil1574782	exodeoxyribonuclease V (recD) [Haemophilus influenzae]	54	36
1	320	311333	312133	gil1209528	D,D-carboxypeptidase [Enterococcus faecalis]	54	40
1	610	577096	579909	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	54	30
1	765	720685	719999	gil290216	[bride of sevenless] gene product [Drosophila virilis]	54	25
1	789	739607	739996	gil473804	'dosage-dependent dnaK suppressor protein' [Escherichia coli]	54	35
1	845	797932	798366	gil1045767	ribosomal protein S6 [Mycoplasma genitalium]	54	35
1	951	894898	893912	gil1303842	YqfU [Bacillus subtilis]	54	28
1	86	96019	97032	gil405550	flagellar P-ring protein [Pseudomonas putida]	53	40
1	89	98331	99215	gil912478	No definition line found [Escherichia coli]	53	35
1	164	159533	158562	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	53	39
1	250	234276	232861	gil1303989	YqkI [Bacillus subtilis]	53	28
1	278	266053	267426	gil1749686	similar to Saccharomyces cerevisiae unknown, EMBL Accession Number Z68194 [Schizosaccharomyces pombe]	53	28
1	302	292150	294309	gil1015945	methyl accepting chemotaxis homolog [Treponema denticola]	53	31
1	364	358298	357702	gil1499620	M. jannaschii predicted coding region MJ0798 [Methanococcus jannaschii]	53	41

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	514	486253	486888	gil940842	orf 06111 gene product [Saccharomyces cerevisiae]	53	28
1	567	541832	540684	gil165254	YlxH [Borrelia burgdorferi]	53	33
1	621	590418	591032	gil1592021	cell division protein J [Methanococcus jannaschii]	53	32
1	805	759748	758537	gil1732203	GlcNAc 6-P deacetylase [Vibrio furnissii]	53	35
1	854	804825	805298	gil1303915	YqhZ [Bacillus subtilis]	53	30
1	884	835705	834944	gil1574399	H. influenzae predicted coding region HI1555 [Haemophilus influenzae]	53	26
1	48	58236	56944	gil1652686	hypothetical protein [Synecocystis sp.]	52	26
1	53	63264	62383	gil42219	P35 gene product (AA 1 - 314) [Escherichia coli]	52	34
1	56	66168	65665	gil1151158	repeat organellar protein [Plasmodium chabaudi]	52	37
1	95	102255	102746	gil1574136	colicin V production protein (pur regulon) (cvpA) [Haemophilus influenzae]	52	24
1	117	115800	116879	gil288998	secA gene product [Anthamion sp.]	52	34
1	220	208898	208446	gil1652602	hypothetical protein [Synecocystis sp.]	52	25
1	285	274152	272764	gnlPIDle2551	trigger factor [Bacillus subtilis]	52	28
1	352	344946	346532	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	52	26
1	368	361087	361800	gil216861	24K membrane protein [Pseudomonas aeruginosa]	52	32
1	376	368462	367695	gil147213	phnP protein [Escherichia coli]	52	47
1	381	373209	372412	gil467459	unknown [Bacillus subtilis]	52	28
1	437	418141	416768	gil1591425	hypothetical protein (GP:X91006_2) [Methanococcus jannaschii]	52	27
1	439	420801	420166	gil1674178	(AE000047) Mycoplasma pneumoniae, MG246 homolog, from M. genitalium [Mycoplasma pneumoniae]	52	40
1	474	443436	443798	gil1573287	aspartyl-tRNA synthetase (aspS) [Haemophilus influenzae]	52	35
1	583	555235	553802	gil496254	fibronectin/fibrinogen-binding protein [Streptococcus pyogenes]	52	29
1	759	715852	715610	gil397703	dihydroorotate dehydrogenase [Plasmodium falciparum]	52	30
1	797	751384	750674	gil1063419	S2 gene product [Borrelia burgdorferi]	52	27
1	820	776768	774852	gil580936	SpoVD [Bacillus subtilis]	52	33
1	869	820887	821516	gil1592298	ATP synthase, subunit D [Methanococcus jannaschii]	52	29
1	888	839581	838106	gil1151158	repeat organellar protein [Plasmodium chabaudi]	52	30
1	916	862856	862110	gil1256625	putative [Bacillus subtilis]	52	25
1	67	83112	81610	gil587604	beta subunit RNA polymerase [Plasmodium falciparum]	51	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	150	147190	146360	gil520844	orf4 [Bacillus subtilis]	51	26
1	194	186516	185275	gil211931	3-hydroxy-3-methylglutaryl-CoA synthase [Gallus gallus]	51	29
1	300	288759	289676	gil142833	ORF2 [Bacillus subtilis]	51	33
1	371	362209	362874	gil1698880	protein antigen LmST11 [Leishmania major]	51	27
1	464	438943	439497	gil1591434	chromate resistance protein A [Methanococcus jannaschii]	51	29
1	819	772935	774842	gnlIPIDle239057	AMP-binding protein [Brassica napus]	51	29
1	926	869257	869955	gil633996	a negative regulator of pho regulon [Pseudomonas aeruginosa]	51	26
1	45	54760	54062	gil505363	ORF2 [Salmonella typhimurium]	50	32
1	94	101155	102261	gil39995	phospho-N-acetylmuramoyl-pentapeptide-transferase [Bacillus subtilis]	50	29
1	118	118397	117096	gil1762996	RING-finger protein [Helicoverpa armigera nucleopolyhedrovirus]	50	25
1	155	151159	150506	gil893358	PgsA [Bacillus subtilis]	50	35
1	239	224187	224744	gil1303843	YqfV [Bacillus subtilis]	50	29
1	274	265044	264040	gnlIPIDle276778	unknown [Mycobacterium tuberculosis]	50	32
1	287	276164	274710	gil147140	peptidase D [Escherichia coli]	50	28
1	310	299525	300778	gil1652202	ComE [Synechocystis sp.]	50	33
1	349	342477	341581	gnlIPIDle220245	frameshift [Plasmodium falciparum]	50	30
1	457	435120	434509	gil144839	beta-galactosidase [Thermoanaerobacterium thermosulfurigenes]	50	29
1	479	448691	447948	gil580905	B. subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]	50	32
1	680	640194	641039	gil882579	CG Site No. 29739 [Escherichia coli]	50	31
1	737	690152	690400	gil1086864	T03G11.2 gene product [Caenorhabditis elegans]	50	39
1	752	708130	709662	gil40162	murE gene product [Bacillus subtilis]	50	30
1	360	353288	354157	gil343314	involucrin [Saguinus oedipus]	49	20
1	44	54046	53216	gil505363	ORF2 [Salmonella typhimurium]	48	21
1	122	119896	120774	gil405908	yejE [Escherichia coli]	48	29
1	161	157504	156653	gil143213	putative [Bacillus subtilis]	48	23
1	316	305940	306995	gil1762962	FemA [Staphylococcus simulans]	48	28
1	459	436152	437315	gil1001478	hypothetical protein [Synechocystis sp.]	48	25

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	628	596267	596566	gil156218	putative [Caenorhabditis elegans]	48	32
1	694	655069	654452	gil1574476	dedA protein (dedA) [Haemophilus influenzae]	48	22
1	731	686392	686129	gil915207	gastric mucin [Sus scrofa]	48	27
1	893	844951	843476	gnlPIDle220245	frameshift [Plasmodium falciparum]	48	32
1	62	74673	72196	gil1766042	outer membrane protein [Neisseria gonorrhoeae]	47	30
1	103	107896	108780	gil1256885	P24A protein (unknown function) (Swiss Prot. accession number P32802) [Saccharomyces cerevisiae]	47	27
1	187	181111	180215	gil1184118	mevalonate kinase [Methanobacterium thermoautotrophicum]	47	30
1	204	195930	196616	gil1573552	phosphoglycolate phosphatase, chromosomal (SP:P40852) [Haemophilus influenzae]	47	21
1	265	251835	251098	gil1209847	repeat motif-containing gene [Borrelia burgdorferi]	47	30
1	334	325837	326529	gil1591893	uridylylate kinase [Methanococcus jannaschii]	47	26
1	356	349581	349991	gil849173	Probable essential component of the nucleoskeleton (Swiss Prot. accession number P32380) [Saccharomyces cerevisiae]	47	27
1	490	460559	459834	gil1592264	type I restriction enzyme [Methanococcus jannaschii]	47	34
1	526	499992	499264	gil710551	ankyrin 3 [Mus musculus]	47	29
1	577	549541	548390	gnlPIDle220245	frameshift [Plasmodium falciparum]	47	27
1	744	701189	699441	gnlPIDle160436	orfA gene product [Borrelia burgdorferi]	47	23
1	755	713050	710765	pirIS41649IS41649	DNA polymerase - Plasmodium falciparum	47	22
1	761	717229	718392	gil1500309	M. jannaschii predicted coding region MJ1428 [Methanococcus jannaschii]	47	37
1	813	767745	768737	pirIG64100IG64100	membrane fusion protein (mtrC) homolog - Haemophilus influenzae (strain Rd KW20)	47	23
1	824	779587	780546	gil687844	contains TPR domain-like repeats [Caenorhabditis elegans]	47	28
1	881	834283	833015	gil1574393	H. influenzae predicted coding region HI1548 [Haemophilus influenzae]	47	24
1	886	837236	836199	gil887563	serine/threonine-protein kinase [Plasmodium falciparum]	47	30
1	47	57001	55880	gil1652686	hypothetical protein [Synechocystis sp.]	46	23
1	160	156659	156171	gil13261	ORF4 protein (AA 1-156) [Paramecium aurelia]	46	30

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	249	231765	232829	gil1142681	Lpp38 [Pasteurella haemolytica]	46	28
1	329	323695	322838	gil562039	NADH dehydrogenase, subunit 2 [Acanthamoeba castellanii]	46	20
1	336	329090	327303	gil457146	rhostry protein [Plasmodium yoelii]	46	18
1	442	422511	421747	gil591598	hypothetical protein (GP:U19364_6) [Methanococcus jannaschii]	46	27
1	452	428632	429375	pirIS41649IS41649	DNA polymerase - Plasmodium falciparum	46	21
1	573	545081	545596	gil1022328	Four tandem repeats of a DNA-binding domain known as the AT-hook are found at the carboxy terminus of CarD. This protein has been purified and found to bind in vitro to a promoter region [Myxococcus xanthus]	46	28
1	617	586903	587865	gnlPIDle33329	ND5 protein [Ascaris suum]	46	29
1	708	668290	666710	gil1573271	apolipoprotein N-acyltransferase (cute) [Haemophilus influenzae]	46	32
1	790	741189	740008	gil458015	TpN50 precursor [Treponema pallidum]	46	29
1	892	843474	841147	gil1574537	outer membrane integrity protein (toIA) [Haemophilus influenzae]	46	19
1	903	853463	852741	gil806562	nebulin [Homo sapiens]	46	26
1	968	908917	909948	gil438455	possible N-terminal signal sequence; mature protein may be membrane-anchored and start at Cys-17. 17.5% identity over 354-aa overlap with Candida pelliculosa beta-glucosidase.; putative [Bacillus subtilis]	46	29
1	208	197467	198516	gil220578	open reading frame [Mus musculus]	45	27
1	462	438197	438949	gil687689	similar to a chromate resistance protein (ChrA) from A. eutrophus, Swiss-Prot Accession Number P17551 [Synechococcus sp.]	45	23
1	742	698657	695295	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	45	23
1	90	99196	98756	gil303895	ORF 8: This ORF is required for the secretion of IpaB, IpaC and IpaD [Plasmid pMYSH6000]	44	26
1	253	235698	234343	gil143245	Na+/H+ antiporter [Bacillus firmus]	44	26
1	709	668406	670430	gnlPIDle236483	F54G8.4 [Caenorhabditis elegans]	44	31
1	850	802490	801045	gnlPIDle220245	frameshift [Plasmodium falciparum]	44	25
1	458	436119	435118	gil1303799	YqeN [Bacillus subtilis]	43	19

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

1	859	810560	809967	pirIS17998IS17998	gene COX1 intron 4 protein - yeast (<i>Kluyveromyces marxianus</i> var. <i>lactis</i>) mitochondrion (SGC2)	43	30
1	935	881179	879701	gil1045905	no score generated - score shown is bogus [<i>Mycoplasma genitalium</i>]	43	27
1	319	311250	309877	gil1591425	hypothetical protein (GP:X91006_2) [<i>Methanococcus jannaschii</i>]	42	19
1	618	587863	588672	gil1045801	hypothetical protein (SP:P32720) [<i>Mycoplasma genitalium</i>]	42	24
1	625	593472	594572	gil343962	VAR1 protein [<i>Candida glabrata</i>]	42	25
1	93	100191	101021	gil413976	ipa-52r gene product [<i>Bacillus subtilis</i>]	41	26
1	574	545523	546581	gnlPIDle16326	MURF2 protein (AA I-348) [<i>Crithidia fasciculata</i>]	41	26
1	740	693458	692403	gil1151158	repeat organellar protein [<i>Plasmodium chabaudi</i>]	41	20
1	3	5792	6796	gil1256888	Similar to chromosome segregation protein Smc1p of <i>S. cerevisiae</i> (GenBank accession number L00602), chromosome segregation protein Cut3p of <i>S. pombe</i> (Swiss Prot. accession number P41004), and <i>C. elegans</i> hypothetical proteins R13G10.1 (GenBank)	40	24
1	228	214440	214742	gil1150836	neural specific DNA binding protein [<i>Xenopus laevis</i>]	40	28
1	318	309735	308377	gil1591425	hypothetical protein (GP:X91006_2) [<i>Methanococcus jannaschii</i>]	40	19
1	453	431037	429700	gil499647	[<i>Mus musculus</i> (strain C3HF/RL) ORF mRNA, complete cds.], gene product [<i>Mus musculus</i>]	40	24
1	795	747813	749516	gil304179	wall-associated protein [<i>Bacillus subtilis</i>]	40	35
1	966	907336	905528	gil1151158	repeat organellar protein [<i>Plasmodium chabaudi</i>]	40	26

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

Contig ID	Orf ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length
1	69	86349	85018	gbIL32144	<i>Borrelia burgdorferi</i> peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	220
1	70	86918	86340	gbIL32144	<i>Borrelia burgdorferi</i> peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	579
1	71	87573	86911	gbIL32144	<i>Borrelia burgdorferi</i> peptidyl-tRNA hydrolase-like protein (pth) gene homologue, complete cds	100	129
1	124	123885	121759	gbIM60802	<i>B. burgdorferi</i> immunogen gene, 5' flank	99	2127
1	126	127421	125700	embIX919651 BBATPBP	<i>B. burgdorferi</i> abp gene	97	284
1	137	136332	139151	gbIL31424	<i>Borrelia burgdorferi</i> (clone BbK3.11) <i>phoA</i> fusion protein gene, partial cds	98	248
1	138	138676	138515	gbIL31424	<i>Borrelia burgdorferi</i> (clone BbK3.11) <i>phoA</i> fusion protein gene, partial cds	96	60
1	165	160705	159932	gbIU17591	<i>Borrelia burgdorferi</i> primary sigma factor (<i>rpD</i>) gene, complete cds	100	774
1	166	162604	160703	gbIU17591	<i>Borrelia burgdorferi</i> primary sigma factor (<i>rpD</i>) gene, complete cds	100	1902
1	167	162835	162602	gbIU17591	<i>Borrelia burgdorferi</i> primary sigma factor (<i>rpD</i>) gene, complete cds	99	232
1	168	164397	162811	gbIU17591	<i>Borrelia burgdorferi</i> primary sigma factor (<i>rpD</i>) gene, complete cds	99	1216
1	210	198495	199028	gbIU61498	<i>Borrelia burgdorferi</i> <i>CheA</i> (<i>cheA</i>) gene, partial cds, <i>CheW</i> (<i>cheW</i>), <i>CheX</i> (<i>cheX</i>) and <i>CheY</i> (<i>cheY</i>) genes, complete cds	98	127
1	211	199527	199069	gbIU61498	<i>Borrelia burgdorferi</i> <i>CheA</i> (<i>cheA</i>) gene, partial cds, <i>CheW</i> (<i>cheW</i>), <i>CheX</i> (<i>cheX</i>) and <i>CheY</i> (<i>cheY</i>) genes, complete cds	99	459
1	212	200067	199549	gbIU61498	<i>Borrelia burgdorferi</i> <i>CheA</i> (<i>cheA</i>) gene, partial cds, <i>CheW</i> (<i>cheW</i>), <i>CheX</i> (<i>cheX</i>) and <i>CheY</i> (<i>cheY</i>) genes, complete cds	99	519
1	213	201455	200046	gbIU61498	<i>Borrelia burgdorferi</i> <i>CheA</i> (<i>cheA</i>) gene, partial cds, <i>CheW</i> (<i>cheW</i>), <i>CheX</i> (<i>cheX</i>) and <i>CheY</i> (<i>cheY</i>) genes, complete cds	99	1410

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

							II (crr) gene, hsp90 (hptg) gene, complete cds		
1	346	339458	338868	gblU518781			Borrelia burgdorferi phosphotransferase enzyme III (crr) gene, hsp90 (hptg) gene, complete cds	100	591
1	388	378955	379590	gblM968471			Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	100	636
1	389	379566	381521	embIX676461 BBHSPRO			B. burgdorferi dnaK gene for heat-shock protein	100	1956
1	390	381512	381943	gblM979141			Borrelia burgdorferi DnaJ gene, complete cds	97	424
1	391	381907	382617	gblM968471			Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	100	687
1	392	382656	383360	gblM968471			Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	95	144
1	393	383005	382688	gblM968471			Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	95	144
1	394	384408	383416	gblU829781			Borrelia burgdorferi phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	956
1	395	384799	384467	gblU829781			Borrelia burgdorferi phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	292
1	396	386169	384733	gblU829781			Borrelia burgdorferi phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	1416
1	397	387733	386144	gblU829781			Borrelia burgdorferi phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	1220

TABLE 2. Borrelia burgdorferi - Coding regions containing known proteins

1	398	394257	387727	gbU829781	Borrelia burgdorferi phenylalanyl-tRNA synthetase alpha subunit (pheS), phenylalanyl-tRNA synthetase beta subunit (pheT) and thioredoxin reductase (trxB) genes, complete cds	99	230
1	421	408559	407981	gbM286811	B. burgdorferi promoter region DNA	98	152
1	427	411019	410132	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	287
1	428	411388	411017	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	96	357
1	429	411676	411386	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	291
1	430	412531	411674	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	98	858
1	431	412852	412529	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	324
1	432	413487	412846	gbU781931	Borrelia burgdorferi tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds	99	642

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	433	414117	413485	gblU781931	S3 (rpsC) gene, partial cds		99	633
					<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds			
1	434	414464	414141	gblU781931	<i>Borrelia burgdorferi</i> tuf-s10 operon: elongation factor (tuf), ribosomal proteins S10 (rpsJ), L3 (rplC), L4 (rplD), L23 (rplW), L2 (rplB), S19 (rpsS), and L22 (rplV) genes, complete cds, and S3 (rpsC) gene, partial cds		100	324
1	435	415714	414503	gblL231251	<i>Borrelia burgdorferi</i> elongation factor EF-Tu (tuf) gene, complete cds		100	1212
1	481	450681	450310	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds		100	148
1	482	450820	450650	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds		100	171
1	483	451208	450897	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds		100	312
1	484	451288	451467	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA),		100	180

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	485	452456	451287	gblU045271	DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	99	1170
1	486	454181	452685	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	1497
1	487	454315	456237	gblU045271	<i>Borrelia burgdorferi</i> 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	98	904
1	488	456228	458681	embL121651B BGRAG	<i>B. burgdorferi</i> gyrA gene encoding DNA gyrase subunit A (partial)	96	289
1	496	463825	464394	gblU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	100	570
1	497	466650	466958	gblU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	96	210
1	498	467437	468033	gblU033961	<i>Borrelia burgdorferi</i> B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	99	209

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	499	468167	468433	gblU03396l	complete sequence Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	98	267
1	500	468391	468999	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	95	386
1	501	470714	470445	gblM88330l	Borrelia burgdorferi 23S ribosomal RNA gene	100	270
1	502	475597	480090	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	97	131
1	535	505532	509017	gblL48488l	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	98	2490
1	536	509015	513166	gblL48488l	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta' subunit (rpoC) gene, 5' end of cds	97	76
1	538	513606	514106	gblU35450l	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	100	82
1	539	514120	515229	gblU35450l	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	99	1110
1	540	515472	516605	gblU49938l	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1134
1	541	516641	517666	gblL24194l	Borrelia burgdorferi immunodominant antigen P39 gene, complete cds	99	1026

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	542	517732	518256	gbL350501	<i>Borrelia burgdorferi</i> (clone pB46) membrane lipoprotein A (bnpA) gene, 3' end, membrane lipoprotein (bnpB) gene, 5' end	98	457
1	543	518168	518779	gbL241941	<i>Borrelia burgdorferi</i> immunodominant antigen P39 gene, complete cds	99	606
1	544	518856	520316	gbU499381	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bnpC) and BmpA (bnpA), BmpB protein (bnpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKC1 (pkci) genes, complete cds	99	1461
1	545	520349	521734	gbU499381	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bnpC) and BmpA (bnpA), BmpB protein (bnpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKC1 (pkci) genes, complete cds	99	1386
1	546	521752	522204	gbU499381	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bnpC) and BmpA (bnpA), BmpB protein (bnpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKC1 (pkci) genes, complete cds	100	453
1	547	522168	522893	gbU499381	<i>Borrelia burgdorferi</i> potential virulence gene cluster membrane proteins BmpC (bnpC) and BmpA (bnpA), BmpB protein (bnpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKC1 (pkci) genes, complete cds	98	130
1	559	535086	534772	embIX787081 BBYSC1	<i>B. burgdorferi</i> (ZS7) YSC1-like gene	99	314
1	560	536461	535058	embIX787081 BBYSC1	<i>B. burgdorferi</i> (ZS7) YSC1-like gene	100	1404
1	561	536545	537144	embIX708261	<i>B. burgdorferi</i> gene for lipoprotein	100	600

TABLE 2.
Borrelia burgdorferi - Coding regions containing known proteins

1	562	537652		BBLA7	B.burgdorferi gene for lipoprotein	100	57
1	563	539695	537191	embIX708261 BBLA7			
1	564	537705	537665	gblM90084	Borrelia burgdorferi 22 kD antigen	100	786
1	565	538395	537968	gblM90084	Borrelia burgdorferi 22 kD antigen	100	264
1	606	574092	538757	gblM90084	Borrelia burgdorferi 22 kD antigen	100	56
			572497	gblU291431	Borrelia burgdorferi periplasmic substrate-binding protein homolog (p30) gene, complete cds	92	805
1	607	575817	574204	gblU291431	Borrelia burgdorferi periplasmic substrate-binding protein homolog (p30) gene, complete cds	100	84
1	616	585458	586936	gblL314221	Borrelia burgdorferi (clone Bb2.13) phoA fusion protein gene, partial cds	100	354
1	629	596586	597983	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1185
1	630	597967	599052	embIX966851 BBCDG	B.burgdorferi cell division genes	99	912
1	631	599050	600153	embIX966851 BBCDG	B.burgdorferi cell division genes	99	1104
1	632	600183	600932	embIX964331 BBFTSWQA	B.burgdorferi ftsW, ftsQ & ftsA genes	99	750
1	633	600905	602173	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1269
1	634	602171	603394	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1224
1	635	603392	604087	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	696
1	636	604085	605041	gblL763031	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flfEFGHI, flbABC genes, complete cds	98	712
1	637	605039	605599	gblU437391	Borrelia burgdorferi fesmid clone 31, complete sequence	100	561

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	638	605535	606938	embIX96685 BBCDG	B. burgdorferi cell division genes	97	1404
1	639	606936	607379	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	444
1	640	607382	607861	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	480
1	641	607831	608208	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	100	378
1	642	608163	609932	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	100	1770
1	643	609930	610982	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1053
1	644	610961	611917	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	957
1	645	611915	613246	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	99	1332
1	646	613222	613674	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	99	453
1	647	613655	614284	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	630
1	648	614250	615470	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	99	1221
1	649	615481	615927	gbIL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flIEFGHI, flbABC genes, complete cds	100	447
1	650	615911	617260	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1350
1	651	617277	617507	gbIU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	231

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	652	617498	618286	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	789
1	653	618280	619068	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	789
1	654	619066	619653	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	588
1	655	619688	620749	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	1062
1	656	620789	621136	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	348
1	657	621114	621755	gblU43739I	<i>Borrelia burgdorferi</i> fesmid clone 31, complete sequence	100	642
1	658	621742	622530	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	99	789
1	659	622028	621822	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	207
1	660	622515	622802	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	288
1	661	622811	623623	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	99	813
1	662	623007	622819	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	189
1	663	623706	623458	gblL75945I	<i>Borrelia burgdorferi</i> flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flhB, flhF, flbE genes	100	249

Borrelia burgdorferi - Coding regions containing know proteins

							fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes			
1	664	623608	624741	gblL75945I			Borrelia burgdorferi flagellar hook protein (fliG), fliD, flagellar motor apparatus (motAB), fliL, fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes	99		1134
1	665	624735	626843	gblL75945I			Borrelia burgdorferi flagellar hook protein (fliG), fliD, flagellar motor apparatus (motAB), fliL, fliM, fliZ, flagellar export apparatus (fliPQR, fliH), fliF, fliE genes	100		2109
1	666	626841	628013	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	100		1173
1	667	627998	628912	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	99		816
1	668	629151	628807	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	100		345
1	669	628910	629398	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	100		489
1	670	629371	631305	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	100		1935
1	671	631314	631634	gblU43739I			Borrelia burgdorferi fmsmid clone 31, complete sequence	100		286
1	676	636891	635476	gblM28682I			B. burgdorferi promoter element DNA	100		78
1	687	646982	649420	gblL77216I			Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	99		2439
1	688	651760	649409	gblL77216I			Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	100		274
1	711	671567	672412	gblU35673I			Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99		542
1	712	672418	672744	gblU35673I			Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100		327
1	713	672751	673083	gblU48651I			Borrelia burgdorferi PIG histone-like protein HBbu (hbb) gene, complete cds	100		327

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	714	673081	673491	gblU356731	<i>Borrelia burgdorferi</i> OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	411
1	715	673553	675118	gblU356731	<i>Borrelia burgdorferi</i> OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	1566
1	716	675164	675424	gblU356731	<i>Borrelia burgdorferi</i> OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	106
1	773	724171	723770	gblU629011	<i>Borrelia burgdorferi</i> thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	97	67
1	774	723891	724181	gblU629011	<i>Borrelia burgdorferi</i> thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	97	77
1	775	725456	724164	gblU629011	<i>Borrelia burgdorferi</i> thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	780
1	776	727348	725441	gblU629011	<i>Borrelia burgdorferi</i> thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	1841
1	777	727854	727336	gblU629011	<i>Borrelia burgdorferi</i> thdF gene, partial cds, putative motility protein (flbF), flagellar hook associated proteins FlgK (flgK) and FlgL (flgL) genes, complete cds	99	519
1	778	727908	729308	embIX956691 BBTHDFGID	<i>B. burgdorferi</i> thdF and gidA genes	98	1185
1	779	729284	731176	embIZ121601B BGIDAG	<i>B. burgdorferi</i> thdF, gidA and gidB genes	99	1893
1	780	731149	731799	embIX956681 BBGIDMOX R	<i>B. burgdorferi</i> gidA, gidB and moxR genes	98	381
1	781	731772	732848	embIX964341	<i>B. burgdorferi</i> gidB moxR genes and ORF	99	789

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

					BBGIDBMO X				
1	782	732815	733738	embIX96434 BBGIDBMO X	B.burgdorferi gidB moxR genes and ORF	100		84	
1	798	752154	751372	gbIU51878I	Borrelia burgdorferi phosphotransferase enzyme II (crr) gene, hsp90 (hptg) gene, complete cds	100		57	
1	800	754266	753118	gbIAF003354I	Borrelia burgdorferi SecA (secA) gene, complete cds	97		67	
1	801	753992	754243	gbIAF003354I	Borrelia burgdorferi SecA (secA) gene, complete cds	96		50	
1	802	754283	757015	gbIAF003354I	Borrelia burgdorferi SecA (secA) gene, complete cds	99		2041	
1	803	756991	757641	gbIAF003354I	Borrelia burgdorferi SecA (secA) gene, complete cds	100		158	
1	806	759909	761930	gbIU66699I	Borrelia burgdorferi flagellar filament cap (filD) gene, complete cds and flagellin protein (flaB) gene, partial cds	98		1149	
1	807	762051	763067	embIX16833I BBFAA	Borrelia burgdorferi gene for flagellum-associated 41kD antigen (flagellin)	99		1017	
1	808	763194	764339	embIX63898I BBHYPP	B.burgdorferi DNA for hypothetical protein	99		1146	
1	809	764337	765245	embIX63898I BBHYPP	B.burgdorferi DNA for hypothetical protein	92		253	
1	826	783276	784400	gbIU23457I	Borrelia burgdorferi RecA (recA) gene, complete cds	99		1122	
1	827	784412	785182	gbIU23457I	Borrelia burgdorferi RecA (recA) gene, complete cds	82		476	
1	828	785142	785918	gbIU23457I	Borrelia burgdorferi RecA (recA) gene, complete cds	99		139	
1	907	855179	857182	gbIU28760I	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI)	94		75	

TABLE 2. Borrelia burgdorferi - Coding regions containing known proteins

1	908	857228	858262	gblU28760	genes, complete cds		99	1035
1	909	858270	859463	gblU28760	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds		99	1194
1	910	859315	860226	gblU28760	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds		99	912
1	911	860224	860604	gblU57683	Borrelia burgdorferi sequence 3' to the triosephosphate isomerase (TPI) gene		97	183
1	912	860645	860316	gblU57683	Borrelia burgdorferi sequence 3' to the triosephosphate isomerase (TPI) gene		95	94
1	913	861447	860704	gblU57684	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds		92	294
1	914	861020	861397	gblU57684	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds		93	244
1	915	861439	862113	gblU57684	Borrelia burgdorferi uracil DNA glycosylase (UDG) gene, partial cds		96	128
1	930	874089	874859	gblL32861	Borrelia burgdorferi 1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC) gene, 3' end; topoisomerase IV beta-subunit (parE) gene, 5' end		99	408
1	931	874877	876679	gblL32861	Borrelia burgdorferi 1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC) gene, 3' end; topoisomerase IV beta-subunit (parE) gene, 5' end		100	252
1	943	887900	886758	embY08885 BBRUVA BH L	B. burgdorferi ruvA, ruvB and queA genes		98	293

TABLE 2. *Borrelia burgdorferi* - Coding regions containing known proteins

1	944	887965	888570	embly088851 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	99	606
1	945	888603	889658	embly088851 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	99	1056
1	946	889615	890271	embly088851 BBRUVABH L	B.burgdorferi ruvA, ruvB and queA genes	97	342
1	948	890719	892404	embly091401 BBPFPB	B.burgdorferi pfpB gene	99	1320
1	950	892893	893909	embly091421 BBYFII	B.burgdorferi yfiI gene	97	919
1	952	894973	895371	emblyX974491 BBPRIAUDK	B.burgdorferi priA and udk genes	88	324
1	953	895308	895991	emblyX974491 BBPRIAUDK	B.burgdorferi priA and udk genes	99	684
1	954	897976	895988	emblyX974491 BBPRIAUDK	B.burgdorferi priA and udk genes	99	1989
1	955	898577	897963	emblyX974491 BBPRIAUDK	B.burgdorferi priA and udk genes	100	152
1	956	899298	898555	embly091411 BBTRUA	B.burgdorferi truA gene	99	741

TABLE 3.
Borrelia burgdorferi - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	1	2330	1134
1	2	3317	2934
1	8	11375	13021
1	9	11673	11386
1	10	12925	13629
1	11	13538	14146
1	17	25212	24700
1	18	25782	25357
1	19	26115	25870
1	21	27308	27051
1	22	29628	30458
1	29	40696	41217
1	30	41201	41992
1	31	42542	41985
1	32	42593	42982
1	34	44234	44031
1	38	48041	47079
1	41	49318	49617
1	43	53234	51810
1	50	59737	58208
1	58	68227	67733
1	65	79757	80404
1	66	81516	80401
1	75	89552	88353
1	82	93338	92766
1	85	95207	95854
1	104	108788	108621
1	105	109764	108943
1	108	112003	111599
1	113	114317	115846
1	114	114522	114316
1	119	118439	118927
1	121	119802	119599
1	125	125688	123967
1	129	128594	129235
1	135	136116	135259
1	136	136558	136298
1	139	139149	139559
1	141	140573	140121
1	143	141738	141412
1	145	142218	142060
1	146	142686	142342
1	154	150528	149074
1	158	153832	153981
1	163	158277	158474

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	171	168052	166205
1	176	171592	171038
1	186	179607	180089
1	189	182345	182046
1	191	182567	182773
1	199	192561	192716
1	205	196592	197476
1	218	207717	206752
1	219	207733	208437
1	221	209337	208915
1	222	209712	209335
1	231	217179	216025
1	238	223660	223418
1	240	224720	225724
1	242	227006	227275
1	248	231761	231501
1	251	232973	233308
1	252	233669	234004
1	254	235115	235456
1	258	241824	242198
1	261	248009	247773
1	269	256846	255872
1	276	265430	265158
1	279	266582	266298
1	281	268474	268280
1	286	274157	274384
1	292	280495	280274
1	294	281344	281042
1	298	287276	285714
1	303	292943	292644
1	304	293273	293037
1	305	294965	294648
1	308	299427	298699
1	309	299051	299212
1	326	320375	319785
1	327	320425	321036
1	331	324198	324413
1	339	332785	332459
1	341	333503	334138
1	342	334116	334739
1	343	334880	335446
1	350	342916	342443
1	351	344789	342897
1	363	357596	356931
1	367	361065	360859
1	370	362519	362196

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	374	366905	366114
1	377	368632	369537
1	378	369928	370560
1	379	370532	371353
1	382	375028	373193
1	383	375102	375542
1	387	378677	378198
1	400	394952	394722
1	401	396247	394937
1	403	397569	398327
1	406	399103	399294
1	436	416160	416570
1	445	424660	423950
1	446	425181	424642
1	450	428559	428200
1	451	428933	428619
1	455	432590	431628
1	461	437823	438092
1	463	438690	438313
1	466	440749	440222
1	470	441568	441350
1	471	442039	441614
1	472	442216	442037
1	473	442666	442262
1	476	445202	445017
1	493	462106	462519
1	494	462893	462549
1	504	482111	481035
1	505	481552	481800
1	509	483249	483668
1	512	484864	485157
1	516	489171	488527
1	519	492989	492375
1	520	493626	492997
1	521	494169	494864
1	524	497185	497385
1	525	497674	499254
1	527	500251	501294
1	528	501281	502156
1	558	533912	533667
1	568	541267	541491
1	571	544436	544257
1	572	544565	545068
1	578	549603	551198
1	580	551508	551657
1	581	552337	551513

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to known proteins

1	585	556051	557271
1	590	561342	561139
1	591	561825	561520
1	592	562536	563360
1	596	565758	566519
1	599	568389	568682
1	602	568680	568856
1	605	570829	571167
1	609	576170	577093
1	612	581549	581091
1	614	582910	584013
1	619	589384	588674
1	624	592665	593465
1	626	594542	595405
1	672	631642	632175
1	677	636650	636892
1	678	637059	638078
1	681	640861	640412
1	686	644887	645207
1	689	649716	649961
1	690	650436	650735
1	691	650733	651056
1	693	653303	653689
1	705	664733	664918
1	707	665979	666770
1	718	679155	678391
1	721	680664	681047
1	722	681523	681849
1	724	681809	682171
1	727	682853	683272
1	734	687648	688067
1	739	691613	692290
1	751	707290	707718
1	763	719197	718904
1	764	720030	719257
1	769	722198	722482
1	783	733736	734647
1	785	735554	736618
1	787	737124	739184
1	792	742924	744801
1	799	753128	752655
1	811	766129	765980
1	812	766438	767772
1	815	770062	769790
1	818	771890	772282
1	831	788219	788836

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

1	832	788824	789615
1	838	793566	793414
1	840	794295	794119
1	844	796774	796586
1	852	803096	802908
1	858	809371	809970
1	864	816108	816497
1	865	816672	817283
1	866	817281	817838
1	872	823841	824836
1	876	828191	828739
1	877	828749	829147
1	879	831328	831714
1	880	831698	833005
1	885	836201	835677
1	890	841171	840590
1	891	840594	840860
1	899	849453	850148
1	902	851608	852687
1	918	862867	863109
1	920	864292	864705
1	923	865660	865346
1	925	868212	869273
1	928	871012	872580
1	933	878576	879166
1	939	884338	883268
1	940	884999	884325
1	949	892388	892924
1	957	900141	899296
1	958	900534	900139
1	959	901526	900510
1	962	902383	903258

TABLE 4.
Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident
69	1	291	4	gil146582	beta-lactamase [Escherichia coli]	100	98
69	2	692	240	gil344797	galactosidase fusion protein [unidentified]	100	99
26	3	1575	2093	gil458219	ORF 4 [Borrelia burgdorferi]	94	76
2	48	41836	41459	gil47453	ribosomal protein S12 [Streptococcus pneumoniae]	92	85
6	20	14234	12951	bbs161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	88	67
52	5	1080	1652	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	88	74
152	1	337	26	gnlPIDle158979	orfA gene product [Borrelia burgdorferi]	86	75
71	2	1421	1128	gnlPIDle160437	orfD gene product [Borrelia burgdorferi]	85	46
131	1	381	674	gil458220	ORF 5 [Borrelia burgdorferi]	85	76
3	113	98152	97367	gil1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	84	65
2	107	108403	109485	gil882454	fructose 1,6-bisphosphate aldolase [Escherichia coli]	81	61
19	4	4059	4754	pirA34520A34520	29K calcium-binding protein, brain-specific - guinea pig (fragments)	81	56
20	9	6084	5791	gnlPIDle201249	ORF-C gene product [Borrelia burgdorferi]	81	72
2	52	49986	49600	pirA02771R7MCML	ribosomal protein L7/L12 - Micrococcus luteus	80	67
14	1	3071	3	gil1522636	M. jannaschii predicted coding region MJEC502 [Methanococcus jannaschii]	80	60
29	2	218	409	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	80	37
32	2	719	925	gil433720	CDC25 [Homo sapiens]	80	73
100	1	2	946	gil1522636	M. jannaschii predicted coding region MJEC502 [Methanococcus jannaschii]	80	60

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	106	107148	108239	gnlPIDle2881 24	glucose epimerase [Bacillus thuringiensis]	79	66
8	4	4878	4735	gil1543076	outer membrane porin protein Oms28 precursor [Borrelia burgdorferi]	79	69
2	55	51661	51218	gil587583	ribosomal protein L11 [Thermus aquaticus thermophilus]	78	58
4	54	39290	38742	gnlPIDle1604 37	orfD gene product [Borrelia burgdorferi]	78	57
5	46	27416	27177	gnlPIDle2532 11	ORF YDL065c [Saccharomyces cerevisiae]	78	57
7	4	2382	2966	gnlPIDle2012 48	ORF-B gene product [Borrelia burgdorferi]	78	60
19	5	5107	4943	gil882579	CG Site No. 29739 [Escherichia coli]	78	42
78	1	1	171	gnlPIDle2012 49	ORF-C gene product [Borrelia burgdorferi]	78	60
105	2	503	742	gnlPIDle2532 11	ORF YDL065c [Saccharomyces cerevisiae]	78	57
2	30	24917	23697	gil143795	transfer RNA-Tyr synthetase [Bacillus subtilis]	77	52
6	34	22722	24080	gil466474	cellobiose phosphotransferase enzyme II' [Bacillus stearothermophilus]	77	50
8	1	688	536	gil1017809	similar to dihydropyridine-sensitive I-type, skeletal muscle calcium channel alpha-1 subunit (SP:CIC1_RABIT, P07293) [Caenorhabditis elegans]	77	55
3	91	81071	82183	gil467376	unknown [Bacillus subtilis]	76	58
11	1	208	2	gil1065989	(pos:5995..5997,aa:Met) [Bacillus subtilis]	76	56
68	1	605	3	gnlPIDle1589 80	orfC gene product [Borrelia burgdorferi]	76	56
2	9	8488	6674	pirC30010IC3 0010	hypothetical ORF-6 protein - Sauroleishmania tarentolae mitochondrion (SGC6)	75	50
2	37	31639	32163	gil1573470	H. influenzae predicted coding region HI0491 [Haemophilus influenzae]	75	55
2	56	52261	51701	gil396321	nusG [Escherichia coli]	75	56

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

20	1	653	414	gil520778	protein p23 [Borrelia burgdorferi]	75	62
20	3	2437	1652	gnlIPIDle2012 49	ORF-C gene product [Borrelia burgdorferi]	75	60
58	1	856	62	gnlIPIDle2012 49	ORF-C gene product [Borrelia burgdorferi]	75	37
68	3	1153	578	gil458217	ORF 2 [Borrelia burgdorferi]	75	55
117	1	744	388	gil520783	unknown [Borrelia burgdorferi]	75	42
130	1	1	684	gnlIPIDle1604 36	orfA gene product [Borrelia burgdorferi]	75	58
2	36	30506	31693	gil1020317	S-adenosylmethionine synthetase [Staphylococcus aureus]	74	57
2	109	111301	109871	gil396501	aspartyl-tRNA synthetase [Thermus aquaticus thermophilus]	74	52
3	101	92143	91103	gil1651962	hypothetical protein [Synechocystis sp.]	74	49
20	5	4080	2974	gnlIPIDle1589 79	orfA gene product [Borrelia burgdorferi]	74	56
36	2	468	1253	gnlIPIDle1589 84	orfC gene product [Borrelia burgdorferi]	74	59
42	1	396	719	gil1655798	CdsK [Borrelia burgdorferi]	74	58
2	10	6810	7022	gil406135	glycoprotein 120 [Simian immunodeficiency virus]	73	53
2	29	23695	21395	gil511145	hemolysin [Serpulina hyodysenteriae]	73	52
3	56	44789	44262	gil1595810	type-I signal peptidase SpsB [Staphylococcus aureus]	73	47
3	73	64881	62341	gnlIPIDle2684 56	unknown [Mycobacterium tuberculosis]	73	54
3	100	89800	91113	gil500705	Similar to Seryl-tRNA synthetase [Saccharomyces cerevisiae]	73	56
3	106	92803	93513	gnlIPIDle2436 81	ORF YGR248w [Saccharomyces cerevisiae]	73	63
4	4	3697	3512	gil562035	NADH dehydrogenase, subunit 5 [Acanthamoeba castellanii]	73	53
7	9	8519	8079	gil694092	emml gene product [Streptococcus pyogenes]	73	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

8	16	17562	17756	gil1500401	reverse gyrase [Methanococcus jannaschii]	73	40
14	3	4280	4438	gil520778	protein p23 [Borrelia burgdorferi]	73	55
19	9	7074	6742	gil1773311	NADH dehydrogenase [Ceanothus cuneatus]	73	36
25	3	2369	2587	gil1655790	CdsC [Borrelia burgdorferi]	73	64
78	2	176	619	gnlPIDie201250	ORF-D gene product [Borrelia burgdorferi]	73	50
108	1	2	382	gil1573074	adhesin B precursor (fimA) [Haemophilus influenzae]	73	41
120	1	97	342	gil1978	heat shock protein 70 [Sus scrofa]	73	46
3	64	51644	54013	gil1574437	sporulation protein (spoIIIE) [Haemophilus influenzae]	72	51
5	6	2899	2654	gil212383	myosin heavy chain [Gallus gallus]	72	41
6	31	22140	21799	gil895748	putative cellobiose phosphotransferase enzyme II' [Bacillus subtilis]	72	46
8	8	8812	9600	gil1655859	Orf1 [Borrelia hermsii]	72	55
10	12	8579	8376	gil536681	ORF YBR257w [Saccharomyces cerevisiae]	72	36
45	2	1440	394	gil1699017	ErpB2 [Borrelia burgdorferi]	72	42
2	2	1342	2796	gil285623	pyruvate kinase [Bacillus stearothermophilus]	71	52
2	31	26272	24911	gilS58522IS58522	glycyl-tRNA synthetase - Thermus thermophilus	71	54
2	64	60156	58684	gil459009	similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]	71	48
3	66	55240	54275	gil217121	ORF1 [Synecococcus elongatus]	71	52
3	104	92345	92175	gil44228	secretion protein Sec Y (AA 1-482) [Mycoplasma capricolum]	71	42
5	43	25567	25734	gil213778	sodium-hydrogen exchange protein-beta [Oncorhynchus mykiss]	71	50
7	3	1179	2384	gil458216	ORF 1 [Borrelia burgdorferi]	71	60
20	4	2964	2392	gil458217	ORF 2 [Borrelia burgdorferi]	71	47
51	2	984	2066	gil1373144	ErpD [Borrelia burgdorferi]	71	41
54	1	251	883	gil145280	ORF1 [Escherichia coli]	71	40

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	54	51233	50538	spIQ06797IRL1_BACSU	50S RIBOSOMAL PROTEIN L1 (BL1).	70	48
2	116	114025	113744	gil1673757	(AE000012) Mycoplasma pneumoniae, phosphocarrier protein HPr; similar to GenBank Accession Number A49683, from M. capricolum [Mycoplasma pneumoniae]	70	41
3	4	1684	2220	gil153906	CheW protein [Salmonella typhimurium]	70	48
3	84	74775	73225	gnlPIDle283919	glycerol kinase [Sulfolobus solfataricus]	70	60
3	107	93500	93273	gil836815	cdc4 gene product which is essential for initiation of DNA replication in yeast [Saccharomyces cerevisiae]	70	35
4	1	926	123	gil167913	Thy1 protein [Dictyostelium discoideum]	70	51
4	47	35616	35807	gil48808	dcIAE gene product [Bacillus subtilis]	70	58
4	65	48320	47976	gil1421734	ORF 5 [Borrelia burgdorferi]	70	48
6	23	16458	15904	gil1655860	Orf2 [Borrelia hermsii]	70	54
17	4	2940	3173	gil1255880	F01G12.6 gene product [Caenorhabditis elegans]	70	40
20	8	5470	5237	gil1236921	Var1p [Saccharomyces douglasii]	70	47
23	5	4173	3970	pirSI6447IS16447	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion	70	47
36	3	1270	1653	gnlPIDle160437	orfD gene product [Borrelia burgdorferi]	70	50
2	69	65752	63860	gil151932	fructose enzyme II [Rhodobacter capsulatus]	69	42
3	114	99712	98150	gil1303856	YqgI [Bacillus subtilis]	69	46
4	36	25614	24694	gil1663561	orf1; product unknown [Borrelia burgdorferi]	69	46
6	21	14584	14204	gil1616644	P30 [Borrelia burgdorferi]	69	47
12	12	7025	7258	gil150176	protein 69 [Mycoplasma hyorhinis]	69	38
12	14	8414	8587	gil13233	ND6 (AA 1 - 296) [Podospira anserina]	69	26
54	2	1332	2402	gnlPIDle158979	orfA gene product [Borrelia burgdorferi]	69	46
2	35	29769	30518	gil473817	'ORF' [Escherichia coli]	68	42
2	79	72330	72980	gil1498049	adenylate kinase [Paracoccus denitrificans]	68	37

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	104	104748	106385	gil1574032	hypothetical [Haemophilus influenzae]	68	42
3	78	68895	68287	gnlPIDle255117	hypothetical protein [Bacillus subtilis]	68	51
3	98	88992	86074	gil927711	D9461.18p; CAI: 0.15 [Saccharomyces cerevisiae]	68	52
3	111	96519	97364	gil1707057	coded for by C. elegans cDNA CEES55F; coded for by C. elegans cDNA yk84a1.3; coded for by C. elegans cDNA yk78g7.3; coded for by C. elegans cDNA yk168g9.5; coded for by C. elegans cDNA yk78g7.5; coded for by C. elegans cDNA yk84a1.5; strong s	68	52
4	56	40648	40046	gil458217	ORF 2 [Borrelia burgdorferi]	68	54
4	57	41916	40678	gil458216	ORF 1 [Borrelia burgdorferi]	68	57
6	24	17296	16520	gil1655859	Orf1 [Borrelia hermsii]	68	43
7	5	2894	3694	gil1655859	Orf1 [Borrelia hermsii]	68	48
29	6	3832	3254	gil458217	ORF 2 [Borrelia burgdorferi]	68	46
72	2	927	1133	gil577175	L8479.4 gene product [Saccharomyces cerevisiae]	68	44
2	57	52752	52558	gil1001264	50S ribosomal protein L33 [Synechocystis sp.]	67	56
3	65	54290	54051	gil710340	ribosomal protein S21 [Myxococcus xanthus]	67	49
3	79	69068	70114	gil460955	TagE [Vibrio cholerae]	67	38
3	81	70653	71150	gil467420	unknown [Bacillus subtilis]	67	42
3	110	94703	96502	gnlPIDle267607	alanyl-tRNA synthetase [Thermus aquaticus thermophilus]	67	51
4	42	30304	31941	bbsl161785	60 kda antigen [Borrelia coriaceae, C053, ATCC 4338, Peptide, 514 aa] [Borrelia coriaceae]	67	49
12	6	3590	2967	gnlPIDle160437	orfD gene product [Borrelia burgdorferi]	67	41
12	9	5524	6276	gil1655859	Orf1 [Borrelia hermsii]	67	51
12	10	6611	6889	gnlPIDle8903	SERA protein [Plasmodium falciparum]	67	48
17	6	4995	5906	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	67	37
34	2	1221	1817	gnlPIDle1589	orfB gene product [Borrelia burgdorferi]	67	47

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

58	2	1347	796	83	ORF 2 [Borrelia burgdorferi]	67	52
2	33	28572	27751	gil458217 gil340613	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	66	40
2	73	69021	69908	gil153903	methyltransferase (cheR; EC 2.1.1.24) [Salmonella typhimurium]	66	42
2	93	93739	94524	gil45713	P.putida genes rpmH, rnpA, 9k, 60k, 50k, gidA, gidB, uncI and uncB [Pseudomonas putida]	66	41
3	9	6009	6902	gnlIPIDle2639 31	OrfD [Streptococcus pneumoniae]	66	47
4	28	20922	20665	gil471731	vacuolating cytotoxin homolog [Helicobacter pylori]	66	50
4	64	47985	47107	gil1421735	ORF 6 [Borrelia burgdorferi]	66	43
6	13	7227	8591	gil1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	66	48
34	4	2556	3161	gil458218	ORF 3 [Borrelia burgdorferi]	66	42
37	1	982	689	gil974334	non-receptor tyrosine kinase [Dictyostelium discoideum]	66	55
3	77	68191	66395	gil1651216	Pz-peptidase [Bacillus licheniformis]	65	47
3	123	105911	104070	gil1575784	DNA mismatch repair protein [Aquifex pyrophilus]	65	45
6	9	5726	7126	gil1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	65	49
8	9	9684	10325	gnlIPIDle2012 50	ORF-D gene product [Borrelia burgdorferi]	65	48
10	1	3	971	gil1373144	ErpD [Borrelia burgdorferi]	65	47
13	5	3956	3411	gil1209872	REV [Borrelia burgdorferi]	65	47
2	76	70509	71069	pirA00547IX YEBET	protein-glutamate methyltransferase (EC 3.1.1.61) - Salmonella typhimurium	64	45
3	61	48610	50838	gil1001335	soluble lytic transglycosylase [Synecocystis sp.]	64	42
4	5	3519	3773	gil1263021	M protein [Streptococcus pyogenes]	64	32
4	53	38288	37824	gil1373141	ORF-10 [Borrelia burgdorferi]	64	50

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

6	10	5985	5824	gil40271	delta-endotoxin CryIG protoxin [Bacillus thuringiensis]	64	30
7	7	7798	4499	gil1041785	rhostry protein [Plasmodium yoelii]	64	35
7	30	19738	19289	gil1209840	2.9-3 ORF-D [Borrelia burgdorferi]	64	46
11	3	1608	2339	gil1652934	hypothetical protein [Synechocystis sp.]	64	30
16	1	537	839	gnlPIDle276380	AARP1 protein [Plasmodium falciparum]	64	44
19	1	308	1177	gil1553115	P35 antigen protein [Borrelia burgdorferi]	64	35
42	3	1928	1788	gil1752736	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w [Saccharomyces cerevisiae]	64	41
142	1	589	2	gil162142	kinetoplast-associated protein [Trypanosoma cruzi]	64	52
2	3	2837	2592	gnlPIDle236274	ZK287.2 [Caenorhabditis elegans]	63	27
2	15	12750	11320	gil1652577	carboxyl-terminal protease [Synechocystis sp.]	63	49
2	32	27753	26266	sp15189ISY E RHIME	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE) (GLURS).	63	48
2	77	71067	72308	gil1041116	TRAB [Plasmid pPDI]	63	34
3	2	1056	58	gil1098641	Bislp [Saccharomyces cerevisiae]	63	43
3	82	71398	71237	gil1339938	EC 1.1.99.5 [Mus musculus]	63	47
3	83	72845	71349	gil763191	glycerol 3 phosphate dehydrogenase [Saccharomyces cerevisiae]	63	37
3	85	75552	74773	gil142997	glycerol uptake facilitator [Bacillus subtilis]	63	45
7	6	3747	4304	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	63	40
7	38	24123	24956	gil467330	replicative DNA helicase [Bacillus subtilis]	63	40
11	5	4161	3853	gil1592217	bifunctional protein [Methanococcus jannaschii]	63	38
12	13	9558	7906	gil633167	adenine deaminase [Bacillus subtilis]	63	48
32	1	753	268	gil520783	unknown [Borrelia burgdorferi]	63	42
2	68	63866	62745	gil146722	phosphomannose isomerase [Escherichia coli]	62	45
2	75	69920	70573	gil145524	cheB peptide [Escherichia coli]	62	28

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	95	96334	95492	gil40031	spoJ93 gene product [Bacillus subtilis]	62	36
3	67	57341	55212	gil1574144	single-stranded-DNA-specific exonuclease (recJ) [Haemophilus influenzae]	62	40
3	76	66414	65677	gil1477770	unknown [Helicobacter pylori]	62	37
6	1	1762	104	gil1072419	gleB gene product [Staphylococcus carnosus]	62	43
18	4	4431	5144	gil1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	62	36
19	8	6743	6976	gil1513302	CigB [Dictyostelium discoideum]	62	56
20	6	4563	4378	bbs144872	Fu=putative serine/threonine kinase [Drosophila melanogaster, Peptide Partial Mutant, 152 aa] [Drosophila melanogaster]	62	37
81	1	56	538	gnlPIDle153957	ORF-A gene product [Borrelia burgdorferi]	62	36
106	2	586	356	gil151158	repeat organellar protein [Plasmodium chabaudi]	62	43
114	1	138	629	gnlPIDle153957	ORF-A gene product [Borrelia burgdorferi]	62	36
2	117	114352	114032	gil173128	ubiquitin-specific processing protease [Saccharomyces cerevisiae]	61	32
3	55	42737	44236	gil143999	dnaK homologue [Borrelia burgdorferi]	61	41
3	57	44821	46083	gil1653709	lipoprotein NlpD [Synecocystis sp.]	61	50
3	125	110052	109261	gil1303863	YqgP [Bacillus subtilis]	61	45
4	63	47119	46478	gil1421736	ORF 7 [Borrelia burgdorferi]	61	34
7	35	21496	22971	gil1655797	CdsJ [Borrelia burgdorferi]	61	44
8	7	8300	8872	gil458217	ORF 2 [Borrelia burgdorferi]	61	48
12	8	5006	5551	gil458217	ORF 2 [Borrelia burgdorferi]	61	50
14	10	9398	8652	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	61	44
15	12	6206	4377	gil836624	methyltransferase [Bacillus aneurinolyticus]	61	38
16	4	2449	2240	gil1066497	Similar to S. cerevisiae hypothetical protein Ykl012p (Swiss Prot. accession number P33203) and C. elegans hypothetical protein ZK1098.1 (Swiss Prot. accession number P34600) [Saccharomyces	61	38

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

29	4	2323	1853	gnlPIDle1604 37	cerevisiae]	orfD gene product [Borrelia burgdorferi]	61	45
50	2	1374	1156	gnlPIDle2763 80	AARPI protein [Plasmodium falciparum]		61	52
2	18	14371	15369	gil1573923	prolipo protein diacylglycerol transferase (lgt) [Haemophilus influenzae]		60	57
3	118	101571	100690	gil1001260	hypothetical protein [Synechocystis sp.]		60	47
3	120	101692	102273	gil1399829	elongation factor P [Synechococcus PCC7942]		60	34
6	32	21869	22162	gil192960	L-type calcium channel alpha-1 [Mus musculus]		60	50
7	37	23373	24101	gil458217	ORF 2 [Borrelia burgdorferi]		60	40
8	11	13570	13851	gil1065989	(pos:5995..5997,aa:Met) [Bacillus subtilis]		60	47
14	5	5327	5091	gil147158	pfs [Escherichia coli]		60	51
15	7	3316	2984	gil153727	M protein [group G streptococcus]		60	36
27	3	2744	3772	pirS40422IS4 0422	hypothetical protein - Staphylococcus aureus		60	31
2	62	57446	58672	gil143002	proton glutamate symport protein [Bacillus caldotenax]		59	34
2	82	74989	74051	gil1651878	regulatory components of sensory transduction system [Synechocystis sp.]		59	38
2	89	92119	91322	gil467425	unknown [Bacillus subtilis]		59	38
2	92	93010	93663	pirA30191IA3 0191	hypothetical protein L - Bacillus subtilis (fragment)		59	39
2	118	115604	114315	gil39269	sigma factor (ntrA) (AA 1-502) [Azotobacter vinelandii]		59	35
4	41	29875	29210	gil1209831	lipoprotein [Borrelia burgdorferi]		59	34
6	4	3323	2058	gil624056	contains 4 ankyrin repeats; similar to D. melanogaster notch protein, Swiss-Prot Accession Number P07027 [Paramecium bursaria Chlorella virus 1]		59	37
6	25	17793	17257	gnlPIDle2012 48	ORF-B gene product [Borrelia burgdorferi]		59	43

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

6	33	22493	22125	gil153677	enzyme III [Streptococcus mutans]	59	36
10	9	6241	6026	gil1339977	skeletal myosin heavy chain [Thunnus thynnus]	59	40
19	6	5383	5970	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	59	30
25	7	4008	3742	gil1055144	similar to galactoside 3(4)-L-fucosyltransferase [Caenorhabditis elegans]	59	37
59	1	835	8	gil1359436	Mag44 [Dermatophagoides farinae]	59	24
2	27	21414	20317	gil974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis]	58	41
3	5	2156	3049	gil1653618	hypothetical protein [Synecocystis sp.]	58	35
3	109	93822	94718	gil790935	flgG [Treponema denticola]	58	31
4	3	2423	3340	gil1553115	P35 antigen protein [Borrelia burgdorferi]	58	39
4	35	24696	24238	gil1663562	orfII; product unknown [Borrelia burgdorferi]	58	32
4	46	35509	34904	gnlPIDle264708	myosin heavy chain [Sus scrofa]	58	31
15	8	3683	3468	gil457336	Pv200 [Plasmodium vivax]	58	32
50	3	1941	1498	gnlPIDle220350	brca2 gene product [Homo sapiens]	58	41
55	1	2322	247	gil1522636	M. jannaschii predicted coding region MJEC502 [Methanococcus jannaschii]	58	32
2	53	50563	50045	gil786163	Ribosomal Protein L10 [Bacillus subtilis]	57	29
3	117	100606	99710	gil1303855	YqgH [Bacillus subtilis]	57	30
6	38	26564	26232	gil1499632	M. jannaschii predicted coding region MJ0809 [Methanococcus jannaschii]	57	40
8	10	12350	13117	gil1553115	P35 antigen protein [Borrelia burgdorferi]	57	33
11	4	3183	2470	pirA45605/A45605	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	57	35
14	8	7117	7899	gil1553115	P35 antigen protein [Borrelia burgdorferi]	57	36
15	6	3027	2818	gnlPIDle261409	nuclear/mitotic apparatus protein [Xenopus laevis]	57	30
17	1	336	1178	gil473817	ORF [Escherichia coli]	57	31
20	2	1654	1064	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]	57	34

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

2	111	113765	111636	gil148316	NaH-antiporter protein [Enterococcus hirae]	56	32
3	80	70112	70669	gil1372995	OrfH [Borrelia burgdorferi]	56	24
3	116	98976	99212	pinE22845IE2 2845	hypothetical protein 4 - Trypanosoma brucei mitochondrion (SGC6)	56	36
6	26	18732	17791	gil1655797	CdsJ [Borrelia burgdorferi]	56	41
7	21	14706	13510	gil1574247	H. influenzae predicted coding region HI1410 [Haemophilus influenzae]	56	32
11	8	6722	7087	gnlPIDle2428 97	aBIM [Lactococcus lactis]	56	28
53	7	2446	2018	gil1421737	ORF 8 [Borrelia burgdorferi]	56	38
61	2	712	1410	gil583161	albumin binding protein [unidentified]	56	35
2	6	3866	3573	gil290487	50S ribosomal subunit protein L28 [Escherichia coli]	55	37
2	14	11322	10585	gil1303811	YqeU [Bacillus subtilis]	55	33
2	34	28640	29782	gil558266	orf gene product [Wolinnella succinogenes]	55	30
2	71	66669	67415	gil397486	endonuclease G [Bos taurus]	55	33
3	87	75924	76550	gil403984	deoxyguanosine kinase/deoxyadenosine kinase(I) subunit [Lactobacillus acidophilus]	55	38
4	66	48434	48958	gil1100900	70 kDa heat shock protein [Theileria parva]	55	32
140	1	322	68	gil15611	gene 17, tail fiber protein [Bacteriophage T7]	55	38
4	34	24244	23867	gil1663563	orfIII; product unknown [Borrelia burgdorferi]	54	31
5	9	5510	4179	gil1513238	ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number Z49132 [Dictyostelium discoideum]	54	25
5	45	27187	25895	gnlPIDle2614 09	nuclear/mitotic apparatus protein [Xenopus laevis]	54	30
7	28	17905	18162	gil36501	C protein [Homo sapiens]	54	41
11	6	4415	5215	gil1707287	putative outer membrane protein [Borrelia burgdorferi]	54	25
19	2	1674	2501	gil392799	G5/D6 ORF [Dictyostelium discoideum]	54	25
29	5	3284	2532	gnlPIDle1589 80	orfC gene product [Borrelia burgdorferi]	54	33
31	3	3328	4137	pirS41649IS4	DNA polymerase - Plasmodium falciparum	54	28

				1649		bud-emergence protein [Saccharomyces cerevisiae]			
32	5	2560	2865	gil499695		Rpilp [Saccharomyces cerevisiae]		54	36
95	1	95	997	gil763227		YlxH [Borrelia burgdorferi]		54	37
2	16	13235	14383	gil1165254		orf 06111 gene product [Saccharomyces cerevisiae]		53	33
2	72	68814	68179	gil940842		cell division protein J [Methanococcus jannaschii]		53	28
3	3	1032	1646	gil1592021		vacuolar aspartic proteinase precursor [Candida albicans]		53	32
4	18	14627	14427	gil1039462		ErpB2 [Borrelia burgdorferi]		53	35
5	63	34850	34152	gil1699017		XLR related protein [Mus musculus]		53	25
10	5	3672	3893	gil398581		TOTC12.4 [Caenorhabditis elegans]		53	27
15	17	8485	8925	gnlPIDle2483 24		coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; similar to matrix F/G (DNA binding protein, SP:MAFG_RAT, Q00910) [Caenorhabditis elegans]		53	28
25	5	3497	3679	gil1055100		XLR related protein [Mus musculus]		53	25
29	1	70	291	gil398581		Orf1 [Borrelia hermsii]		53	27
34	3	1787	2527	gil1655859		fibrinectin/fibrinogen-binding protein [Streptococcus pyogenes]		53	42
2	1	3	1265	gil496254		asparyl-tRNA synthetase (aspS) [Haemophilus influenzae]		52	29
2	110	111638	111276	gil1573287		rhoptry protein [Plasmodium yoelii]		52	35
4	8	5323	6150	gil457146		repeat organellar protein [Plasmodium chabaudi]		52	24
4	44	32562	31999	gil1151158		ORF YGR023w [Saccharomyces cerevisiae]		52	26
7	29	18485	18808	gnlPIDle2439 27		YHR146w gene product [Saccharomyces cerevisiae]		52	26
25	4	3287	3499	gil500655		NADH dehydrogenase, subunit 5 [Allomyces macrogynus]		52	35
92	2	38	241	gil1236411		NADH dehydrogenase, subunit 5 [Allomyces macrogynus]		52	52
148	2	119	322	gil1236411		chromate resistance protein A [Methanococcus		52	52
2	120	116131	115577	gil1591434				51	29

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

					jannaschii]				
4	9	6362	7153	gil1553115	P35 antigen protein [Borrelia burgdorferi]			51	26
10	10	6603	7196	gnlPIDle256393	anti-P.falci-parum antigenic polypeptide [Saimiri sciureus]			51	34
11	12	10333	9422	pirA42771A42771	reticulocyte-binding protein 1 - Plasmodium vivax			51	31
19	7	5919	6179	gil173241	ZIP1 protein [Saccharomyces cerevisiae]			51	38
23	1	3	287	gil1498320	cell wall-associated protease precursor [Bacillus subtilis]			51	25
2	105	106383	107126	gil580905	B.subtilis genes rpmH, rnpA, 50kd, gidA and gidB [Bacillus subtilis]			50	32
3	1	1	195	gnlPIDle220201	rps5 gene product [Plasmodium falciparum]			50	38
3	62	50808	51653	gil882579	CG Site No. 29739 [Escherichia coli]			50	31
3	119	100766	101014	gil1086864	T03G11.2 gene product [Caenorhabditis elegans]			50	39
4	32	23555	22992	gil1663565	orfV; product unknown [Borrelia burgdorferi]			50	36
5	8	4168	3470	gil49402	M1.1 protein [Streptococcus pyogenes]			50	27
10	7	5190	4612	gnlPIDle158981	orfE gene product [Borrelia burgdorferi]			50	28
11	2	1277	504	gil1553115	P35 antigen protein [Borrelia burgdorferi]			50	26
13	3	1948	1634	gnlPIDle268243	p21 [Borrelia afzelii]			50	32
92	3	582	941	gnlPIDle201250	ORF-D gene product [Borrelia burgdorferi]			50	40
148	1	339	4	gnlPIDle236901	unknown [Saccharomyces cerevisiae]			50	34
28	3	2001	2630	gil499325	STARP antigen [Plasmodium falciparum]			49	22
3	10	6881	7180	gil156218	putative [Caenorhabditis elegans]			48	32
3	75	65683	65066	gil1574476	dedA protein (dedA) [Haemophilus influenzae]			48	22
3	112	97006	96743	gil915207	gastric mucin [Sus scrofa]			48	27
7	23	14743	14970	gil172294	protein-tyrosine phosphatase [Saccharomyces cerevisiae]			48	33

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

11	11	7980	9293	gil1046137	M. genitalium predicted coding region MG422 [Mycoplasma genitalium]	48	28
28	4	2628	2825	gil1591322	chorismate mutase subunit B [Methanococcus jannaschii]	48	30
2	8	5526	6677	gnllPIDle220245	frameshift [Plasmodium falciparum]	47	27
2	60	55075	55803	gil710551	ankyrin 3 [Mus musculus]	47	29
2	94	94515	95240	gil1592264	type I restriction enzyme [Methanococcus jannaschii]	47	34
4	11	9057	9941	gil1553115	P35 antigen protein [Borrelia burgdorferi]	47	32
2	12	9986	9471	gil1022328	Four tandem repeats of a DNA-binding domain known as the AT-hook are found at the carboxy terminus of CarD. This protein has been purified and found to bind in vitro to a promoter region [Myxococcus xanthus]	46	28
3	89	78904	77324	gil1573271	apolipoprotein N-acyltransferase (cute) [Haemophilus influenzae]	46	32
6	36	24361	25719	gil1592272	ribosomal protein S19 [Methanococcus jannaschii]	46	23
10	13	9895	8816	gil160299	glutamic acid-rich protein [Plasmodium falciparum]	46	21
13	4	3412	3648	gnllPIDle275506	C41G6.i [Caenorhabditis elegans]	46	37
138	1	632	15	gil157006	bicaudalD protein [Drosophila melanogaster]	46	23
3	124	109271	105909	gil1499043	M. jannaschii predicted coding region MJ0263 [Methanococcus jannaschii]	45	23
4	17	14212	15465	pirIS30782IS30782	integrin homolog - yeast (Saccharomyces cerevisiae)	45	23
23	4	3950	4852	gnllPIDle236901	unknown [Saccharomyces cerevisiae]	45	27
92	1	258	4	gnllPIDle236901	unknown [Saccharomyces cerevisiae]	45	27
3	90	79020	81044	gnllPIDle236483	F54G8.4 [Caenorhabditis elegans]	44	31
12	7	4075	5019	gil1151158	repeat organellar protein [Plasmodium chabaudi]	44	26

Borrelia burgdorferi - Putative coding regions of novel proteins similar to known proteins

17	3	1735	2142	pirIA42771IA4 2771	reticulocyte-binding protein 1 - Plasmodium vivax	44	26
22	7	4179	2827	gil563812	XCAP-C [Xenopus laevis]	44	20
31	2	1682	2761	gil1438951	cutinase negative acting protein [Fusarium solani f. sp. pisi]	43	23
3	7	4086	5186	gil343962	VARI protein [Candida glabrata]	42	25
28	1	110	496	gil157804	laminin B2 chain [Drosophila melanogaster]	42	23
28	5	2889	3833	pirS30782IS3 0782	integrin homolog - yeast (Saccharomyces cerevisiae)	42	18
34	1	209	1234	gil1655797	CdsJ [Borrelia burgdorferi]	42	27
65	3	1035	1415	gil1654220	variable major protein 16 [Borrelia hermsii]	42	34
2	11	9544	8486	gnlPIDle1632 6	MURF2 protein (AA 1-348) [Crithidia fasciculata]	41	26
3	122	104072	103017	gil1151158	repeat organellar protein [Plasmodium chabaudi]	41	20
18	6	5122	6366	gil1591494	M. jannaschii predicted coding region MJ0797 [Methanococcus jannaschii]	40	20
6	6	4662	3964	gil600448	var1 protein (aa 1-339) [Candida utilis]	39	24
4	10	7637	8914	gil1293695	microfilament sheath protein SHP3 [Litomosoides sigmodontis]	37	19

TABLE 5. Borrelia burgdorferi - Coding regions containing to know proteins

Contig ID	Orf ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length
2	20	15372	17402	gb M90084	Borrelia burgdorferi 22 kD antigen	100	786
2	21	16672	16310	gb M90084	Borrelia burgdorferi 22 kD antigen	100	56
2	22	17362	17099	gb M90084	Borrelia burgdorferi 22 kD antigen	100	264
2	23	17415	17876	emb X70826 B BLA7	B.burgdorferi gene for lipoprotein	100	57
2	24	18522	17923	emb X70826 B BLA7	B.burgdorferi gene for lipoprotein	100	600
2	25	18606	20009	emb X78708 B BYSCI	B.bergdorferi (ZS7) YSC1-like gene	100	1404
2	26	19981	20295	emb X78708 B BYSCI	B.bergdorferi (ZS7) YSC1-like gene	99	314
2	38	32899	32174	gb U49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	98	130
2	39	33315	32863	gb U49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	100	453
2	40	34718	33333	gb U49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1386
2	41	36211	34751	gb U49938	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1461
2	42	36899	36288	gb L24194	Borrelia burgdorferi immunodominant antigen P39	99	606

Borrelia burgdorferi - Coding regions containing to know proteins

2	43	37335	36811	gblL35050l	gene, complete cds	98	457
2	44	38426	37401	gblL24194l	Borrelia burgdorferi (clone pB46) membrane lipoprotein A (bmpA) gene, 3' end, membrane lipoprotein (bmpB) gene, 5' end	99	1026
2	45	39595	38462	gblU49938l	Borrelia burgdorferi immunodominant antigen P39 gene, complete cds	99	1134
2	46	40947	39838	gblU35450l	Borrelia burgdorferi potential virulence gene cluster membrane proteins BmpC (bmpC) and BmpA (bmpA), BmpB protein (bmpB), putative protein 4, Mg ion transporter MgtE (mgtE), protein kinase C1 inhibitor PKCI (pkci) genes, complete cds	99	1110
2	47	41461	40961	gblU35450l	Borrelia burgdorferi membrane protein D (bmpD) gene, complete cds	100	82
2	49	46052	41901	gblL48488l	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta subunit (rpoC) gene, 5' end of cds	97	76
2	51	49535	46050	gblL48488l	Borrelia burgdorferi RNA polymerase beta subunit (rpoB) gene, complete cds, RNA polymerase beta subunit (rpoC) gene, 5' end of cds	98	2490
2	83	79470	74977	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	97	131
2	84	84351	84620	gblM88330l	Borrelia burgdorferi 23S ribosomal RNA gene	100	270
2	85	86923	86066	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	95	386
2	86	87637	87041	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	99	209

Borrelia burgdorferi - Coding regions containing to know proteins

2	87	88424	88116	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	96	210
2	88	91249	90680	gblU03396l	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile-tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	100	570
2	96	98846	96393	embZ12165IB BGYRAG	B. burgdorferi gyrA gene encoding DNA gyrase subunit A (partial)	96	289
2	97	100759	98837	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	98	904
2	98	100893	102389	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	1497
2	99	102618	103787	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	99	1170
2	100	103786	103607	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	180
2	101	103866	104177	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	312

Borrelia burgdorferi - Coding regions containing to know proteins

2	102	104254	104424	gblU04527l	ribosomal protein L34 (rpmH) genes, complete cds	100	171
2	103	104393	104764	gblU04527l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	148
3	11	7200	8597	gblU43739l	Borrelia burgdorferi 212 DNA gyrase b subunit (gyrB) and ribonuclease P protein component (rnpA) genes, partial cds, DnaA protein (dnaA), DNA polymerase III beta subunit (dnaN), and ribosomal protein L34 (rpmH) genes, complete cds	100	1185
3	12	8581	9666	emblX96685lB BCDG	Borrelia burgdorferi fesmid clone 31, complete sequence	99	912
3	13	9664	10767	emblX96685lB BCDG	B.burgdorferi cell division genes	99	1104
3	14	10826	10614	emblX96433lB BFTSWQA	B.burgdorferi ftsW, ftsQ & ftsA genes	100	213
3	15	10797	11546	emblX96433lB BFTSWQA	B.burgdorferi ftsW, ftsQ & ftsA genes	99	750
3	16	11519	12787	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1269
3	17	12785	14008	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1224
3	18	14006	14701	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	696
3	19	14699	15655	gblL76303l	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flhEFGHI, flbABC genes, complete cds	98	712
3	20	15653	16213	gblU43739l	Borrelia burgdorferi fesmid clone 31, complete sequence	100	561
3	21	16149	17552	emblX96685lB BCDG	B.burgdorferi cell division genes	97	1404

Borrelia burgdorferi - Coding regions containing to know proteins

3	22	17550	17993	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	444
3	23	17996	18475	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	480
3	24	18445	18822	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	378
3	25	18777	20546	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	1770
3	26	20544	21596	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1053
3	27	21575	22531	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	957
3	28	22529	23860	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1332
3	29	23836	24288	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	453
3	30	24269	24898	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	630
3	31	24864	26084	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	99	1221
3	32	26095	26541	gblL76303	Borrelia burgdorferi ftsA gene, 3' end of cds, ftsZ, orf230, smf, hslVU, flgBCE, flieFGHI, flbABC genes, complete cds	100	447
3	33	26525	27874	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1350
3	34	27891	28121	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	231
3	35	28112	28900	gblU43739	Borrelia burgdorferi fesmid clone 31, complete sequence	100	789

Borrelia burgdorferi - Coding regions containing to know proteins

3	36	28894	29682	gbU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	789
3	37	29680	30267	gbU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	588
3	38	30302	31363	gbU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1062
3	39	31403	31750	gbU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	348
3	40	31728	32369	gbU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	642
3	41	32356	33144	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	99	789
3	42	32642	32436	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	100	207
3	43	33129	33416	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	100	288
3	44	33425	34237	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	100	813
3	45	34320	34072	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	100	249
3	46	34222	35355	gbIL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flil, flim, fliz, flagellar export apparatus (fliPQR, flhB), flhF, flbE genes	99	1134

Borrelia burgdorferi - Coding regions containing to know proteins

3	47	35349	37457	gblL75945I	Borrelia burgdorferi flagellar hook protein (flgE), flbD, flagellar motor apparatus (motAB), flilL, flilM, fliz, flagellar export apparatus (flpQR, flhB), flhF, flbE genes	100	2109
3	48	37455	38627	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1173
3	49	38612	39526	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	99	816
3	50	39765	39421	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	345
3	51	39524	40012	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	489
3	52	39985	41919	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	1935
3	53	41928	42248	gblU43739I	Borrelia burgdorferi fesmid clone 31, complete sequence	100	286
3	58	47505	46090	gblM28682I	B. burgdorferi promoter element DNA	100	78
3	68	57596	60034	gblL77216I	Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	99	2439
3	69	62374	60023	gblL77216I	Borrelia burgdorferi (strain B31) protease (lon) gene, complete cds	100	274
3	92	82181	83026	gblU35673I	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	542
3	93	83032	83358	gblU35673I	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	327
3	94	83365	83697	gblU48651I	Borrelia burgdorferi PIG histone-like protein HBbu (hbb) gene, complete cds	100	327
3	95	83695	84105	gblU35673I	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	411
3	96	84167	85732	gblU35673I	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	99	1566
3	97	85778	86038	gblU35673I	Borrelia burgdorferi OrfR gene, partial cds, and S20, Hbb, OrfH and Rho genes, complete cds	100	106

Borrelia burgdorferi - Coding regions containing to know proteins

4	2	1935	1147	gblU611421	Borrelia burgdorferi outer membrane porin protein Oms28 precursor (oms28) gene, complete cds	99	789
4	12	10037	11002	gblU594871	Borrelia burgdorferi P35 antigen protein gene, and 7.5 kDa lipoprotein gene, complete cds	100	966
4	13	11365	11153	gblU598591	Borrelia burgdorferi strain B31 6.6 kDa lipoprotein gene, complete cds	100	213
4	14	11577	12230	gblU594871	Borrelia burgdorferi P35 antigen protein gene, and 7.5 kDa lipoprotein gene, complete cds	100	373
4	15	12578	13414	gblM852161	Borrelia burgdorferi 27kD protein antigen gene (p27), complete cds	78	370
4	16	13511	13753	gblU224511	Borrelia burgdorferi 49kb linear plasmid small 12kDa lipoprotein gene, complete cds	99	243
4	23	18668	17793	gblL314271	Borrelia burgdorferi (clone BbK2.1) phoA fusion protein gene, partial cds	100	169
4	49	36694	36347	gblU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	99	329
4	50	36351	36929	gblU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	99	564
4	51	36838	36692	gblU758671	Borrelia burgdorferi decorin binding protein B (DbpB) gene, complete cds	100	147
4	52	37001	37624	gblU758661	Borrelia burgdorferi decorin binding protein A (DbpA) gene, complete cds	93	533
4	55	40073	39318	gblU425991	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	69	731
4	58	43349	42447	gblL231371	Borrelia burgdorferi (27985CT2) OspA gene, 3' end and OspB gene, complete cds	99	903
4	59	44228	43347	embIA040091A04009	B. burgdorferi OspA gene and 5'flanking region	100	882
4	60	44792	44403	gblL197021	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete cds	88	370
4	61	45198	44758	gblL197021	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete	89	375

Borrelia burgdorferi - Coding regions containing to know proteins

4	62	46440	45382	gblL19702l	cds	Borrelia burgdorferi outer surface protein A (ospA) and outer surface protein B (ospB) genes, complete cds	85	622
4	67	49363	50622	gblL34016l	cds	Borrelia burgdorferi (clone 8) S1 gene, complete cds	99	1260
4	68	50708	51580	gblL34017l	cds	Borrelia burgdorferi (clone 8) S2 gene, complete cds	99	837
4	69	52203	51655	gblL31423l	cds	Borrelia burgdorferi (clone BbK2.14) phoA fusion protein gene, partial cds	99	292
4	70	53018	52488	gblL41151l	cds	Borrelia burgdorferi (clone 8) s3 gene, complete cds	99	297
5	1	535	71	gblU60642l	cds	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	91	465
5	2	1526	546	gblU60642l	cds	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	89	374
5	4	2395	2129	gblL31425l	cds	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	98	135
5	11	6832	6542	gblS66708l	cds	{target sequence for detection of Lyme disease agent} [Borrelia burgdorferi, B31, 30-kb circular plasmid pIP87, Plasmid, 416 nt]	97	290
5	12	7422	6817	gblU44914l	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	87	595
5	13	8167	7565	gblU44914l	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	84	147
5	14	9408	8284	gblU44914l	cds	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	72	568
5	15	10122	9427	gblU30617l	cds	Borrelia burgdorferi BbK2.11 (bbk2.10), complete cds	93	560
5	16	10533	11324	gblU44912l	cds	Borrelia burgdorferi plasmid cp32-1, erpA and erpB genes, complete cds	93	790
5	17	11590	11330	gblU44913l	cds	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	95	261

Borrelia burgdorferi - Coding regions containing to know proteins

5	18	11761	11588	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	96	173
5	19	13256	11808	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	95	1431
5	20	14187	13636	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	552
5	21	14727	14185	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	511
5	22	15588	14788	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	99	801
5	23	16097	15519	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	98	579
5	24	17276	16158	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94	1075
5	25	17558	18526	gblU45425I	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	86	927
5	26	19040	18564	gblU45422I	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	379
5	27	19712	19116	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	85	596
5	28	20164	19775	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	390
5	29	20504	20121	gblU45426I	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	99	384
5	30	20799	20446	gblU96714I	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	99	354
5	31	21006	20797	gblU45426I	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	97	210
5	32	21903	21076	gblU96714I	Borrelia burgdorferi B31 BlyA (blyA) and BlyB	95	440

Borrelia burgdorferi - Coding regions containing to know proteins

5	33	21470		21625	gblU96714I	(blyB) genes, complete cds			
						Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	94	151	
5	34	22518		22051	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90	467	
5	35	22806		22516	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	93	286	
5	36	23082		22840	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	242	
5	37	23397		23080	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	96	317	
5	38	23768		23388	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	381	
5	39	24331		23750	gblU45421I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90	495	
5	51	29986		29417	gblU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97	300	
5	52	30414		29980	gblU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	99	435	
5	53	30803		30357	gblU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97	447	
5	54	31204		30740	gblU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	465	
5	55	31775		31215	gblU60642I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374	
5	59	33577		32804	gblL31425I	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds	87	135	

Borrelia burgdorferi - Coding regions containing to know proteins

6	16	9678	9022	gblU01894l	Borrelia burgdorferi B31 outer surface protein C (ospC) gene, complete cds	100	657
6	17	9836	11425	gblL25883l	Borrelia burgdorferi 26 kb plasmid GMP synthetase (guaA) gene, complete cds	98	1590
6	18	11435	12664	gblU13372l	Borrelia burgdorferi 26 kb plasmid IMP dehydrogenase (guaB) gene, partial cds	100	1212
6	19	12195	11686	gblU13372l	Borrelia burgdorferi 26 kb plasmid IMP dehydrogenase (guaB) gene, partial cds	100	510
7	1	695	3	gblU85588l	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	99	693
7	2	1081	677	gblU85588l	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	98	375
7	39	25041	25847	gblU45423l	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	77	437
8	2	1420	746	gblU45424l	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	80	193
8	12	14287	14087	gblU84396l	Borrelia burgdorferi 16 kb plasmid DNA fragment	95	140
8	17	18352	17876	gblU85588l	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	96	362
9	1	2815	2507	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	309
9	2	3522	2767	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	756
9	3	5188	5862	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	675
9	4	6809	7255	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	447
9	5	8621	7467	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	1155
9	6	9079	8735	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	345

Borrelia burgdorferi - Coding regions containing to know proteins

9	7	10224	9214	gblU43414I	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	911
9	8	10370	10972	gblU43414I	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	603
9	9	11844	11107	gblU43414I	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	738
9	10	13299	13027	gblU43414I	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	273
9	11	13612	13241	gblU43414I	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	372
10	2	2164	1604	gblU45422I	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	78	278
10	3	2686	2886	gblU12332I	Borrelia burgdorferi 16 kb plasmid hypothetical protein gene, complete cds	97	143
13	1	3	842	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	91	290
13	2	1525	983	gblU16625I	Borrelia burgdorferi exported neurotoxin-like protein gene, complete cds	99	531
13	6	4098	4901	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	86	713
13	7	4691	4467	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	88	224
13	8	6348	5041	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	82	1202
13	9	6673	7788	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	81	519
13	10	7786	8355	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	78	414
13	11	8393	8968	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	84	576
13	12	9290	9544	gblU03641I	Borrelia burgdorferi lp21 circular plasmid, complete sequence	91	210

Borrelia burgdorferi - Coding regions containing to know proteins

14	6	5768	6217	gbL316161	Borrelia burgdorferi protein p23 gene, complete cds	89	396
14	7	6126	6671	gbL316161	Borrelia burgdorferi protein p23 gene, complete cds	85	242
16	5	3660	2854	gbIM974521	Borrelia burgdorferi outer surface protein D (ospD) gene, complete cds	100	807
19	3	3136	3657	gbL411511	Borrelia burgdorferi (clone 8) s3 gene, complete cds	77	267
21	1	849	4	gbU609631	Borrelia burgdorferi plasmid cp32-1 PCR target site, partial sequence	95	296
21	2	1427	834	gbU449141	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	93	594
21	3	2168	1581	gbU449141	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	83	130
21	4	2946	2257	gbU809561	Borrelia burgdorferi strain 297CH putative outer membrane protein (ospF) gene, complete cds	91	350
21	5	3794	2964	gbU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	100	401
21	6	4334	5143	gbU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	99	413
21	7	5362	5183	gbU449131	Borrelia burgdorferi plasmid cp32-4, erpH gene, complete cds	91	180
21	8	5581	5360	gbU425991	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	97	221
22	1	306	4	gbU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	303
22	2	664	317	gbU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	336
22	3	1230	658	gbU454211	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	406
24	1	69	4058	gbU764061	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete	97	2305

Borrelia burgdorferi - Coding regions containing to know proteins

24	2	4056	5108	gblU764061	sequence	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	94	750
25	1	383	760	gblU434141	complete sequence	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	378
25	2	1333	1536	gblU434141	complete sequence	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	204
26	1	684	82	embIX871271B BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96	603
26	2	903	682	embIX871271B BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96	221
26	4	2181	2573	gblAF0002701		Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	94	362
26	5	3073	2621	gblU454271		Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	80	220
26	6	3745	3149	gblU454231		Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	87	478
26	8	4663	4355	gblU454241		Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	98	309
27	1	997	434	gblL316151		Borrelia burgdorferi (clone BbK2.5-6) unknown protein gene, complete cds	96	219
27	2	1395	2258	gblL316161		Borrelia burgdorferi protein p23 gene, complete cds	98	610
30	1	252	686	embIX871271B BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	97	419
30	2	760	1545	embIX871271B BPBRGEA		B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	100	786
30	3	1543	2157	embIX871271B		B. burgdorferi repeated DNA element, 30.5 kb	100	615

Borrelia burgdorferi - Coding regions containing to know proteins

30	4	2158	BPBRGEA	circular plasmid copy			
30	5	3247	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	100	645	
33	1	450	4230 gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	95	976	
33	2	1008	995 gblU72996I	Borrelia burgdorferi plasmid cp32-5, erpI gene, complete cds	100	546	
33	3	2253	2159 gblU78764I	Borrelia burgdorferi plasmid cp32-1, erpA and erpB2 genes, complete cds	100	1152	
33	4	3050	2882 gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	98	379	
35	1	3	3628 gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	93	577	
35	2	976	176 gblU03396I	Borrelia burgdorferi B31 Ala-tRNA (alaT), Ile- tRNA (ileT), 16S rRNA, 23S rRNA (rrlA and rrlB), and 5S rRNA (rrfA and rrfB) genes, complete sequence	91	174	
36	1	1	737 gblM88330I	Borrelia burgdorferi 23S ribosomal RNA gene	100	240	
38	1	672	525 embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	77	159	
38	2	850	28 gblU44914I	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	92	571	
38	3	1516	653 gblU42598I	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	100	133	
38	4	2200	983 embIX82409IB BOSPG	B.burgdorferi ospG and bapA genes	100	534	
38	5	2602	1604 embIX82409IB BOSPG	B.burgdorferi ospG and bapA genes	100	597	
39	1	967	3132 gblU42598I	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	99	529	
39	2	1505	665 embIX87202IB BBRGBCDE	B.burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	97	170	
39	3		957 embIX87202IB	B.burgdorferi plasmid, orfA, B, C, D, E, & G	89	176	

Borrelia burgdorferi - Coding regions containing to know proteins

39	3	2353	1553	BBRGBCDE gblU42599l	genes, clone pOMB10 Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	91	137
39	4	2574	2284	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94	291
39	5	2874	2572	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	91	284
39	6	3028	2861	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	93	168
40	1	596	132	gblU76406l	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	100	465
40	2	1753	575	gblU76406l	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	100	1179
40	3	3000	1732	gblU76406l	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	1269
41	1	1	411	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	99	411
41	2	342	1127	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	80	785
41	3	1172	1747	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	80	572
41	4	1745	2338	gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	65	571
42	2	1133	1384	gblU85588l	Borrelia burgdorferi transposase-like protein (tra) gene, partial cds	93	236
43	1	360	4	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	96	356
43	2	635	1741	gblAF000270l	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like	90	392

Borrelia burgdorferi - Coding regions containing to know proteins

43	3	2242	1784	gblU45423I	orfI gene, partial cds		85	421
43	4	2860	2318	gblU45421I	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds		95	259
44	1	1158	178	gblU60642I	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds		89	374
44	3	2531	1761	gblL31425I	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb		99	135
45	1	287	3	gblU78764I	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds		84	153
45	3	2037	1453	gblL13924I	Borrelia burgdorferi plasmid cp32-1, erpA and erpB2 genes, complete cds		90	386
45	4	2663	2893	gblU44912I	Borrelia burgdorferi outer surface protein E (OspE) gene, complete cds		90	230
46	1	174	338	gblU42599I	Borrelia burgdorferi plasmid cp32-1, erpA and erpB genes, complete cds		96	91
46	2	259	966	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds		100	692
46	3	964	1527	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds		100	564
46	4	1509	2111	gblU42599I	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds		99	603
46	5	2537	2851	embIX8720IIB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17		98	315
47	1	2	526	gblU45425I	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds		95	525
47	2	1245	724	gblU45424I	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds		94	483

Borrelia burgdorferi - Coding regions containing to know proteins

47	3	1971	1321	gb U45424	Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	651
48	1	363	25	gb U44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	87	327
48	2	412	1182	gb U72997	Borrelia burgdorferi plasmid cp32-6, erpK gene, complete cds	100	91
48	3	2047	1244	gb U72997	Borrelia burgdorferi plasmid cp32-6, erpK gene, complete cds	99	804
49	1	713	18	gb U76406	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	606
49	2	2308	704	gb U76406	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	98	1596
51	1	613	2	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	99	612
51	3	2203	2487	gb U44914	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	86	269
52	1	3	236	emb X87202 B BBRGBCDE	B. burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	94	146
52	2	179	319	emb X87201 B BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	94	140
52	3	250	1050	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	86	146
52	6	1650	2201	gb U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	81	422
53	1	93	581	gb AF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	99	489
53	2	883	719	gb AF000270	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like	100	101

Borrelia burgdorferi - Coding regions containing to know proteins

53	3	1107	811	gblAF000270I	orf1 gene, partial cds		100	289
53	4	1447	1064	gblAF000270I	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds		96	381
53	5	1742	1380	gblU45427I	Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds		93	362
53	6	1949	1740	gblU45426I	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds		98	210
57	1	3	434	gblU45422I	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds		92	326
57	2	1580	471	gblAF000270I	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds		98	362
57	3	1837	2109	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy		84	246
58	4	1573	1800	gblL31425I	Borrelia burgdorferi (clone BbK3.168) phoA fusion protein gene, partial cds		90	118
60	1	668	1111	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17		75	519
60	2	1479	694	embIX87127IB BPBRGEA	B.burgdorferi repeated DNA element, 30.5 kb circular plasmid copy		72	786
60	3	1907	1410	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17		95	498
62	1	284	3	embIX87201IB BBRGABCD	B.burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17		79	260
62	2	878	282	embIX87202IB	B.burgdorferi plasmid, orfA, B, C, D, E, & G		74	501

Borrelia burgdorferi - Coding regions containing to know proteins

				BBRGBCDE	genes, clone pOMB10		
62	3	1704	910	gblU42599l	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	78	351
64	1	563	54	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	510
64	2	1320	1117	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	204
66	1	647	75	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	93	300
66	2	1075	641	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	435
66	3	1530	1018	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	94	440
70	1	3	275	gblU96714l	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	98	207
70	2	217	600	gblU45426l	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds	99	384
70	3	557	946	gblU45423l	Borrelia burgdorferi 2.9-3 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	98	390
70	4	1424	1083	gblAF000270l	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	99	342
75	1	2	925	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374
75	2	936	1328	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	96	393
76	1	464	12	gblU45422l	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	85	281
76	2	1256	540	gblU45425l	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete	91	552

77	1	433	2	gbIU45422I		cds			
						Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	90		379
77	2	1159	509	gbIU45424I		Borrelia burgdorferi 2.9-4 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97		651
81	2	657	1034	gbIU43414I		Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	80		255
83	1	3	1202	gbIU76406I		Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99		1198
85	1	1	360	gbIU45421I		Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	91		347
85	2	358	1008	gbIU96714I		Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	84		440
85	3	791	636	gbIU96714I		Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	80		151
86	1	891	289	gbIU45422I		Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	86		486
86	2	1151	954	gbIU45427I		Borrelia burgdorferi 2.9-7 locus, ORF-A-D, REV, and lipoprotein (LPA and LPB) genes, complete cds	97		148
88	1	137	3	gbIU60642I		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	97		135
88	2	325	131	gbIU60642I		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98		195
88	3	565	323	gbIU60642I		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98		243
88	4	954	508	gbIU60642I		Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98		447

Borrelia burgdorferi - Coding regions containing to know proteins

88	5	1091	891	gbU60640i	Borrelia burgdorferi plasmid cp32-2, sequence at position 5kb	98	201
91	1	927	34	gbU45422i	Borrelia burgdorferi 2.9-2 locus, ORF-C gene, partial cds, ORF-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	313
93	1	162	578	gbU45421i	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	331
93	2	572	940	gbU45421i	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	96	368
94	1	3	245	gbU45425i	Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	97	243
94	2	749	282	gbAF000270i	Borrelia burgdorferi strain B31 2.9-like locus, OrfC, OrfD, Rev (rev), lipoprotein (LP), and 36 kDa-like orf2 genes, complete cds, and 36 kDa-like orf1 gene, partial cds	90	458
97	1	506	3	gbU44914i	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	94	472
98	1	827	264	gbU42599i	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds	70	380
99	1	175	408	gbU43414i	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
99	2	329	757	gbU43414i	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	98	220
101	1	207	440	gbU43414i	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
101	2	361	837	gbU43414i	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	477
102	1	3	911	gbU76406i	Borrelia burgdorferi putative vls recombination cassettes Vls2-Vls16b (vls) gene, complete sequence	99	889
104	1	388	242	gbU45426i	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes,	100	146

Borrelia burgdorferi - Coding regions containing to know proteins

104	2	595	386	gblU96714l	complete cds and REP+ gene, partial cds		
107	1	2	811	gblU45425l	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	210
109	1				Borrelia burgdorferi 2.9-5 locus, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	789
109	1	264	4	gblL31616l	Borrelia burgdorferi protein p23 gene, complete cds	86	201
109	2	598	173	gblL31616l	Borrelia burgdorferi protein p23 gene, complete cds	93	396
109	3	807	580	gblL31615l	Borrelia burgdorferi (clone BbK2.5-6) unknown protein gene, complete cds	99	228
110	1	1	456	gblU45421l	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	95	456
110	2	450	761	gblU45421l	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	93	310
111	1	787	215	gblU45421l	Borrelia burgdorferi 2.9-1 locus, ORF 5-8, ORF-A-D, REP+, REP-, and lipoprotein (LP) genes, complete cds	89	405
119	1	653	84	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	300
121	1	719	123	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	98	374
122	1	403	2	gblU44914l	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds	85	391
128	1	175	408	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234
128	2	329	700	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	356
129	1	458	697	embIX87201lB BBRGABCD	B. burgdorferi plasmid, orfA, B, C, D, E, & F genes, clone pOMB14 and pOMB17	100	238
132	1	234	467	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	100	234

Borrelia burgdorferi - Coding regions containing to know proteins

132	2	388	660	gblU43414l	Borrelia burgdorferi linear plasmid lp16 DNA, complete sequence	99	171
133	1	3	560	embIX87127IB BPBRGEA	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	80	243
134	1	339	4	embIX87202IB BBRGBCDE	B. burgdorferi plasmid, orfA, B, C, D, E, & G genes, clone pOMB10	78	331
141	1	554	33	gblU96714l	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	513
141	2	124	276	gblU96714l	Borrelia burgdorferi B31 BlyA (blyA) and BlyB (blyB) genes, complete cds	100	153
143	1	67	498	gblU42598l	Borrelia burgdorferi plasmid cp32-3, ErpG (erpG) and BapA (bapA) genes, complete cds	98	432
144	1	497	3	embIX87127IB BPBRGEA	B. burgdorferi repeated DNA element, 30.5 kb circular plasmid copy	94	495
146	1	193	2	gblU03641l	Borrelia burgdorferi lp21 circular plasmid, complete sequence	86	144
147	1	3	542	gblU60642l	Borrelia burgdorferi plasmid cp32-4, sequence at position 4-6kb	88	296
153	1	352	2	gblM96847l	Borrelia burgdorferi GrpE protein homologue gene, DnaK protein homologue gene, and DnaJ protein homologue gene, complete cds's	97	351

TABLE 6.

150

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
2	4	2730	3554
2	5	3559	3410
2	7	5464	3869
2	13	10502	9999
2	17	13800	13576
2	19	15368	15204
2	28	21155	21400
2	50	41944	42186
2	58	53786	52911
2	59	54816	53773
2	61	57393	55813
2	63	57882	57682
2	65	60898	60203
2	66	61441	62070
2	67	62078	62692
2	70	65896	66540
2	74	70203	69910
2	78	71818	71399
2	80	72956	74032
2	81	73515	73267
2	90	92181	92525
2	91	92968	92555
2	108	109872	110057
2	112	112408	112812
2	113	112858	113037
2	114	113035	113460
2	115	113506	113724
2	119	114325	114852
3	6	3279	4079
3	8	5156	6019
3	54	42256	42789
3	59	47264	47506
3	60	47673	48692
3	63	51475	51026
3	70	60330	60575
3	71	61050	61349
3	72	61347	61670
3	74	63917	64303
3	86	75347	75532
3	88	76593	77384
3	99	89769	89005
3	102	91278	91661
3	103	92137	92463
3	105	92423	92785
3	108	93467	93886
3	115	98262	98681

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

3	121	102227	102904
3	126	111308	110055
4	6	3751	4179
4	7	4218	5042
4	19	16115	15516
4	20	17028	16075
4	21	17379	17092
4	22	17735	17397
4	24	19243	18785
4	25	18942	19196
4	26	20677	19259
4	27	19431	19751
4	29	21376	20876
4	30	21899	21423
4	31	22918	21845
4	33	23951	23553
4	37	26253	25627
4	38	26991	26332
4	39	28181	26931
4	40	29175	28522
4	43	30605	30342
4	45	34906	33548
4	48	35750	35932
5	3	2102	1527
5	5	2656	2393
5	7	3460	2900
5	10	6544	5645
5	40	25278	24322
5	41	25235	25600
5	42	25665	25276
5	44	25881	25663
5	47	27883	27410
5	48	28351	27881
5	49	29028	28324
5	50	29454	29026
5	56	32199	31666
5	57	32571	32200
5	58	32826	32569
5	60	32913	33245
5	61	33766	33575
5	62	34173	33742
5	64	35514	34861
6	2	954	1181
6	3	1590	1763
6	5	3400	3954
6	7	4691	5218
6	8	5187	5699

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

6	11	6498	5983
6	12	6975	6727
6	14	7978	7448
6	15	8479	7976
6	22	15106	15636
6	27	19999	18842
6	28	20036	20668
6	29	21814	20690
6	30	20949	21269
6	35	24136	23630
6	37	25697	26248
7	8	8100	7792
7	10	8145	8288
7	11	9374	8517
7	12	9771	9325
7	13	9652	10185
7	14	10163	9765
7	15	10517	10173
7	16	11363	10524
7	17	11904	11392
7	18	12495	11902
7	19	13516	12473
7	20	12807	13154
7	22	15149	14697
7	24	15855	15046
7	25	15503	15826
7	26	16638	15853
7	27	19344	16636
7	31	19473	19727
7	32	20067	19675
7	33	20762	20049
7	34	21136	20738
7	36	22975	23406
7	40	26667	25870
8	3	2907	4118
8	5	5898	6059
8	6	7399	8313
8	13	15645	15899
8	14	17281	16331
8	15	16905	17111
10	4	3211	3684
10	6	3857	4456
10	8	5982	5599
10	11	8038	7802
10	14	10255	10100
11	7	5688	5828
11	9	7248	7685

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

11	10	7672	8028
11	13	9642	10154
12	1	101	370
12	2	982	680
12	3	1390	1115
12	4	1528	1388
12	5	1913	1431
12	11	7308	6616
14	2	3588	3328
14	4	4657	4815
14	9	7981	8511
15	1	1	327
15	2	325	1077
15	3	1478	657
15	4	2360	1758
15	5	2839	2507
15	9	3922	3743
15	10	4145	3900
15	11	4112	4270
15	13	7677	6127
15	14	7852	7709
15	15	8052	7825
15	16	8222	7857
16	2	1733	1936
16	3	1905	2063
16	6	5212	4220
16	7	8903	8505
17	2	1500	1709
17	5	4097	4660
17	7	6344	6189
18	1	1635	2465
18	2	2509	3306
18	3	3332	4390
18	5	4933	4727
18	7	6353	7084
18	8	7098	7625
20	7	4700	4557
22	4	2175	1228
22	5	2132	2314
22	6	2829	2173
22	8	3254	3601
22	9	4408	4169
22	10	4875	4402
22	11	5343	4873
23	2	2283	1537
23	3	3564	2617
25	6	3677	4147

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

26	7	4251	3889
28	2	732	1739
29	3	310	885
31	1	28	195
32	3	935	1603
32	4	1637	2332
37	2	1379	1059
42	4	2708	2388
44	2	1734	1159
44	4	2942	2532
47	4	2336	2115
50	1	908	120
52	4	674	501
56	1	152	1465
56	2	611	459
56	3	1479	2150
58	3	1691	1329
58	5	1867	2046
59	2	2018	1044
61	1	1	657
61	3	1389	1907
62	4	1115	1345
63	1	663	325
63	2	769	446
63	3	1759	1013
65	1	472	903
65	2	901	1236
67	1	387	4
67	2	979	401
67	3	1482	961
68	2	451	612
69	3	840	574
71	1	363	4
72	1	586	933
73	1	300	4
73	2	824	279
73	3	1396	1145
79	1	22	1119
82	1	701	303
82	2	1188	775
84	1	331	134
84	2	983	348
87	1	277	2
87	2	1136	267
96	1	434	57
96	2	748	557
97	2	976	659

Borrelia burgdorferi - Putative coding regions of novel proteins not similar to know proteins

103	1	301	2
103	2	886	299
105	1	36	509
106	1	425	3
106	3	761	600
112	1	416	799
113	1	685	59
118	1	1	489
118	2	487	753
120	2	299	691
124	1	1	630
127	1	702	322
135	1	287	3
135	2	649	407
136	1	1	645
140	2	619	332
145	1	1	480

(1) GENERAL INFORMATION:

- (i) APPLICANT: Human Genome Sciences, Inc. et al.
- (ii) TITLE OF INVENTION: *Borrelia burgdorferi* Polynucleotides and Sequences
- (iii) NUMBER OF SEQUENCES: 155
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Human Genome Sciences, Inc.
 - (B) STREET: 9410 Key West Avenue
 - (C) CITY: Rockville
 - (D) STATE: Maryland
 - (E) COUNTRY: USA
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 - (B) COMPUTER: HP Vectra 486/33
 - (C) OPERATING SYSTEM: MSDOS version 6.2
 - (D) SOFTWARE: ASCII Text
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:

157

- (A) NAME: Brookes, A. Anders
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PB370PCT

(vi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATATAATTTT TAATTAGTAT AGAATATGTT AAAC TTTACC CTTGAATTTT TCTACTCTAT	60
TTGTATATTC TATAGAAAAA ACGATTAGAA TTAAACAAAG CCATAACTGA ACCAACGGTA	120
ATTAGTAGAT AAAGGGATCA AAATATTTTT TATTGCAGCA AGAATACCTT GGTATATTAG	180
AAAAACCAAA AGTCATAGTC AAATCATCTT TTGATAACAA TCCCCAAATC TATAATTTAT	240
TATGAAATTA ATTGCTCCCT TGAAAAGATT AGTTTTTAAA ACTACAAGAC TACTATCAAT	300
CACTATCAGA TAGATTAAAA CAACCTTTAC AAGAAAAAAA TCTTACTACT ATTTTATTGT	360
AAATGTATTA TAAAATAAGT TCATGCAAAA ACTTACAATT TTCACAACA AACTACAATA	420
AAATCATGTA AACAAACAAT TTCTTTGAAA ATTAAGCAAA TTTATAAATA TAAATTATAA	480
AGATATATAT TTTTATATGA TCAATAATAA AAATTAATAG GATACTTATT TGGAAAAATT	540
ATTGAAAAAA CAATAAGCAT GAATTGCCAC AATAAGCTAA TTGTCACCTA ATAATTCTTG	600
TTTACTAGAC CACATTAGTA TAAACTCAAA TATTGGCTAC TATAATATAG GGGCTTTATA	660
CGCCACATGT TTAATGATAA CATAAGAAAA TATTGCAATA ATAAAAAGAT TGAAATATCT	720
TTATTAGAAA AGAATCTCGA TAATTTAGAA AACAGAATAA AAATCATAAC TAATAAATAT	780
AACGTTGAAA AAAATATATT CAAACTTTAA CTATACAATT AATTACACCT TAAAAATGCG	840
TTACATAAAA ATTAAGGACT ACTATAAATA GAAAACACCA CATAACCTAC AGACTCTAAA	900
GGAATAATTA AATCCTCATA TTTCAGTTCT CCAAAGTTT AAATAGGGGC CTTTTACTTT	960

TCTTGATTAG CATATACATT ATTAAAGGCA TCTTCTTGGG CACTATCCTA AACTTTTTTA 1020
CATTATTATT ATTTTATTCT TTATTATTAC AAGATAATTC AAGAATCTAG ATTACAAGAT 1080
ATCAATCCTG CCATTAGTAG TTCAATAAAA CATTTAGAAT ATTTATACAT TATTTAATGT 1140
ATTTTTTTCA TTTTGGAAAT AATATTGTTA TAACTTAACT TAATAAGATA TTTGATTTCT 1200
TCAACTTGAG AATCCGATGT ACATAGAATC TGAACATCTC CTCTGCCCCA TTTGCCAATA 1260
TTCTTAATAT ATCTAGTAA ACCCTCTTTT AAAATTATTT GATCTAGAGC AACAGTAATA 1320
GTAATATTAA TTTTATTTAC CCCAGGTCTA AAGCTAAAAT CTACAAAATA TCCGCCCTGT 1380
ACTTTAAATC CTGTATAGCA CTGTGTTTCA ACTTTCTCAA TTTCATTAAA ATTTAAAACA 1440
AAAATAAAAT CTTCTAATTC TTTATATATT GCTTTTCATAT CGGAATTTAA TTTTCAAAT 1500
TTTTTTTAAAT TTTCGGTTTT AATATTATTA TCTTTTATAC CAGAATCTGT GTCATCTTCT 1560
ATGTCACTTT TCTTGCTGTT TACTAATACA TCGCTTTTTT TTTCATCAAA AAACATACTA 1620
AAAATATTTT TAATAATATC ATTAAATATT TTATCTGAAT ATGTTTTTTT AAAACCAATT 1680
TTAGCTTTAA AAAAATCAAG CAAATCAACA CTTGGATTTT TTGTTTCCTT TTTTAAATAA 1740
GCTGAAAATT TGTCTGTATA TTTTTTTTCT AATGCAAAAG ATCTAGCCTC TTCAACATTC 1800
AAAGAATTTT TAGAAACTT TTTAAGATAT TCAAAATCCT TAGATGTTAA TTTTCTAAA 1860
TTAACAACCA TAAAAGGCTC ATTGTCTAAC AAATTATCTT TATCTAGGTC AGTATAGAAT 1920
CTATATTCTA TGCCATCTGT TAATATACCA AATTCAACTC TCTTTGCTTG AGAACGAATA 1980
TTTTCAAAAT AAGGTTTTAA TTGCTTTAGA TGATTTTCAA GCTTTTCCCT GCTATTATGA 2040
TATTTGGCCT CTATTAAAAT AGTGGGTCTC TCATCCTTTT TTGTTGGATA AATAACATAA 2100
TCAACCCTTT TTAGTCCATC TTTAAGAATA TCTGCCTTCT CTTCAACTTT AACAATTGAA 2160
ATATCAGTAT GATCATAGCC CATCGCATCT AAAAATGGAT CAATAAGATT TTGTCTTGTT 2220
TGTGCTTCAT TTTCAATAAG ATCCTTATCC TTTTGAATTT TTCTACTTAC AGCTTTTATT 2280
GAATTTTCAA AATTTATATC TTTGTATTCA TTTGGCATAA TTATATTTTA CCAATAAAAT 2340
TAAAAATTAA TAATTCTAAA AATAAATTTT CAAAATGTTG TCTATTTTAA ACTCTTAACT 2400
GATACCTTAA TTCTTTTTTC TACCTAATTT TTTAGTTTAA AATCTTATTT TTTAATTTTA 2460
TTATTTTTTC CTACCTTAT TTATACTAAA ATTTTtagTA TTTAGCGAAT AATTTTCATA 2520
TCCTTTTATT AAAGACAAA TATGATTTTC TCTTTTTTGT TTTTAAATAC CTTAAAATCA 2580
CTAAGCAAAG TAATAAAGTC TTCTTTGGTT AATGAATAAA AGACTAGCTA TAATAAAATT 2640
ATTTTATTTT TCTTTACTAA ATTCAAAATG CTCTAAATAA AGCAAATTAG AGAAATTCAA 2700

AGGATCATTT	TTAGCTATTA	GCAGAGAAGT	GTTTTTTTACC	AAAGTTAGAC	ATAATGAACT	2760
AGCCAAAATT	TCTTCTTTGG	GTTGAGGCAT	TGGACATTGA	CAAAGAAATG	ATTTTACAAT	2820
GTCGGTATTT	TAAAACAAAT	CTTCTAATCA	TAAAATCAAA	TACAGTGCAT	TGAAAATAGA	2880
TATAATAAAC	AATTTTTTTAT	AAAAAGATAT	TGGTATTTTC	TCACAATTCA	TATCTATTTT	2940
ATAGAAACAC	AATAATAATT	TTTAGGAGAT	AAAGTGCTAA	TCATGGTTCT	TTCATTTGTA	3000
TTGCTTGCAA	TTCTTCTATA	AAATATTCTT	TCATTTGGGT	ACTGATCATC	TTTAGTTAAG	3060
ATTTTTTCTA	AATCTTCTTT	ATATCCTATC	CATAAAAGCT	TATAACCTTC	TTTTACATAA	3120
TCATAAGTAA	AAAATCTTAA	ATTAAATTGA	TAGATATTAG	CCCCAGAATA	AAGAAATATA	3180
AAGTTTTTCAT	TATTATATTC	CTTTAATAAA	GATTTGCGAT	TCTTTATACT	TGGATCTGGC	3240
CCTTTTTTAA	AATTAATATC	TTCTTTACTA	AGAATACTAA	ATGAACTAAA	TATTTTGTTT	3300
AATTTGGCCC	ATGTTTAATT	CAATTCCTTT	ATAAGGATTT	TCTTTGCAGT	CTTTTAAGTC	3360
TCTAGTTATT	CCTTAATAAT	ATTATCACTA	CTTTGAATAA	CAAATTTTGC	TTTAAAATTT	3420
AATGTAAAAG	TTTATTACTA	CGAGGAAATA	TCGCAAATTT	AAAACCTGAA	TGCATATCTT	3480
AAAACCTTTT	TTTGTTTTCA	AACTGATAAA	TAAGTTAAGT	TTATAATTAC	TAAATATATG	3540
CTTTCTTAGC	AAGCTAAGAC	CAAATATCAC	AATAGAAGTA	ATTCTCAATA	AACAAAATAC	3600
AAAAAGTAGT	TATCATATCG	TCTTTAACCT	TAAATAAGGT	TGCTATAAAC	AACCAAGATA	3660
TTTAATTTCT	TTTAAAACCC	TTATTCAATC	TTTTTAAGCA	TAGGATCTTA	TAATTATAAG	3720
AATATAATTT	TATTTACATC	TCTATATTAA	TAGAAAGATG	CAAATATGTG	ATCAAATTGT	3780
TATTTTTGTA	ATATGGAATA	GTCCTTTATA	GGGACGCTTA	ATGCTCTATA	CTTAAGATTG	3840
GAATTCTCTA	TGAAAATATA	TACTCGCTAC	CCATGTAAAG	CTGACTTATT	TTAGCACGTA	3900
TCGCTTAAAC	AATTATATTT	ATATTATCTT	TTATAAAGTT	AATTTTTTCT	TGTAGATTAT	3960
TTTTTAATAA	AAAAGGCACA	AATTACCACA	ACAAGTTCCA	GTATAAATTA	ATAGTTCTTA	4020
TCTCAACACT	AAAGTACATA	AACATCAAAT	ATCAAAAATA	TATAAGAACA	ACATACTACA	4080
TTGTTTTAAT	GAAAACCTTA	AAAGGAATGG	TTAAACTCTC	ATTAAGCTAA	AACCAATGCA	4140
AAAATATCTT	TATAAATTAG	CAAAAGAACT	AAAAGTCACA	AACAACTACC	ATAAAAATTT	4200
GGTAGTAAAT	TCTGGAACGT	AAATTTACTA	TAAACTCAAT	TATTCATAAA	AAAATATTGC	4260
CTTAAATTAA	AGAATGCCTT	AAAAAAACAA	AATGCTCTGA	TTTAAACCTA	TACCCAAAAT	4320
ACAAATTTAC	TAAAGAAGAA	GATATAGATT	TAGAGAAGAT	CTTAATAATA	AAAATATTAA	4380
TATAAAAGTT	GCTCAGTATG	CTAAAGGCAA	AGAGTTTAAG	TCAAGTTTAG	AAATTACAAA	4440
GAGTAAACT	ATAAACTTCC	TTTAAGAATG	AAAATTTATT	TTTATACTTA	CTTGGCTTAA	4500

TATTAAGATT TTTTATCT TTTTCATAATA ATCTCTTCTA TCACTTAACA TTTTGCTATA	4560
CAAAAATCTT ACACATCTAA ATACTTTTTA AAAAAATTTG ATTAGTGTTA GAATATATTC	4620
TATATTTATA AACTTTATTA GCACTCATAA TTTTACTAAA TTAATATATT ATATTTAATT	4680
TATTTTTTAAA ATTTATCTCC ATTTACCAAA AAAACTAAAA TAAACTCTC CAAACTTATA	4740
AATAAAAAAA TAAGGCAAAA CCCCAACAAA CTCAAGATCT ATAATACAAA AATACAATAT	4800
AAGAATCCCA AGCTTAAAAA CAACCCCCTA AAATCTTTTT TTATTGGCGT TTTTAAATAA	4860
TGGTAATAAA GAATTCCAAT CAACACGATC CCCCTACAA CTTTCAAAC CCTATAGCTT	4920
GGCTTTTTTAT ATTATTTTTA AATTTACATG TCACAACAAT AGATAATGCA TAAAATAAGT	4980
ATTAATAAAA CAAATACATT TATAGAACCT ATACAATTAT TGAGCATATG GCTAGTACTA	5040
AAAATGAAAA TGTACAAGAT AATATGCTAT TAATAAAAAAT TAATGGCTAC TAAAAC'TTTT	5100
GAATCCACAT TTTTCTTTA AAAAAATTCT AAATTATTAA AATAAATAGA AATTAAATT	5160
ACCAAAAATA TTATTATAGT AATAAATATG TAAAGCTATT TTTATTAAAA CTGATAATAA	5220
AAATATAATA GCTAAAATAA CATAAATTAA CTTTAAATTA TATCAAAGAC TTAGATTAA	5280
AATATTTAAT AAAAGGCAAA GCTATAAACA CCATATACTT ATTTTATTAT TTTTTCATT	5340
TTATTTAAAT TAATTTAAAT AAGACTCAAT CAAATAATCA ATCAAACATA TTGGGTGAAG	5400
AAAAAATAGG GTATCTTGG TGAATCGTTT TAAAGGGGG TATAGTAAGC TAAAAAACTC	5460
TTATTAAAGA GGATGTTTAT AGACTTAAAA GTCTAATTCA ATATGAAAGA GGCTTTTAA	5520
AGCTAAAAAT GTTAAAGAAA ATCAAATTAA GCAACAAGAT GGTTTTGTTT CTATAAATAG	5580
TTTTAAAGAA TATATACATT TGCACATACC CTTCAATTATA ACATCTACTA ATTACACAAT	5640
AAAAATAAAA ATGATTTATT AAGAATTATT AGTAACTTAT AAAA'ACTTTA TAAGTTACAT	5700
AGTCAAAAAAT ATAAAAAATT AAAACAAAAA ATTAACGATA TGGAAAAATT GTATTTTATA	5760
GAAATAGAAA TATATTTGCA TTAAACA'ACT ATGAATTTAT AAAGATTCTA GTAGGAGAGA	5820
AAATATGAAA AAAAAAAATT TATCAATTTA CATGATAATG CTAATAAGTT TATTATCATG	5880
TAATACAAGT GACCCCAATG AATTA'ACTCG TAAAAAATG CAAGACAAGA ACGTGAAAAT	5940
TTTAGGATTT TTAGAGAAAA TTCAAGCAGA TAATAAGAA ATTGTTGAAA AACATATAGA	6000
AAAAAAGAA AAACAAATGG TGCAGGCTGC TTCTGTAGCA CCTATTAATG TAGAGAGTAA	6060
TTTCCCATAT TATCTTCAAG AAGAAATAGA GATAAAAGAA GAAGAGTTGG TTCCAATAC	6120
TGATGAAGAA AAGAAGGCAG AGAAGGCAAT TAGCGATGGG AGTCTTGAAT TTGCTAAATT	6180
AGTTGATGAT GAAAATAAAC TTAAAAATGA ATCTGCGCAA TTAGAATCTA GTTTTAATAA	6240

TGTTTATAAA GAAATCTTAG AACTTGCAGA TTTAATACAA GCAGAGGTGC ATGTTGCAGG	6300
AAGGATAAAT AGCTATATAA AAAAAAGAAA GACCACTAAA GAAAAAGAAT ATAAGAAGAG	6360
AGAAATTAAG AATAAGATAG AAAAACAGGC TCTAATTAAG TTGTTCAATC AGTTATTAGA	6420
AAAAAGAGGC GATATTGAAA ATCTTCATAC TCAATTAAAT AGTGGACTTA GCGAGAGAGC	6480
ATCTGCAAAA TACTTTTTTTG AGAAAGCCAA AGAACTTTA AAAGCTGCTA TTAAGTAAAG	6540
ATTAAATAAC AAACGTAAAA ATCGGCCATG GTGGGCAAGA AGAACACATA GTAATTTAGC	6600
AATACAGGCA AAAAATGAGG CAGAGGATGC TTAAACCAA TTAAGTACTT CTTCTTTTAG	6660
GATACTTGAA GCAATGAAAA TAAAGGAAGA TGTA AACAG CTTCTTGAAG AAGTAAATC	6720
TTTTCTAGAT TCTTCAAAGA GCAAATCTT TTCTAGTGGC GATAGATTAT ATGATTTTTT	6780
AGAGACGAGT AAATAAAAAA ATATATTTTA AAGGCTAATA ACTTAAATC AAAGTCTTCT	6840
GTAAAGGAA GACTTTTTTA TAATTTTATT TAAATAACGA AAAGCTTGAT AGTTAAAAA	6900
TCTTTTTTAT TAAAAATATG TTTACTAAAC AGAGCTCAA AATGACTATA TTTAGTATCT	6960
CTATAAAAGA ATTTTCAAT ATTTTAAAAA ATTTATAGAT AAACATAATC TAAAACCATG	7020
CATTAATACA AACCTAAAC ATACTTGGTC ACTTGTA AAA GTAAATTGTA TCTAACTTTT	7080
TTTATTTATT GAATATACGT AAAAATCTT TATAATTTCT ATTTTAAAC GCTGCTATTT	7140
AGCAATACAA TAAAAGGCAT TACAGATTGC AATCAAACA ACTAAAGTTT AAATAAAATA	7200
TTACCCTCTG TTCTAATCCT ATCAAACAAG GTAATAAATT CTTTAAATTT CTAAAAGCCT	7260
AACTTTAAA AGAACTTGTC GAAAAATAA TTTCTCTTAA AAAAGGTTCT AATCTTTTAT	7320
TTATAAGAAC TTTTATACTA TTATAAAAAA GTATCTTGCC TTGATATATT TGTATTCTTT	7380
ATAAATCAAG CCTTCTACTT TTTTAAAGAA TATTTCTATT TTTTATAAAC TAGTTTTCTA	7440
CAATAGAAAA GAAATAACCC AAAGCCCTAA AACTTAAAT AAATGTTAGC TATAATAACT	7500
AAAATAGAGA TAAAAAACTC AATCATAAAT AATGGTAAAA CAACTTAAA CCACGTACCA	7560
TAACCTCAATC TGGATATCCC CAATACAGCC ATTATAACTC CGCTGGTAGG TGTATCAAA	7620
TTAATAAGCC CAGATGCAGT CTGCATGGCA ATAACAACTG AAGCTCTTGG AATTGACAAA	7680
AAATCGGCAA GAGGAGCCAT TATTGGCATA GTGAGACTAG CATGTCCTGA TGAAGATGGA	7740
ACAACAAATC CTATAAATAT TTGAATAATT TCATTCAATA TGATAAAAAG GGGTCTTGGA	7800
AGATTGTATA AAAAATTAGT AGCAGCATTT AACATAGTAT CTGTAATCAA CCCATCATCA	7860
CATACTATCA TAACACCTCT AGCAAGTCCA ATAACAAGAG CAGCGGTTAG CAGACTTTCA	7920
GAACCTTTCA CAAACGCATC CCACATTTCA GTTTCACCTA ATTTACAAAT AAAAGCCGAT	7980
ATAATAGCAA CTCCAAGATA CAACATTGTC ATTTCTTGCA TCCACCAACC AAGATTAACA	8040

ATGCTAAATA TCAAAATCAA TATCATAAAT CCAAATAAAA GTAAAACTAA TTTATGAGCA	8100
AAAGTAAACT CAAGAGCATT CTGAGCATT TCTCCGGTAG AAAGTCCATC TTTTAAACA	8160
AAATATTGAT AATGTTTCATC TTTTGGAGAA TACACAAGCG ATTTTGAGGG ATCCTTTTAA	8220
ATTTTAGACG CATAAACACA AACATAGGTT ATAGCAGCCA ATACTGATAC AAAATAAAGA	8280
ACAATTCTAA AATAAAATCC ATCCTGCAAG CTAATAGAAG CTATTGCAGA TGCAATTCCT	8340
GTCGCAAATG GATTTACAGT AGAAGCCATA GTTCCCACTC CAGCTCCTAA AGCAATAATA	8400
GCCGCTCCAA CAAGACTATC ATAACCCAAA GCTACTATCA AGGGAATCAT AACAAAATAA	8460
AAAGGAAGGG TCTCTTCACT CATTCGGGT ACAGTTCCAC CAATTGAAAA AATAAACATT	8520
AACAAAGGAA TAAGCAACTT ATCTTTGTGC CCCAACTTCT TGATTAAAAA ATAAATTCCC	8580
ACATCTATTG CTCCAGTTTT CATAATAATC CCATAAGCAC CCCCAACAAT TAAAACAAAA	8640
ACAATAACTT CAACTGCATG TTCCATCCCC TTTGACATTG CGGTTAAAT AGTCATAATA	8700
GGATGTAAAA ATCCCCTAGA GCCTCGATCT ACATATTGAT AAGTTCCAGC AACAATTATT	8760
TCCCTTTTAG ATCCATCACC CATTTGCTTA AATTCTTTAT CAAACTTACC GGCAGGAATC	8820
ACATACGTTA AAATGGTAAC AAATACAATT AAAGAAAATA TTATTGTAAA ACTACTTGGC	8880
ATTTTGATCA TAACGTTTCT CCTAAATAAT TTCATAAATT TAATTCACA TAAAAATAC	8940
TGTTATCCCA AAGTTGATAC CATAATAGCT TTAATGGTAT GCACCTATT TTCAGCCACA	9000
TCAAAAACAA CTGAATTTTT ACTTTCAAAA ATTTCTTCTG TAACTTCAAT TCCATCAAGT	9060
CCGTATTTAT CAAAAATATC CTTACCAATC ACAGTGTTTA AGTCATGAAA AGCAGGCAAG	9120
CAATGCATAA ATATTGCATC ATCTTTTGCC ATGCACATTA TCTCTTTATT AACCTGATAA	9180
GCCTTTAGAA GATTTATTCT ATCTTCCCAA TTAATCTCCC CCATAGATAC CCACACGTCT	9240
GTATACACAA CATCAGCACA TTTAACAGCC TCTTCTTTAG AATCTGTAAT TGTAATTTTA	9300
CCCCCACTCT CTAGGGCTAA AGACCTAGCC TTAAGCGTCA AATCGGGGTC TGGAAAAAGC	9360
TCTTTGGGAG CAAAAATTCT AAAATCAAGC CCCATAATAG CACAGCCTTT CAATAAGAA	9420
TTAGCAACAT TCCCCCTACC ATCGCCACAA AACACTATTT TAATCCCTTT CAACTCCCC	9480
TTATGTTCTT TTATTGTCAT TAAATCGGCT AGTATTTGGG TTGGGTGAGA AATATCTGTC	9540
AATCCATTGT AAACAGGAAC ATTAGAATAA TTCGCCAAAC ATTCAACAGT CTGTTGAGAA	9600
AAGCTCTAA ATCCAATAGC ATCATACATG CGTCCCAAAA CTCTAGCGGT ATCTATCATA	9660
GACTCTTTTG AGCCCATTTG ATTACCCTTA GATCCCAAAT AAGTAATATT TGCCCTTGA	9720
TCATAGGCTG CGATCTCAA AGCACACCGG GTCCTTGTTG AATCTTTCTC GAAATTATA	9780

ACTATATTTT TACCTTTAAG TTTTTCACCT TCAATTCCTG CATATTTTGA CTTTTTTAAA	9840
TTAATCGATA AATCAAGTAA ATATTTAATA TCTTTGCTTG TAAAATCTAA AAGATTTAAA	9900
AAGCTCCTAT TTCGTAAATT ATACATCAAC CACCAACCTT TACAATCAAG TTTTAAAAA	9960
CTCATTTAAC TCATGCTTAA ACATGCTTAA ATATTAAATA TCCTCTCTTA CTAAAGACAT	10020
AGACATGCAT CTTGGCCCAC CACGACCCCT TGAAAGCTCG CTAGACGGAA TTCTGTGAAC	10080
TTTAATACCA TTTTCTTCAA ACAGCTTATT AGTTACATGA TTTCTAGAAT AAGCAATTAC	10140
TTCTCCTGGA GCTATCGCCA AAACATTAGC ACCATCATTC CATTGTTCTC TTGCACCATG	10200
TATTAAATCT CCACCCGCAC ATTTTATTAT GTCAATTTTT CTGCCTAAAT AAAAGCTCAA	10260
AACATCTTTA AGCTTGCTT TTTCTTTTTT AATATTAATT TTATTAGAAT TTGAATTGTA	10320
AGTTAAAAACA TAAATTGAGA AATACATATC ATCACTTGTA AAAGTTGTA AAACGCTATA	10380
ATCAATTTGG GTAAAACTG TGTCTAAGTG CATATAGGCT CTGTTTTTTG GAATTTTAAA	10440
AGCCAAAATT GTGCTAAATG GAGCCTTATT TTTAAAAAGA CTAGCAGCTA GTTTTTCTAC	10500
AGACCCCGCT TCTGTTCTTT CTGAGATTCC AATAACCAA AGATCTTTAT TTAACAAA	10560
CTCATCCCCA CCTTCCAAAG AAGTTTCTTC CCATCTATTA AACCAAATTG GAACATTTTC	10620
TTTGTAAGCG GAATGATATT TAAAAATATA CTCTGCAAAT ATTGTCTCTC TACGTCTAAC	10680
CTTGGTATAC ATTTTATTTA TTGTAATTCC ATTGCCAATA CTGGCAAAG GATCTCTGGT	10740
AAATAAAACA TTGGGCATAG GATCAATAAC AAAAGACTT GAACCATTA CCAATCATC	10800
AAGCGAAAAT TCACAATCTT TAAGCTCTTC TCTTGCAACG CCGGAAATCA TTTTAGAAAC	10860
CATATTATCA ACGGTAAAT TAGAAAAATA ATCTTTTAAA ATATTAATTA CACCATCTGT	10920
TTTTATTTCT GCTTCCAGAA TAAATTGAGA TATAAATTTA TTTTGAGCG CTACAGAAGA	10980
AGCAAGAACT TCACTAACAA GATCCTCAAC ATACTCAATT TCAACTGAAT TATCTTTTAA	11040
AATATTTACA AAAACTTCAT GCTCTGTCT TGCAACTTTA AGATAAGGAA TATCATCAA	11100
TAAAAAATTT TTCATAATCA AGGGTGTC AAATTTCTAAT TCTTCTCCTG GCCTATGAAG	11160
CAAACTTTT TTCAAACGAC CTATTTCCGA AAATATATTT ATTGGATTTA AATATCTTC	11220
TTCCATCGAT TTCCCCCTTT ATGAAAATTG TCATATATTA AAATACTATA GTTTATATTA	11280
AAAAACATCA ACTATTTTAA ATAATATTAA AAATATAATA TAAATATAAA AAATTGAAAA	11340
AATAAAAGTT CTAAAAACT TCAAATCAAA AACATAAACA AAAAATTATG CTAAAAACT	11400
AATCATGAAG AATATTAATA GATTAATATT ATTAATATTA ACTACACACA CTTTATTATT	11460
CTCTTGCGC TTAATTGCAG ATAATAAGTC AAAAAATTTA AGCACATCAG AAATCATATT	11520
AACACAAAAA AACTACTAG AAAGCTCTT AATAAAAAAT CTTCTAATG TAGAATATCG	11580

AATACCAATA TCCAGTATCC AAGAAATTTT AAACAATAAC AATGATTCTT TTTTAATAAA	11640
AAAAACAGCA GCAAAAATCA AAATAAGCCC TCAAAAACCTT GAAGAAATAA AAAACTATCT	11700
AAATGCTTAT AAAAATTATC TAAATAATGA AACAGAATGG ATAAAGTTTA TAGATCAAAG	11760
TAGCGTCAAT GGAAATTTAA CAATTAAAT TGATACTGCT TTTGAAAAAA AAACAAATTT	11820
TAATCATACA AATTCAGATA ATGAAAATTT AACAGAACTA ATAGAACTAC AAATGCATCT	11880
GGAAAAAGAA ATTTTAAACT TAATTGAGCA AACATTTTCAT GATAAAAATT TAGGATATAT	11940
ACAATTAAGT CACATCAACT CATTCCTTCC TCAAGAAAAT ATAACTCAA TAACAAAAGA	12000
AATAATAGAT GGAAAAGAAT ATATTGCACC GCACATAATA GCAATCAAT TATTAAAAAT	12060
AAAAGATAAA AAATATTTTG AACAATTTAT GCACTTTTTTA AAAGTTGAAA ACAGCAAAAT	12120
AAAAACAATA ATTGAAAAAC AAAAAATTC AGATCTTCAC AATGAACTGT ATTATTCAAA	12180
ACAATCCCCG CCCAGAAGAA GAAAAAGGTC AACTGCCGAT TCCGATAATA ACAATAAATA	12240
CGATATAATA CCAAAAATAA TAGACCCAAA TACAGGCATT GAAATAACTC CTAAAAATTT	12300
AAGATCTATT TTATCAAATG GCGACATAAT ACTAATAAAA CCAAAAATAG ATTGGACAGA	12360
ATTTTTTTAT TTTTGGAAC ATGTGGGAAT ATTTGATGAA GAAAAATATG AAGCCACTAA	12420
AAAAATTGCA TTCAATGGAA TTGATAGCTT TGATATAAAA TCAATAATTA CAAGCAATCA	12480
AATCAAATTC GATACAGCAT CTAATCAAGG TTCAGGATAC GAAAAGCTTT CAACATACGT	12540
ACAATCAAGA ATATTAAAAA TATTCTCACC AATAACAGAC ATAAGAACAA TTCAAAAAGC	12600
TATTAATTTT GGAAGAAGTA GATACATTGA CAATAACTTT GGATATATGG TTCCATTAAT	12660
ATCCTCTAAT TTATGGACAG ATTCATTCAA TCTTGAAGAA ATTCACAACA AAACCTATTG	12720
CTCTTTAATG GTTGATAGAA TATATAAAAT AGCAGGACTT AATGTATCAA GAAATTACGA	12780
AATTTCCGGA ATAATTACTC CTGGAGAAAT AAATGCAGCA GCTTACAATT TTTACATGTC	12840
TTATACGATT GCAGGAATAC TTCCAAGCGT GCTTCCAAAA AGGCTCATTA AACCAACATT	12900
AAAAGAAAAA TTCATTGGTT ACAATAAAGA AATAGTAGAT GCAATAGAAT TAAAAAATC	12960
GAAAGAAAAA ATTTTTGGGA GAGCTTGCAA CATTACAAAT CTCTGGTGCT CAGGAAGTTA	13020
ATACTACCCA TGAACAAATA TTATGCCTGT ATTTTGATTA ACAGCAATGA AAAAATTATT	13080
TTCAAATCCT GGGAAGAATG CAAAACCGCT ATTAAAGGAA AAAACAATAA AATAAAAAGC	13140
TTCAAAACAA TAGAACAAGC TCAAATTTGG CTATTTAATA ATGAGAATAA AATTCACCAT	13200
CACCCAAATG GAATATATTT TGATTCTGGA ACGGGAAGAG GAAAGGGCAT AGAAATTAGA	13260
GTTGTAAACG AAAAAAGAAT TTCAATATTG GATAAAATCT TAGATAAATC CTTGATTAAT	13320

GAATATGGAA ATTATTATGT CAAAAATTTT CAAGGAATTA GCAATAATTT TGGGGAAGCTG 13380
CTTGCCCTAT ATACAGCTCT CAAAAAGACA TTAAAAGAAA ATATAATAAA CATATTTGGG 13440
GACAGTAAAT TAATAATTGA CTATTGGTCA AAAGGAATCT ATAATAGCAA AAAATTAACA 13500
CAAATTACTA TTAATTTAAT CAAAAAGACA ACTGAACTAA GGAAAAAATT TGAAGAACAA 13560
GGTGAAAAA TTTCTTTTAT TCCAGGAAAT GAAAATATTG CAGATCTTGG TTTTCATAAA 13620
ACTAAGTAGA AATATTGTCA AAAAATACAT AAAACAATA TTTCTGATTT CAATGGTTTA 13680
TTTTTATTGT TGTACGACAA TAAAAATAAA CCATGATTAT GAAACTGATT TTAAAGTTCT 13740
AGAATCTCCC TCTAAATACA TCAATATAGA TGTAATTAAA GCTACAAATG AATATATTTA 13800
TATTCAAATT ACAACAATA GCTTAGACGT AGTAAAAATA AATTGGCAAA AACTAGTCT 13860
TAACAACGAT AAGATCGTCT TAAAAAAGA AGATCTTACA ATAAACAATG AAACAGGGTA 13920
TAAAAATAAA TACAGAGAGT TTTTTATTGG TCCTAAACT TCATTTAAAT TTAAAGTATA 13980
TCCACTAAAA ATTCATTCTA AAAACAAAA TAGCAATAAC TTAAGCTCAA CTATTAAATA 14040
TCCGTCTATT TTTAAGCTCA ACATAACAAA AGTAGGAATT GAAGCAAAAA AAACAATAAA 14100
TGTTTTAATA ACAAGAACTA CAAAAATTAA TATTACTAAT AAATGAAAAT CATTATTATT 14160
TTTTTGTTTT TCTATTAATA ATAACTCGT AGTTTGTATC TTTGTTGTTT TCAAATGACG 14220
CTTTTATAGG AGCAAAAAAG TTCCAAGAAA TATAAATTGT AAAATTATTT CTCCAAATAG 14280
GAGAATAAAT CCCATCAGAT CCCCTTAATA AATCTGGTTC TAAATTATAT TCTCCAACAA 14340
ATTTCCAATC ATAAAAATTG AATTAAAGC CTGATGAAAA TTTTTTAATT TTAAAAAGTG 14400
AATCTTTTCT GTCTTGAGAA TTAAAGAAAT TGAAAGATTT TGATAAATCA ACAAAGAAAT 14460
TAACAGGTTC TAGACCAATT TGGTCCATAT ACCCTTTAAA ATATTTAAAA GTCTTAGTAT 14520
TAATAGATAA AGTAGAAAAG TAAATTTCTA AAAATTCTGT ATATTTAAAC TTCAAAGTCA 14580
ATGCAGATCG AAGTTCATTA TCCGTAAATT TCTGCAAATT TATTTTCCAA CCAACATCTA 14640
CCCCCAAGGT AAAAGAAAGC TTATTGTCAA AAAAGTTAA AACGTACAAT TCCTTTTTGT 14700
AACTAGAATC TAAAGAATAT GGAACAAGTT TGGTTGTAGT ACCAATCTTG GAAAAATCTC 14760
CTTTTAAAGG ATCATAATTA TATTCAAAGT CGTCTTTCAT AGCAAACAAA AATTGAAAAT 14820
CAAAAACATT AAGCTTAAAA GAAAGTTCAG AAACCTCTATT TATCAAAGGA TCATAGGCGA 14880
CTAAAAAAT AAATTTAAAA TAATCCAAAT ATCTCGGCTC AATTTTATAA TACAAAGCAG 14940
GAGACATTC TAAATTTTTA TAAGGCGATG ATGGTTTTTG AGGCTCCAAA GGACTTTGAA 15000
CAGCAGAAAT TCCAGAGTTT TTCATAGCAT CTTCTTTAAA CTTTTTATAA TATTTAATTC 15060
CAATCCCAGC TTCTTGTAGC AAATAAGGAA AATCTAAAGA AAGTTTAAGC TCAGAAGAAG 15120

CTTTAATATC TTCAAACTA TTTTSTAATT CACCTGAAAG CTCAGTAGTA AAATAATCAT	15180
AATCATAAAT TAAAGAGGCT GTTAACTTT GATAAAAAGT TTCCGGATCA GATAAAAAA	15240
TACTACTATT CTTATTAACC AAAGATTTTA CATCAGAATC ATATTTTSTA TTAATGAAT	15300
ATAAAGTAGC CTTATTTTCA AACTTTAAAG TACTTCTAGA AAATAAAGGA TATCTAATAA	15360
AAGGAAGCAA GTTTAAATTT ATTTGGTTAA TAATAGAGTG CTCACSTTTT TTATCTTTAT	15420
CTTCAACTTT AAAATCTTTA TTTAAAGGAC TATACTCAAT AGTATTAAGA TATAATAAAT	15480
TTTCAAAAAGT AATTAAACGA TTGTAAAAAT CAGCATGAAT TTTTATATCC GTTTTATTTT	15540
TTATATCAAA TAAATAATTT TTTATTTTAT AATTAAAGTC CTTTGGACTT GTTATGCCAT	15600
AATTATCAAA AAAACATTA TTTCTTAAAT AAGGATTAAT GCCAAACCTA ATAAAAAAG	15660
AATCGGATTG ATCAATATTT TTTAAAGTAA TTGGTCTCTGG AGGAATATAT AAATCTTTGG	15720
TTAATTCTGT TGTTTTTTTA GTATTTTCT CTTTCACT CTTTTTATCA TTATCTTTAT	15780
CTTCTAGATT TTTAATTTCT GGGCGCATT TCATTTCTTT AGTATCAGCT GGAAATGTCC	15840
ATTGGTTATT GTAAAGATCT TTTTGAAAA TCAAATCAAT ATATGGAGCA TAAATCTCT	15900
CCAAATAAAA CCATTTTCTT GTAGGATCAT TAACATCTTT TGGTTTCTCT AAAGGAGATT	15960
TAACATAAAG ATTTTCATAG CCCGACAATT TAAACTTAA ACCTAAATTA TTTAATTTAT	16020
AATCTAAAAT CGAACCGTCA TTAAATGTTT GCTTATAAAA AGAAGATAAA TTCCAATCAA	16080
AAGTGCTAAT GCTAGTTTGC TCTTTAACCG AATCTTTATC TAAATTTAAA AGAGAAAAA	16140
ATGTAGCACT TTCTATCCTA TCTCTAAAAT CAATATTAAC ATACGGGTCA GAATAGTGCT	16200
CTAAAACAAC CGAGAAAAGT GCATCACTTA AAAGAAATTC TGTTTTAAAT TTAAATAAAT	16260
ATCTAAAAGG AACTTCAAAC CCAAATACAT CTCCTTTGTT AAGATTGGAA AAATAAAAA	16320
GAGATTGTTT TAAAGTCCTA TTATCAAAAG GATAATATCC TCCATCGTAA CTATAAACAT	16380
TCCTGGTAAA ACCCAATCCA AAATTTCTTT CCAAAGTTTT AAAATGCCCC AAAGTATTGC	16440
CCAAATTAAA ATCAATTCCA GAATAAAATC CCAGATTAGC ATAAATGTCA AAAATAAGCT	16500
TAACATAATC TTTATTAACA CTGGGTGCTA AATTTTCTGC AAAAAATAA GTTAAATATC	16560
CATTTCTTAT ATAAGGTTTT TTACCCGAAT TATAAACAGA ATTGAAATCA AAATCCAAAA	16620
AAGAAGAATC TTCACTTGAA GATTTATTAC CAAAAGATA AACGGTATTA AAAACAGAAA	16680
AACCTTTTCG TGGATTAGA CCTAAAGATG GATTAAAAA CAACTATCT CCCGGTCTGA	16740
AAAAAAAAGG AATATAAAAT ACTGGAATC TTCCCATGTA AAATATGGCA TTTAAAAACC	16800
CAAAATCTCC CGAGGGCAAT GCCCATATTT TAGAAGCCTT GATTGAATAG TAAGGCTCTG	16860

GAATTTTACT AGTTGTTGCA AAAGCTTGTT CCAAAATGGT AACATCATTG TCTATCTTTT	16920
TTAAAACCTT TCCTCCAAAC GAAAGAATAT GATCTATTTG ATTTTTTTTGC ATTTTTTTTT	16980
GAAGAATACC ATTTTTTAAT AAAAAATTTT GAGAATCAAA ATCGACAAGA AATTCATTGC	17040
CATAAAAATA AAGCTTTTCA TTGGTATCCA TATCAAGAAT ATATTCAACA TTTCCAATAG	17100
CATAAAGTTT TTTAGAGTTC TTATTAAGGA CTATTCTGTC GCCTTTAATA TTGTGCTTTT	17160
TATTTTCTTT AATATCTTCA ACCAAGATAT TAACTCTTCC TTCAAAAATA ATACTTTCAT	17220
CTTTAGTAAG TCCATAAGTG AAATTTTCAA GATTATCTGC AGTTTCAATG ATTATTTTAT	17280
ATCTACCAGA TCCGGCAAGT CCCTTTCCTT TGATAAAAAG CTCAGGATCT ATTCCAAACT	17340
TTTTTAAAG CAATTCTCGT ATTTTGTAAA CATCTGTTTC TTTTAAACCC TCTTTTAAGG	17400
CCCATTTTTT TAAATCCTCA TCGGTTGAAA GCTCAAGTTC TCTTAAATAA GATTTTTGAC	17460
TTAAAGTTAG CTTATCCCTT TTTTLAGAAT TTTCATCATC TATAGTCTGG GCAAAAATTG	17520
CATTAGAAAA TGTAAAAAA ATTAATAATA CTATAAAGA TTTTTTAAAA ACATTCCTGT	17580
ATAGGAATTC TCGCATTTTG CAACCTCTTC AGGAATACCA GAAACAACGA TATTCCCCC	17640
TGCCAACCCA CCATCAGGAC CCAAATCTAT TATATAATCT GCCTGTTTAA TTACATCCAA	17700
ATTATGCTCT ATTAGTACAA CTGTATTACC ATTGGAACT AACCGCTGCA AAACCTCTAA	17760
CAACTTCTTT ATGTCATCAA AATGCAGCCC AGTTGTTGGT TCATCAATAA TATAAAGGT	17820
TTTACCCGTG CTCTTTTAC TTAACCTCAA AGCCAACCTA ATGCGCTGAG CTTCTCCTCC	17880
TGATAAAGTT GTTGCAGATT GTCCTAATTT AATATATTCA AGTCCAACCT CAATTAAAAA	17940
TTTTAATAA TGACTAATTT TTGGGACATT CTCAAAAAT TACTTGCCT CAAAAACACT	18000
CATCTCTAAA ACATCATGTA TATTTTTTCC TTTGTATCTA ACTTCTAAAG TTTCTTCATT	18060
GAATTTTTTA CCCTTACATA AATCACAAGG AACAAAAACA TCTGGTAAAA AATGCATTG	18120
AATATTAAGA TACCCATCTC CTTGACATTT CTCACACCTT CCACCTTTAA CATTAAGA	18180
AAATCTGCCG GCTTTAAAC CCCTTGACTT TGCATCTGGA AGCTTGCAA AAAGCTCCCT	18240
AATTTCTGTA AAAAATCCAA CATAAGTTGC TGGGTTTGAT CTTGAAGTTC TCCCTATTGG	18300
TTTTTGATTT ATTTGAATAA TTTTATCGAT TTTTCATAC CCAACAATAT CTTTAAAGCC	18360
ATCACAATAC TTTTCATTAA GCTTTAATCT ACTATCAAGA GCTGGATATA ACACCTCGTT	18420
AAGTAAAGTA CTTTTTCCGC TACCAGAAAC ACCTGTTATT ACGGTAAAAA CTCCCAAAGG	18480
GATACTTAAG TCTATATTTT TAAGATTATT TTTATTAGAG CCCAAAAGCA AAATTTCTCC	18540
CTTATCTGCC TTTCTCTAG AGCTTGGAAC ATCTATTTTA AACTTGCCGC TAAGATATTG	18600
ACCAGTTAAA CTATTTTTGC TATTTAAAT ATCAATCAAG GCTCCCTTTG CAACTATTTT	18660

CCCTCCAAGA ATTCCAGCAC CAGGACCCAT ATCAATAATA TAGTCCGCAG TACGCAAAGT	18720
TTGCTCATCA TGTTCACAA CAATTACAGT ATTACCAAGA TTTTAAAGAT TAACAAGAGT	18780
AGAGATTAAT TTTTCATTAT CTCCTTGATG AAGACCAATA CTTGGCTCAT CAAGAACATA	18840
AATAACACCC GAAAGTGCTG ATCCTATTTG AGTAGCAAGC CTAATACGCT GAGCCTCGCC	18900
ACCAGATAGA CTACCTGATA TTCTATTTAA ATATAAATAA GAAAGGCCAA CATCAATTAA	18960
AAATTTAAGC CTAATTTTAA TTTCCTTTAA AATTTCTTTA GATATTTTTT CGTCCACCAT	19020
ATCAAGCTGC AAGTTTTCOA AAAATACATA AGAATCAAAT ACTGACAAAT TGGTAAGATC	19080
TTGAATGTCT TTTCCATTAA TTTTCACAGT TAAAGCTCCA ACGCTTAGGC GTTTACCTTT	19140
GCATGAATTA CATATTTTTT TAGACATCAA ATTTTCGTAA AAAATTTTAG TACTCTCTGA	19200
TTCTGTTGCA AGATATCGCC TTTTAAAG GGGCAAAAGT CCTTCAAATG TTTTAGAATA	19260
ATGAAATCCT CCATCTAGCT CTTTTGCTTC CATTTCTTTG GACTGGTAAA TAAAATCTAT	19320
TTTTTCATTT GAGCCGTATA AAATCTGTTT AAGAACTTTA TCTGGAATGT CTTTTATGGG	19380
AGTATTTAAG TCAAAATTAT AATGTTTAGC AAGTCCTTTA AAAATAGCCA CAGACCAAGA	19440
TGAAC TTGTC TTAAACGTAA GAAAAGCATC ATCATTAATAA GAAAGACTAG TATCAGGACA	19500
AATGCTCTCA AAATCAAACCT CAAGTGTAAC GCCAAGACCA GAGCACTCAC TGCAAGCACC	19560
AAATGGACTA TTAAATGAAA AAAGTCTGGG TTCTATAAGA GGAAGTGAAA ATCCACACAA	19620
AGGACAACCTG TTGTGCTCTG TAAATAGTTT GTCTATTTTT TCCAAATCAT TATCAATTTT	19680
CACTCTTAAA TATCCATTAG AAACAGCAAG AGAAGTCTCA ATAGATTCCG CAAGTCTAAC	19740
TCGAACATTA TTACCAAGCT TAATCCTATC AACTATAATT TCAATGGTAT GTTTTTTATT	19800
TTTATGTAAA TTAAATTAA GTGCATCTTC TATTAAATAA TCTTCAGAAT TTATCCTAAC	19860
TCTATTAAAA CCTTGATTTA ATATTTTTTC TAAACCTTT TTATGAGAGC CTTTAGACCC	19920
CCTTACAATT GGTGCAAAAA GTATAACCTT GGATCCTTCA GAATAACTTA AAATAGTATT	19980
AACTATTTTA TCTAAAGATT GCTCTTCTAT TAATCTACCA TCATTTGGAC AGTATGCTTT	20040
ACCAATTTTT GCAAATATTA GTCTATAGTA ATCATAAATC TCAGTAATTG TTCCAACAGT	20100
AGAGCGGGGA TTATTGCTTA TTGTCTCTG CTCAATAGCT ATAGAAGGAG AAAGTCCATC	20160
TATATAATCA ACATTGGGTT TTTTCATTAC ACCTAAAAAC TGCCTTGCAAT AAGCTGAAAC	20220
AGATTCCATA TACCTTCTTT GCCCTTCTGC AAAAATAGTA TCAAAAGCCA GAGAAGACTT	20280
GCCAGAGCCA CTCTTGCCAG ATATTACAAC TAAACCATCT TTTGGAATAT CTACATCAAC	20340
ATTTTTTAAA TTATGTTCTT TTGCTCCTCT GACAATAATT TTTTTTTTCA AACTTTTTTC	20400

CAAAAATTAC ACCTCTCTTT TTTTATTACG AGCTATACTA ATTTTGCTAC TAAGCTCTTT	20460
TATTTTATCT CTAAAAACAA TTGCGTCTTC AAATCTTTCA TCATTAACAG CTCTCTCTAA	20520
GTCAAATTTA AGCTTATCAA TAAGCTTTTT TTTAGACAAT CTCTCACCCG AAATAATTTT	20580
TTCAAAATCA TAGCCAACAT TTTTATTTTT ATTATTAAGT TCCTTTTCTA AAATATTTTG	20640
AATCTTTTTA ACAATTGTCT TAGGAGTAAT ATTATTTTTT TTATTATAAT CAATCTGAAT	20700
TTGACGTCTT CTATTAGTCT CCTCAATTGC CTCCCGCATA GCTAAACTAA TTTTGTCGTA	20760
ATACATTATT ACAAGTCCAT TAGAATTCTT AGCAGCCCTA CCAATTGTTT GTATTAATGA	20820
AGTAGTAGAT CTTAAAAATC CCACCTTATC AGCATCTAAT ATTGCAACAA GAGATACTTC	20880
TGGAATATCT AAGCCCTCTC TAAGCAGGTT AATCCCAACA ATAACATCGA TTTCAGATTT	20940
TCTAAGCAAC GAAATAACTT CCACTCTCTC AAGGGTATCA AGCTCTGAAT GTAAATATTT	21000
TGCCCTTACG CCAAGATTTA CCAAATATTC AGTCAAAATCC TCAGACATTT TTTTGTCAA	21060
AGTAGTAATT AAAACCCGCT CTTTAAGAGC CACTCTTTTT TGAATTTTCGC TGTAAAGATC	21120
TTCCATTTGC CCATCAGAGT GCCTAGTAAT AATTTTCAGGA TCAACAAGAC CTGTTGGACG	21180
AATTATTTGG TCAACAACCA CACTACTTTT CTCATTCTCT TCAACACCCG GGGTTGCAGA	21240
TACAAACACA ACCTGATTAA TTAATGCTTC AAATTCATCA TATTTAAGAG GTCTGTTTTT	21300
AAGCGCTGCA GGAAGTCTAA ACCCAAAGTT AACAAGATTT AATTTTCTAG AATGATCTCC	21360
ATTATACATT CCCCTAAATT GAGGCAATGT AACATGAGAT TCATCTACAA ATAATAAGTA	21420
ATCTTTTCGGA AAAAAATCAA AAAGACAATA AGGTCTTTCC ATTGTAATTC CACTCAAATA	21480
TTTAGAATAA TTTTCAATGC CCGAACAAAA CCCTGTTTCT CTAAGCATTT CCAAATCATA	21540
CTCTACCCTC TGTTTGAGTC TCTCGGCTTC TACAAGTTTG CCATTGTCTT TAAAATATTG	21600
ACATTGAAGA CTAAATCAT GAGATATTTT GGGTATCGCT TCTAATACAT TTTCATAAGG	21660
AATTACAAAA TAAGATTTAG CAAAAAGAGT AAAACTATTT GTAGCTCCTA AATTTTTTTT	21720
AGAAAATGAA CTAATCTAT ATATTTCAAC AATTTTCATCA AAATCTAAAC AAATTCGATA	21780
AGCAAATCTT CCATGTTTAC TGCTAGGCCA AATTTCAACA ATATCTCCCT TAATCGAAAA	21840
TTTATCTCTT TCTAGATTCA TTAAAGTTCT CTCATAATAA AGCTCTACAA AAATATCTGA	21900
TATTTCTTTA ATAGAAATCT TTTGACCTAC AAAAAATTCT CGTGCTGATT TTTTGAAAAA	21960
ATCTGGAGAT CCAAGAGCAT AAATTGAAGA TACGGTTGCA ACAACAATTA CATCTCGTCT	22020
TTTAGCAAGA GACGTTACCG TTCTTATTCG CTTAATTTCT ATCTCAGTAT TAATAGTGGC	22080
TTCTTTTTCA ATAAATAAAT CTTTGAAGG AACATAAGAT TCTGGCTGAT AATAATCATA	22140
ATAAGAAACA AAATACTCAA CAGCATTATT TGGAAAAAA TCTTTAAACT CTCTATAAAG	22200

CTGTGCTGCT AATGTTTTGT TGTGACTGAC AACTAAGGCA GGCCTGTTTA GATCTTTTAT 22260
TATATTTGCA ATTGTAAAAG TCTTTCCACT GCCTGTAACA CCTTTTAAAG TTTGATATTT 22320
ATTTCCAAGC AAAATAGAAT TTTCAATCTC TTTTATTGCC TTAGGCTGAT CCCCAGCAGG 22380
AAGATATTCT GACTTCAAAA AAAAATCTAT CATTAATTTA ACGACCAAAA TTAAATACAC 22440
ATTCTTATAA ATTATATGAT AATAAATTCT ATATCAAGTA TATAATTCAT TATAAATCAA 22500
TATAATTTAA TTAATCTTTG TTTAATAAAA TAAAAGGAAA TATTGATGCT AAAAATCGAA 22560
GCTAAAAGAA AATTGAAAAA TTATATTCTT CTTGAAGAAG ATATGCATTT TAAAGAAGAA 22620
GCAATAAAAA TTCAAAAAC AAATAATTCA ACAGAAATTT TAAATAGATT TTACAAAGAT 22680
CTAGAATTTG GCACTGCTGG AATAAGGGGA ATCATTGGAG CTGGAACATG TTACATGAAC 22740
ACATATAATA TAAAAAAAT AAGCCAAGGA ATATGCAATT ACATACTTAA AATAAACAAA 22800
AACCCTAAAG TTGCAATAAG CTATGATTCA AGATATTTTT CAAAAGAATT TGCTTACAAT 22860
GCTGCTCAAA TTTTTGCCTC AAATAATTTT GAAACATATA TATATAAAAG TTTAAGACCT 22920
TCCCCACAAC TATCTTATAC AATAAGAAAA TTTGACTGTG ATGCTGGCGT TATGATAACA 22980
GCAAGTCATA ATTCAAAAGA ATATAATGGA TATAAAGCAT ATTGGAAAGG TGGAATCCAA 23040
ATAATACCAC CTCATGACAC ACTAATAACT AATGAAATTA AAAATACAAA AAACATAATA 23100
AATACAATTA CCATAAAAGA AGGCATTGAA AAAGGGATCA TCAAAGAACT TGGCAATGAA 23160
ATAGACGAAG AGTATGTGAA AGCAATAAAC AAAGAATTGC CTGATTTTGA AAAGAATAGC 23220
AAAGAAACAA ACTTAAAAAT AGCCTACACA GCATTACATG GCACCGGTGG GACCATAATA 23280
AAAAAACTCT TTGCAAAATAG CAAAATACGG CTTTTTTT TAG AAAAAATCA AATACTACCA 23340
AACCCTGAAT TTCCAACAAT AAATTATCCT AATCCAGAAA AACAAACATC AATGCTTAAA 23400
GTAATAGAGC TTGCAAAAAA AAAAGATTGT GACATTGCCC TTGCAACAGA TCCAGATGCC 23460
GACAGAATAG GGATTGCATT TAAAGATCAA AACGAATGGA TATTCTTAAA CGGAAATCAA 23520
ATATCATGCA TTTTAATGAA CTATATACTC TCAAAAGAAA AAAATCCTAA AAATACATTT 23580
GTAATATCAT CGTTTGTAAC AACACCAATG CTAGAAAAAA TTGCAAAAAA ATATGGTTCT 23640
CAAATTTTGA GAACCTACAC AGGATTTAAA TGGATAGGAA GCTTAATTAA TGAAATGGAA 23700
AAAAATGAAC CAAATAAAAA ATTTGCTTTT GCATGCGAAG AAAGTCATGG ATATCTAATA 23760
GGAAGAAAGG TTAGAGATAA GGATGCATTT TCAGCCATAA AAGGAATTTG TTCTTTAGCA 23820
CTTGACTTAA AAGCCAAACA ACAAACAATT AAGGATTATC TTGAAAAGAT ATACAAAGAA 23880
TTTGATATT ATGAAGAATT TAATATAGAA AAAAATTTT AGGGGGCCAA TGGAGAAATT 23940

CAAAGAGAAA AGTTAATGCT AAAACTAAGA AAAGAACAAA AAGTACAATT TGCAGGAATT	24000
AAAATAATTG AAAAATTAGA CTATAAACT CTTAAAAAGA TTAAC TTAA AAATGAAATT	24060
TCAGAAATTA AAGAATATAA ATACCCCAT AAGCAATAA AATTTATACT TGAAAACGAA	24120
ATTGCAATAA TTGTAAGACC CTCTGGAACA GAGCCGAAAA TTAAATTTTA CATATCTGTA	24180
AAACTAGAGT ATAAGGAAAA ACATAAAATA TTTGATATAA TAAATGCAAT AAAGATGGAG	24240
ATAAAAAAAT ATTAACATAA CAGAAAATTT AATAAATTTG GTAGAAATAG ACTCAAAGA	24300
AATTGCAAGA AAAAATAAAA ATAAAGAGGT TTCAATTTGG CACTTATTAA TGTCTATAAT	24360
TACCACTCCC AAAAATCCG AAATAAAATT TATAGATAGC AAACTCTAA AAAACATTAA	24420
ACAAGAAGTT ATATCTGAAA TAGATAAATT AGAGAAAATT TTAATAGAAA AAAACGAAAT	24480
AATTATTCCC AAAATCAATA AAGAAATCTT TGCTCTCATA AAAGAAGCTA AAAAGGAATT	24540
TAAATCCAAA CCTTTAATAG GGGCAAAGA AATTTTTTAT CAAATATTAA AAAATAAAAA	24600
ACTTCTTAAA AACATAAAC TAAGTAAATC TAGCTTTAAC TTAAAGATC AAAATATATT	24660
AGAATACATG GAAAAAATA AAATAAGATT AATTGAAACC TACAAAGAAT TTGATGAAGA	24720
AATACGACTT GAAAATGAGC ACTTTGAAAT TGGAAAGTAT GTCAAAAATT TAACAGCACT	24780
TGCAAAAGCC AAAAATTAG ACCCCTTGGT TGGAAGAGAA GCAGAGATTA AAACCTTAC	24840
AAATATACTC TTGAGAAGAA ATAAAAATAG TGCAATGCTA ATAGGCGAAC CTGGTG TGGG	24900
AAAAACAGCA ATAGTTGAAG GCCTTGCATC AAGCATAGTG CAAAAAATA TAAGTAGCAA	24960
ACTACAAGAC AAAACAATTC TAATGCTTAA GGTTCAAAC TTGGTATCGG GAACAAAATA	25020
TAGAGGCGAG TTTGAAGATC GTTTAAATAA TATAATTAAG TATATTGAAA AAAACAAAAA	25080
CACAATCATA TTTATTGACG AAATACACAC TCTAATAGGA GCTGGAACT CTGAAGGAGC	25140
TCTTGATGCA TCAAATATAC TAAAACCATC ACTTCTAGA GCTGAAATAC AAATTATTGG	25200
CGCAACTACT TACAATGAAT ATCGAAAAATA TATTTCAAAA GACAAAGCAT TCGCCAGAAG	25260
ATTCCAAACA ATTACCGTAA AAGAGCCTGA TGAAAAAGAT aCACTAAAAA TAATCGAAAA	25320
TATTGCAAAA AATTTTGAAG ACTATCATGG AGTGATCTAT GAAAAAGCG CGCTTTTAAA	25380
TATAGTAAAA CTTTCATCCA AATATCTAAT AAATAAAAGA TTTCCAGATA AAGCAATAGA	25440
TATAATAGAC ATTGCCGGCG CAATTAAAAA GGAAGAACTT ACAAAGACA ACATCATAAC	25500
ATCAGATGAT ATACAAAAGG CAATAAATGA AATATTATCT ATTAACAG CAAATAACAC	25560
TAAAGAAGAA ATTTTAGAAT TAAAAGAAAT AGAAAGCGAA ATAAATAAAA AGGTGATCGG	25620
ACAAAAACAT GCGGTAAGCG AACTTATCAA AGAAATTATT AAAGTCAAAC TTGGACTTAA	25680
TGACGATTCT AAGCCTTTAA CTTCAATATT GTTAATAGGA TCAAGTGGAT GTGGAAAAAC	25740

TGCTTTAACT GATGAAATAT CTAAAAAAT TATCAAAGAT CAAAATTCAG TATTAAAACT	25800
AGATATGTCA GACTATAAAG AAGAAAAC TC TATTTCAAAA TTAATTGGCA CAAATCCAGG	25860
ATACGTAGGC TACTCTGATG GAGGCATTCT GACAAATAAA TTAAGACATT CATTTGAAAC	25920
TTTAATATTG TTTGAAAATA TTGAAAATGC CCACAGCTCT GTATTAAACC TAATAAGTCG	25980
AATGCTTGAA AACGGAGAAC TTATTGACAG CAAAGAAGAT AAAATACTAT TTAAAAACAC	26040
AATTATAATA ATGACTACAA ACATTGGATC TAGAATGCTT CTTGGAGAAA AAAATATTGG	26100
ATTCAACAAA AATCAACAAA AAAGCTTAGA AACAAAAAGC TTTAAAGAAG AAATAAACCA	26160
AGATCTTGAA AAAAGATTTA AATTATCCTT TTTAGACAGA ATTCAAAAAA AAATCATCCT	26220
AAATATCCTT ACaAAGGAAA ATGTAGAAGA AATTTGCAAA AACTACTTAA ACACCCTTAA	26280
AACAAAATTT CACTCTAAAG GAATCGAGAT AGAAATAAAA AAAGATGTTG ACAAATTCAT	26340
AACCACAAA TACTATAAAA AAAATTCAGG AGCAAGAAGC GTAATTGCTG CAATAAAGGG	26400
GAAAATAGAA GAAAATATTA TCACCAAAAT AGCTGAAAAT CAAAACATAA ATAAAAAATC	26460
GATTTATTTA GAAAAAGAAA AAATAATAAT AGAATAAAGA GGAATTATAA TATGTTTAAA	26520
AAAGTAGAAA ACAAGGCAAA TTTTCCTAAA ATAGAAGAAA AAATATTAAA ATTTTGGAAT	26580
GACAATAAGA TCTTTGAAAA ATCAATAAAG CAGAGAGAAG GATGTGAAGA ATTTACATTT	26640
TATGACGGAC CGCCTTTTGC AACAGGACTT CCTCATTTTG GACATTTTGT TCCAAACACA	26700
ATAAAAGACA TAATTCCAAG ATATCAAACA ATGCAAGGCA AGTATGTTAA AAGAAATTTT	26760
GGATGGGATA CTCACGGACT ACCTGTTGAA TACGAAGTAG AAAAAAATT GGAATTTCT	26820
GGAAAATACG AAATAGAAAA TTATGGCATT GAAAATTTTA ACAAAGAATG CAGAAAAATA	26880
GTAATTAGAT ATACAGAAGA ATGGAAAAAT ATAATCTTGA GACTTGGACG ATGGGTAGAT	26940
TTTGAAAAGG GTTACAAAAC CATGGATATA AGCTTCATGG AATCCGTGTG GTGGGTATTT	27000
AAAAATCTTT ATGAAAAAGG TTTAATCTAC GAAAGTTACT ATGTACTACC CTATTCCCCA	27060
AAGCTTGCAA CTCCGCTTTC AAATTTTCGAA GTGAATCTTG GAGAATATAA AGAAGTCAAT	27120
GACCCATCAT TAACAATAAA ATTTAAAATA AAAGATAAAA ACGAATACTT ACTAGTGTGG	27180
ACAACCACCC CCTGGACATT GCCCTCAAAC CTTGGAATTG CAGTAGGACA AGAAATAGAA	27240
TATTCTAAAA TTTTGTGACAA AACAAAAGAA GAGATTTTAA TACTTGGATC AAAAAAGCTT	27300
AATAGCTATT ACGATGATGA AAATTCATAT ACTATTATAG AAAAATTCAA AGGCAGCAAG	27360
CTTGAAGGCA TAGAATATGA ACCTATTTTT AACTACTTTT TAGAACAAAA AGATAAGGGG	27420
GCTTTCAAGG TACACACAGC TGATTATGTT ACAACTGACG ATGGAACAGG AATTGTTTCAT	27480

ATTGCTCCTT TTGGAGAAGA AGACTACAGA ATACTCAAAA AACACACAAA TGTCGATATA	27540
ATAGACCCCT TAGATGCTGA ATGTAAATTT ACAAATCAGG TAAAAGATTT TAAAGGACTT	27600
TTTGTAAGAG ATGCTGATAA AAAAATAATA GAAAACCTAA AATTACGCAA TTTTTTATTC	27660
AAAAGAGAAA ATTATCTACA CAGGTATCCA TTTTGTATA GAACAACTG CCCAATTATT	27720
TACAGACCAA TAAGTTCGTG GTTTGTAAAT GTAGAAAAAA TAAAAACCAA ACTTTTAGAG	27780
GTAAATGAAA AAATTAATTG GATGCCAGCC CATTTAAAAA AAGGAAGATT TGGAAAATGG	27840
TTAGAAAATG CAAAAGATTG GGCAATAAGC AGAAACAGAT TTTGGGGAAA TCCAATTCCA	27900
ATTTGGATAT GCTCAAAAAC AGGAAAAAAA ATTTGCATTG GATCAAAAAA AGAGCTTGAA	27960
AACCTATCTG GCCAAAAAAT CGAAGACTTA CATAAAGACC AAATAGATAA AATAACCTGG	28020
CCAAGCAAAG ACGGTGGCAA ATTTATCAGA ACAAGCGAGG TTCTCGATTG TTGGTTTGAA	28080
TCTGGAGCAA TGCCTTACGC AAGCAACCAT TATCCATTCA CAAATGAAAT TAATTTTAAA	28140
AATATATTTT CTGCTGACTT TATTGCAGAA GGTCTAGATC AAACAAGAGG ATGGTTTAT	28200
ACTCTTACAA TCCTGGGAAC TGCTCTTTTT GAAAACACAG CATTCAAAAA CGTTATTGTA	28260
AATGGACTTG TGCTTTCAAG CGATGGAAGA AAAATGTCAA AATCCTTTAA AAATTATACA	28320
GACCCAATGC AAGTAATAAA CACCTTCGGA GCTGATGCTT TAAGGCTTTA TTTAATAATG	28380
AGCCCTGTAG TTAAAGCTGA TGATTAAAA TATAGCGACA ATGGAGTAAG AGACGTTCTT	28440
AAAAATATAA TAATACCCAT TTGGAACGCT TATTCATTTT TCACAACTTA TGCAATAATT	28500
GATAAATTCA AACCTCCAAA AAATCTCAGC CTGGCTAAAA ACAATAACCT TGACAAATGG	28560
ATCATAAGCG AACTTGAAAG TCTAAAAAAA ATACTAAATA CAGAAATAGA CAAATACAAT	28620
CTAACAAAAT CAATAGAATC TTTACTTGAA TTTATAGATA AATTAAACAA TTGGTACATA	28680
AGAAGATCAA GGCGAAGATT TTGGAATCA GAAAACGATA AAGACAAAAA TGATGCCTAC	28740
GAAACATTAT ATTATGCAAT CAAAACCTTA ATGATTTTAC TTGCACCTTT TATTCCATTT	28800
ATAACAGAAG AGATTTATCA AAATTTAAAA ACTGATGAAG ACAACAATC AATACACCTT	28860
AACGATTATC CAAAAGCAA TGAAAATTTC ATTAACAAAA CAATTGAAGA GAAAATAAAT	28920
CTCGCAAGAA AAATAACTTC AATGGCAAGA TCACTCAGAT CATTGCACAA TATAAAAAATA	28980
CGCATGCCTA TTAGTACGAT ATATATCGTC AAAAAAATC AAAATGAACA AAATATGCTA	29040
ATGGAAATGC AAGAAATAAT ATTAGATGAA ATAAATGCAA AAGAAATGAA AATAAAAGCT	29100
AACGAAGAGG AGCTTATAAC TTACAAAGCA AAAGCAAACCT TTAAAGAACT TGGGAAAAAG	29160
CTTGAAAAAG ATATGAAAGC GGTATCTACT GAAATTAGCA AGCTAAAAAA TGAAGACATA	29220
ATAAAAAATA TAAATGGAAC ATCCTACGAG ATAAAAGTAG CCAATGCAAA GCATTATTTA	29280

TCATTAAATG ATATAATATT AGAAAGAGAA GAAAAAGAGA ACTTAAAAGT AATAAATGAA	29340
GAATCCATTA CAATAGGAAT AGACTCACTA ATCACTAAAG AGTTGTACTT GGAAGGGCTG	29400
ACAAGAGAAT TTGTAAGGCA AATACAAAAT TTAAGAAAAG AAAAAAATTT TGATGTTAGC	29460
GATAGAATAA ATTTATACAT AGAAAAATAAT GAAACTTTGA AAGAAATGCT AAATAAATTT	29520
GAAAAATACA TTAAAACTGA AACATTAGCC TTAAATATCA TATTAAACAA AAGTAAGCTA	29580
GAAAAAATAA TAAACCTTGC CGATGACATA TTTACACTAA TAGGAATTGA AAAATGTTAA	29640
AAACATTAAC AAAAATAATT ACCATTTTCAT GCCTCATAGT GGGATGCGCA AGCCTGCCTT	29700
ACACTCCTCC AAAACAAAAT CTAAATTACT TAATGGAACT TTTACCTGGC GCAAATTTAT	29760
ACGCCCATGT AAATTTAATT AAAACAGGT CTATTTATAA CTCTTTAAGC CCTAAATATA	29820
AATCAGTTCT TGGGCTTATA AGCAATTTAT ACTTTAGCTA TAAAAAAGAA AATAACGATT	29880
TTGCTCTACT AATAATGGGT AATTTCCCAA AAGATATTTT CTGGGGAATT CATAAAAATA	29940
GAAATACAGA ATCAATAGGC AATATATTTA CAAATCCAAA ATGGAACTT AAAAATTCAA	30000
ATATATACAT TATTCCAAAC AAAGCTAGAA CTAGCATTGC AATAACCCAA AAAGATATAA	30060
CCGCAAAAGA CAATAATATG CTAACAACAA AATATATTGG GGAAATAGAA AAAAATGAAA	30120
TGTTTTTTTG GATTCAAGAT CCAACATTAT TGCTCCCAA CCAAATAGTA AGCAGCAAAA	30180
ATTTAATTCC CTTTAGCAGT GGAACTTTGT CTATAAACAG CTTAAATCAA GAAGAATATA	30240
TTTTTAAATC CTTAATCAA ACAAATAATC CACCAATACT AAAAATATTG TCAAAAAAGT	30300
TAATTCCAAC CGTCTTGACA AACATGACAA ACCTCACAAT ATCAAGCCAC ATAAAGACCA	30360
CAATAAAAGA CCAAATACG GTTGAAATAG AATTTAATAT TCAAAAATCT AGTGTTGAAA	30420
GCCTTATAGA AAAACTAGCT TCAAATATTC AAACCTAAAA TTTCTGCCAC TCCACTAAAA	30480
TGAGGTATTA TTTTGATTTT TGCAAGTAAA ATAATGAAAC AAAGCTCCAA TTTTACCAGA	30540
TTCATTATTA AATTTAGTAG GCTCAAGTGC TACAAGATTT TTTATATTAT TATTATTATC	30600
AAAAGCCATT TCTAAAGACC ATAAATTTTC TAATTTTTC TATATTCTAT CTATTAAATC	30660
GGGTCTTGCG CTTATTCCTC CTCCGATCAA AATTTTTTCA GGATTCAAAA TAAAAGTTAA	30720
ATTAAAAATA CCAAATGACA AATTCTCAA AAATCTATCA ACTTCATTTT TGGCATGAAT	30780
ATTCCCATT TCAGCTAGAT CAAAAACAAA TTCTCCTGAA ACCTCTTTTA AAGGTTTTC	30840
TAATCGCATA GCAACTCTTT TTCTTAAAGC CGAAACAGAC GCAATGGATT CCCATTTGCA	30900
ATTAAAGGGA ATATTGTTGC TAATACCTCC AGTAATCATA AATCCAACCT CTCCGGACAT	30960
AAAAGAATTT CCTCTTAAAA GCTTGCCATT TGCAAAAATT CCAGCACCAA TTCCTGTGCC	31020

AAGAGTTATA GCAATAAAAT TATTAGAGTC AATAGCATTA CCCTTAAATT TTTCTGCTAA	31080
GGCTACACAA TTAGCATCAT TTTCAATCTC TGTACTTACT CCGGTTAAAG ATTCTAATCG	31140
CTCTTTTAAA GGATAATTAA CAAATCCAGA AATAGCATTT ACCCTAAGAA CATTTCCCTT	31200
AAGATCAACA AACCCAGGAA TACAAATTGC AACTCCCGCA ATATCACTTG ATTCTTTGTA	31260
AGAATTAATA ATATTAATA AAATATTTAC TTGTTCGTCA GAAGTAGCAC CTGTGCTTAT	31320
TTCATTTTTTA TCAAAAAAAA CACCGCTTGA ATCTGAAAGC GAATATTTGG TACTAGTCCC	31380
GCCAATATCA ATCGCTAAAT AATGTTTCAT ATTTATCCTC AAGGCCTAAT TGTACATAAA	31440
TGATCATAAA TTTTCTATAG CAATATAAGA AATTTTAGAA ATCTTGTTTA TAACTATTTG	31500
CGCTTTAATC ATCTCCTTCA AATAAGAAAC ATGGGAAATT ATGCCAATTT GTCGCCCAGT	31560
CATCATTTGA AACTTAGAAA GCTTAGGCAT AACTTGAGCC AAAGTATCTT CATCAAGATT	31620
GCCAAAACCT TCATCTAGAA AAAAAGCCTC TATTTTAAAC TCACTATCCC TTATTTTATC	31680
AGATAAAGCT AAGGACAAAG CTAAAGACAC AAGAAATTC TCACCCCCAG ACAAAGTTTT	31740
TACCGTTCTT ATTTTATTAA CATCTTTTTT GTCTTCAATT AAAAAATCAA ACTCTTTGCT	31800
CTCTTTGTTT GTTTTGAGCT CAAAATCAGG AAAAATCCAC CTAAATACT TTTCAATTTG	31860
CAGTCTTAAA ATATCATTA TTAaaaaaAGT TTGAACATAA TATTTCAATC CAGAAGATCT	31920
AATAACGACC TTCCTTAATA CATCTAGCTT ATCTTTCCTT TCTTTAGCAA GATTTAATTC	31980
ACCCCTTAGC GAGTCTAAAT TAATTTTTTG TTGATTAATC TTTTTTTGAA GAGTTTGAAA	32040
ATTTAAAAGC TTGATTTTAT ACTTTTCAAT ATCTCTGGAT AAAAAATCAA GCTTAGAACT	32100
AATTGATAAA CTCAATTTTT GCAAAAAAGA CAGACTATTC TTATTAATTT GCTCTAAGTC	32160
AGTTGTTGAT TCAAAAGAAA ATGAACTAAA AAAAACATTT TTTAAATTTG AAATTAGATT	32220
AATAAAATTA TTTTGCTCTT CATTTAATCT CGCTTTTAAA GTCAATATAG ATTCCTTTGT	32280
AAATTTAATT TGTGTTTCGG TTTTAATTTT TAAATCTTCT AAATTTTAA GATTTAAAAC	32340
AAGCATATTC CATTCATTTT CCACACTTTT CTGCTTAGCC AAAACAACAT TAAATTCCTT	32400
TTCCAAAGAA GAATAATCAT TAAACTTAA ATTTAAATTA AGTTTAAACA ATAAATCCTT	32460
AATCTTTAAA AGATTTTGAT CAAAATTTTT ATTTTCAAAA GAAATTTCAA TTTTAAATC	32520
TTTTTTCTTA GCCTTAAATT GTTCAAGCTT TTCTAATTTA TTTTCAAATG CTAAAATTTT	32580
TTCTCTGTCA AAATAATTTA TGTATTTGTC AAATAAATTT TTTCCAATCA ATCTTAAAT	32640
TTCAGCATTA TTCTTTTCAA ACTCCAAAGC ATTAACCTCT TGTTTAGAGA TTTCTTCTTG	32700
TCTACAAGAT AGCTGATATT TAAGCTCATC AATTTGATTT TGTATCAAAT GAAGCTTTGA	32760
ATTTAAAGCG TAAAGCTCTT TCAAACTGCA AAGCGATAAT TTATCTTTAT GCTGATAATT	32820

TTTATATTCA GCCTCAATAT ATTTTAGCTT CTCTTTATCA CTCTCAATAG AAAAATTTTT	32880
ATCATCAAGA TATTTTAACA ACTCTTTATA CAAGTCAATC TTAATAATAT TTTTTCCTT	32940
ATTTTATTA AAATCTTCTT TGCCAGTAGA TTTTAATAAA AATTCTAGCC TATCTCTATA	33000
TTTTGAAATC AACTCATCAT TAAAAGTTTG GAACAATTTT AATGCTTCAT AGTAAACATA	33060
TTTGTCAAAA TCAAAATTAG ATTTCTCAGA AGAAATGCTT TTAATCTCAT CATTTTTTTT	33120
GCTCTGAGAT CTTAATAATT CTTTTTTTTT ATCCTCAAGA CTATTTTTCC TTAAAGCAA	33180
GCTTTGATAA TCATTCTCAA CAAGTTTAA ATTAAGAA TGCAATTTT TATTATAAAG	33240
CTCCTTAAACA TAATTAAAT TAAATCATT GCTATACAAA TCTTTAATTT CTTCTAAATT	33300
ATTCATCACT TTTGAAAGTT CTAAATCAAG CAATCCAATA TCATTAAACA ATTCGCCTTG	33360
TACAGCAACT AAATTTTTCA AACTCCAAA ATCTGAACAT AAATAAACTT TTCGATCCAA	33420
ATCCAAATTT TCTTTTAATT TCTTTGAAG GGAATGATCC TTCTCTAAAG AATTAAATA	33480
TTAATCTGA GAAGATAATT GATCGTTTAG AGAAGACATT TCAATTTCCA AGCCCAAATA	33540
TCTCTCATTA GACGCTATTG CCTGATTACA TAAAGAAATA GCTCTTCTAA TATTTTCAAG	33600
ATCAATTTCT AATCGATCAA TATCAACCAA ATCCAAATAA CCTTTAAGGG ATTTACACTC	33660
ACTCTCATCA TAATCAAGAA TTGATTTTTT ATAAGATTCA GAATTCAACA ATTTATCTAT	33720
ATTAAACTTT GTGCGCTCAA AATCACTTTT TAAATAAAAT TCCAAATTAT CATATTTTTT	33780
CAAATTAATA ATATTATCAA TTATTGCAGC TTTCTCTTTG GGAGTTGACG TTAAAAATTC	33840
TTGAAAATTG CCTTGTGCTA AAATTACAGT TTGACAAAAT TGGTTAAAGT CTAATCGACA	33900
AAGACTTTTA ATATGCTCTA AACATCGGT TCGACCCTCT ATAATCCTAT TATCAAAAAA	33960
ACAATTAAGC AACATGCTCT TAGGAGTCTC TATATTTTTT ACATTAAGCT CAACAAAAGA	34020
TTCATAAATC TTCCCAGAAA TAGTAAACGT TAATTTAACA TAAGCGCTAG TCTCGCCTTT	34080
TGATATAATA TCTACAATTT TTTTCCAAG TCTGTAAACA CGAGCATATA GTGCCAAAGT	34140
TATGCAATCT AAAATGGTGC TTTTGCCTGA TCCAGTATTA CCAGAAATTA AAAAATGCC	34200
CGATTGTCTT AAAAGAAGTG TATCGAAAT CAACTCATGT TCGCCTTTAT AAGAAGCAAT	34260
ATTTTTAAAT ATGAGCTTAT TTATCCTCAT ATTCACCCAA ATATCCGTTA GCTAAAACCT	34320
CGTTAAAAAG AGAAATAAGC TCTTCTTCTT TAAATTTGAT ATCCCTAATA ACACCGTTCT	34380
CAAAATCCCA TCTCAACTTT TTCTCAAAAA AATATTTTTT ATCCATTTCA AGCACTTCAA	34440
GTTCTCCAAT AAAGTTGGAA TCGTCTTGCA AATCCTGACT TGAGGGTAAA GAATAGGAAA	34500
TAGAACTAA ATTCATAAAA TTAAGCCTTG CTAAATCATA AATAGACTCC TCAGCGCTAG	34560

TATCAACTGC CTCATTAAGT TCAATTTTCA AATAAATAGT AAAAGACTCT TCTTTTTTTGG	34620
AATTAGCCAA AAAATCAAGA ACTTCATTTA AAGAACCTTT AGCAAAGATT AATTTATTGA	34680
AAATCGGCAC CGGAAATGCT TCTTGCAAGA TTAATTTATT GTCATTAAAA TGTA AACGT	34740
TTATGTATTT ATCACAGGTC TCATTAAATG AATATTGCAT AGGAGATCCT GAATAACAA	34800
TATTATCTCT TAGTTTCATG AACTTATGAA TATGCCCAAG AGCAACATAA GAAAAACCAT	34860
TTCCAAAAAC ATTAAAAGGG ATAATATAAC TACCTCCCAA GGTGTCAATC TTTTACTGC	34920
TGCCAAAAAA AGAATGCGCC ATTAATATCT TAGGAATTCC TTTATACTTG TTTTCTAAAA	34980
AATTAGATAA ATTTGATATT TTTTCTCTGT AGGCATTTTC TAAATTTTCA AGAAATAGTT	35040
TGCTGGAATA CTGATCTTCC AGTCCAAAAA TATTGTCAAA ATTTTGACCT AAAATAAGCC	35100
TTTCATTTAT ATGCGGAAGA CAAACAACAA TAACTTAAG ATTTCCATTA TCTTTTAATA	35160
AAACTATTTG CTCATCAGAA TCATATTCAG TTATTAAAAA AAAATTAAAC CGTGAGAGAA	35220
GTTTTTTAT TATACTCAAA TAATCCTTTT TGTCATGATT TCCAGAAATA ACCACACACC	35280
ATTTACAAGA AGTAAAAGAA AGTTCATAAA AAAAATTATT CACTAATCTT TGCTCTTCAA	35340
ACCCAGGCCT TTTGGAATCA TAAACATCCC CGGCAACAAG TAAAAGATCT ATATTTTCTT	35400
TTTTAATAAA TTCTAAAAGA AAATATAAAA AATTTTCTG CTCCTTAAGA ATTGAAAAAT	35460
TTTCAATTTT TTTTCCAATG TGCCAATCTG AAGTATGCAG AATTTTATAA TTGCTCACAA	35520
AATACTCTCA CTTTTTTTAA TTCTTAAATT ATATTTATAT ATTATAATAC AATATATAAA	35580
CATAGGGAAT TTATGCAAAA TAAAAAGTTG ATAATAGTTG AATCGCCAAC AAAAGCCAAA	35640
ACAATAAAGA AGTTTCTCGA TGAATCATTT CTAGTAGAAG CATGCATTGG ACATGTAGTA	35700
GATCTACCAA ACAACGCAAA AGAAATCCCA AAAGAATATA AAAAATACGA ATGGGCAAAT	35760
ATTTCTATAG ATTATAACAA TGGATTTAAT CCAATTTACA TTATTCCCAG CAATAAAAAA	35820
CCAATTGTAT CAAAATAAA AAAATTAGTA AAAACAATAA ATGAAATATA TCTTGCAACC	35880
GACCAAGACA GAGAAGGAGA AACTATAGCA TTTCACCTAA AAGAAGTATT AAAAATCAAA	35940
AACTACAAAC GGATGATATT TCATGAAATC ACAGAAACCG CAATAACTGA ATCACTAAAA	36000
AATACTAGAA ATATAGACAT GAACCTTGTT AATGCCGGGG AAGCTAGAAG AATATTGGAC	36060
CGACTATACG GGTATACAAT CTCTCCACTA CTTTGAAAAA AAGTAGCTTA TGGACTTTCT	36120
GCTGGGCGAG TACAATCTGT TGGATTAAAA TTATTAATAG AGAAAGAAAA AACTAGAATA	36180
AATTTCAAAA AGGCAAATTA TTATTCAATT TTAATTCAAT GTAAACACGA GAAAAAAAC	36240
TTGTTGCTTG AAGCAAAATT AGAAGAAATT GACGGCAAAA ATATAGCAGA GGGTAAAGAC	36300
TTTGTAATG AACTGGAAA ACTTAAAAAT ATTGCCAAAA CAACAATAAT AACCCAAGAT	36360

TTAATGATAG AGCTTGAAAA AGAATTAAAA AATGGACAAA AAATTGAATT AATTTCAATA	36420
GAAACTAAAA AAATAAAAAT ACCTCCTCCA AAGCCATTTA CCACCTCTAC ACTTCAACAA	36480
GAAATAAATA AGCGTCTTAA AATTGGAACA AAGCAAATCA TGCAACACGC TCAAAAACCTT	36540
TACGAACACG GATACATTAC CTATATGAGA ACAGACTCTC ATAATATTGC TAAAATTGCA	36600
AAAGATAAAA TAACAAAAAT AATAAAAAAT AAATATGGGA AAGAGTATAT AGAGGAAAAA	36660
GATAGAATTT ATGAAAAAGA AAAAATGGCT CAAAATGCAC ATGAGGCAAT AAGGCCTTCT	36720
GAAATATTTA TTCCAAATGA AACCATAGAA ATAGAAAGCA AAACCGCTAA AGAAATTTAC	36780
AAAAATAATAT GGGATAGAAC CATTATTTCT GGAATGAAAG ATGCAATAAA AGAAAATATA	36840
AAACTGACTT TTAAATATAA AAACCTAATT TTCAGATCAA GTTTTACAAA AATAATTTTTT	36900
GATGGATTTT TTAACACAC TAAAGAACAA GATGAACATC TTAACATAAA TTTTGACTTA	36960
ATTAAAAAGG GAGATACATT TTCCATAGTT AAAATGAAAA CAAGTGAGCA CGAAACAAAG	37020
GCTCCATTTA GATACACAGA AGCGTCTCTT GTGCAAAAAA TGGAAAAAGA AGGAATAGGT	37080
CGTCCCTCGA CCTATTCTAC AATTATATCA AACTTTTtag AAAGAGAATA TGCATTCAAA	37140
CTTAACAACA CATTAATGCC AACTATAAAA GCGGCTGCTG TAATAAATCT TCTTGAGAAA	37200
TATTTTCCAG TACTCATTGA ACTAAATTTT ACCTCTAATA TGGAAGAAAA ATTAGACAAA	37260
ATAGCAATAG GAAAACTAGA TAAAATAAAA TATCTAAGTA AATTTTATAA TGGCAAAAAA	37320
GGACTAAAAG ATACAGTAAT GCAACTAGAG CCTAAAATTG ATTCCCTCTGA ATTTAGAACC	37380
GTTATTGAAA GTCAAAAAAT AGAAAAATAA AATAGCATTA ATTACACAAT AACATTGGT	37440
AAATATGGGC CTTATTTGAT ATTCAAAGGA CATAATTACT CAATTAATGC AAAAActCCA	37500
TTAGAAAATT TGTACAAAAA AGATGAAATA GAAAAAATAA TAAATGAAAA AGAGCTAAAA	37560
CCCAATATAC TTGGGGTTGA TCCTTTAACA GGACTTAATG TGATCTTTAA AAATACAATT	37620
TACGGAAACA TTGTTCAACT TGGAGAAGAT ACCCATGCCC CTCAAGAATA TACAAAAAAA	37680
GGAAAACCTA AAAAATTAAA AATAATAAAA GCAAAAAAAG CATCAACTAA AAAAATTGAC	37740
CCTGAAAACA TAACATTGGA GCTTGCTTTA AAATTGCTCT CACTGCCAAA ACCAATTGGC	37800
AAACATCCCC AAACCAATGA ACAAATCATT GCTGCAACTG GTGTTTTTGG GGATTATATT	37860
AAAACTGAAA GCGGAAGCAT TGCTTGCTCG CTAAAAAAG ATTTAAAAGC ATATGACATA	37920
AACTAGACA AGGCCATCAG CCTACTCAAC GAAAGAGCCA ATAAAGTGGG TATAATCGTT	37980
AAAACAATCA CATTTTCTAA AAACAAAATT GGCAACAAAA TATATATTTA CAAAAAAAC	38040
GACAAATTTT ATGCTAAAAT TAAAAGAAAG AAGATTGATT TACCTGATAA CATTAATCTT	38100

GAAGAAATAA ATGAGAAATA TGTATTCAGC TTGTTATAAA TATGAATGAT TTCAAACCTCC	38160
CAATTTATAA ATACAAAGAT GAATTAATTA AAGTACTAAA AAACCACAAT GTTTTAATTG	38220
TAGAAAGTCC AACAGGTAGC GGAAAAACCA CCCAACTACC AAGAATAATA TATGAAGCGG	38280
GTTTTGCAAA ATTAGGAAAA ATTGGAGTAA CTCAACCAAG AAGAATAGCT ACAGTATCAA	38340
TAGCTGAATA TATTGCCAAG CATATTGGCG TAAATGTTGG AGAAGAAGTT GGCTATAAGA	38400
TAAGATTTGA AGAAATTACA AGCCCCAAAA CCAAATCAA ATTAATGACT GACGGAGTGC	38460
TTCTGCAAGA GCTAAAAAAA GATACACTGC TTTATGAATA TGATGTAATA ATAATAGACG	38520
AAGCACACGA AAGAAGTTTA AACATTGATT TTATATTGGG TCTTATCAAA GACATTTCAA	38580
GGAAAAGGGA TGATTTTAAA ATCATAGTTT CGTCTGCTAC AATAAACACA AAAATATTTT	38640
CAAAATATTT TAATAATGCA CCGGTTGTTA GTATTGAAAC TATCACTTAC CCAGTACAAA	38700
TAATATACAA TCCTCCTCTT TTAAACACAT CAAAAGGAAT GATATTAAAA ATAAAAGAAA	38760
TTGTCTTAAA CGTAATAAAA GAAAAAAAAG CGGGAGATAT TCTTATATTT TTATCTGGAG	38820
AGAAAGAAAT AAAAGAACT ATAAAAGAAT TACAAGAATT AAACTCAAAA AAAAATTTAA	38880
TAATATTTCC TTTATACGGC AGAATGCCCA AAGAAGCTCA AGAGCAAATA TTTATGACTA	38940
CTCCTAAAAA TAAAAGAAAA ATAATAGTGT CAACAAACAT AGCAGAAACT TCAATCACAA	39000
TTGAAAATAT TAAAATAGTA ATAGATAGTG GAAAAGTTAA AACAAATAAA TTCCAAACAA	39060
AAACTCATAC CTATTCGCTC CAGGAAGTTC CAATTTCAAA ATCATCAGCA ACTCAAAGAG	39120
CTGGTCGAGC AGGAAGACTT TCAAAAGGAA CTTGCTACAG ACTTTACAAA AGAGAAGATT	39180
ATCAATTAAG AGAAGATTAT CAAAAGAAG AAATATATAG AACAGACCTA TCTGAGGTAG	39240
TGTTGAGAAT GGCAGATATT GGAATTAGAG ATTTTACCCA CTTTGACTTT ATCTCAAAAC	39300
CATCAACGCA TTCGATTCAA ACTGCAAGCA AAATATTAAA ATCTCTGGAT GCTATAAACA	39360
ATAAAAACGA ACTTACAGAA ATTGGGAAAT ATATGATACT ATTCCCATTA ATACCAGCAC	39420
ATTCAAGAGC ATTAGTCGAA GCAATGATAA ATTACCCACA AGCGATCTAT CAAACCACAA	39480
TAGGTCTATC ATTTTATATCC ACAAGTGGAA TTTTCTACT ACCCCAAAAT GAAGAAATGG	39540
AAGCTAGACA AGCTCACTTA AAATATAAAA ATCCAATGGG AGATTTAATT GGGTTTGTTA	39600
ATATCTTTGA AGATTTTAAA AAAGCTCTAA ATAAAGAAGC TTTCACAAAG GAAAATTATT	39660
TAGATCTACA AGGACTTGAA GAGATAGCAA ATGTGCAAAT GCAGCTTGAA AACATTATTA	39720
GCAAATTAAA TATACCAATA ATACAAAAAG GTGTTTTTGA CAACGAAGGA TATTTAAAAAT	39780
CAATAATGAG AGGAATGAGG GATTATATTT GCTTTAAAAC TTCAAAAAG AAATATAAAA	39840
CCATCAAGGC TCAAAACGTA ATAATTCATC CTGGATCACT TATTAGCACC GATTCTGTGA	39900

AATATTTTGT	TGCAGGAGAA	ATTATAGAAA	CTACAAAAAT	GTATGCAAGA	TCTATTGGTG	39960
TCTTAAAAAA	AGAATGGATT	GATGACATTA	TCCTTAATGA	AGAGTTTAAA	CATAACGACA	40020
TATCTAGCAA	AGAGAACCAA	ATAACAAATA	CCGGGCAGAC	AAAAATTATC	AATGAAATCA	40080
AAATAGGGAA	AAAAATTTTC	AAAGCGGAAT	ACAAAAATAA	CATTTATGTA	ATAAAAAATTA	40140
ACCTAGAAAC	GCTAAAAGAA	ATAATTTTTA	AAAACGAACT	AAACAATCAA	AATAATGAAG	40200
ATCTCAAAAA	AATTAAAAATA	CAATTGATGC	ATAAAAAATAT	AACGGTTTTT	AACAACAAAA	40260
AATTTTTAGA	AACTATAGAA	ATAGTCAAAA	ACATGGGAAA	AGATTGGCAT	TGTATAAAAA	40320
AATATGAAAC	AAAGAATGTA	AACATTGACG	AACCTGAAAA	AATGAAAAAT	CTTTTAGAAT	40380
GCACAATGCA	ATTTATAAGC	TTTCCCCCCA	AAAAAACGCG	TCTTTTTTTA	TCGTTGGAAA	40440
CAGATTATTC	TGGAAATTTT	AGACTAAAAC	CCAAACAAAA	TTTCATAATG	GCAATAGAAG	40500
AATCTATAGA	AAGCATAAAA	AGCCTTATAG	AAAACAAAGA	ATACATACAA	AAGTTACATT	40560
TTATAAAAAA	ATTAATAAAT	AAGGTTTACA	AAAAATTAAA	TTACTTTTTT	TAAAAACTAA	40620
ACTTTGAAAG	CCTTGTTATA	ATATAAAATA	TAATAATCAA	ATATTATTCA	AAGTTAACAG	40680
CAATGAAGTT	TATAATAAAT	TATGAACTGG	CTATCCTTTT	TTTATGTTTT	ATTATTTTTA	40740
TTAATTTTTC	CTTTTGAATT	ACAGAGTAAT	AATAAAGAAA	ATATAGAAAA	TTTAATAAAG	40800
CTACATATGC	TTTATGATTT	AACCAATAAC	CTGTCAAAAG	AATTAGAAAC	AATAAATAAA	40860
ATTAAAAATT	TTGACTTAGA	ACAACATTAT	CTGCTAATTA	CAAAATATTA	TCTAAAAATA	40920
AAAAAATATA	AAGAAGCTAA	TGATTTTTTA	AAAAAAATAA	ACCAAAAAAA	GATCAAAAAT	40980
CAAAAAATAA	AAAACGAAAT	CATTTGCTA	AAATTAAGAA	TAAATGAAGA	TAATATTAAT	41040
GAAGAAGAAA	TCAAAAAAAT	TTTAAATAAC	GAAAAAATA	TAGATGTCAA	AATAATTTAT	41100
CAAATATTCA	GTCTTATAAA	ATTTAAAAAT	AAAAAATTAG	CAAATAAAAT	TAAAAACATA	41160
ATACTAACAA	ACTATCCCAA	AAGCATTTAT	TCTTATAAAA	TAAAAAGAAA	TGAATAAAAA	41220
AATATTAACA	CTGCTAGTAT	TGATTTTAAG	TATTTTCATCA	GTACTAATGC	TGTCCAAATC	41280
AATCACCAAA	AAATCCAAAT	ACAAAATTAT	TAGGGATTAT	TTCATAAACA	GCAATTATGT	41340
TCTGGTGAAA	ATTGAAAATA	AAGATCTAAA	ATTTACCATA	TCAAAACCTA	TTTACGACAA	41400
AAAGCTAAAT	AATTACTTCT	TTAAAGGCCA	AACAACAAGC	CATTTCTTAA	TTTCTAACAA	41460
TGTTGACATT	GCAATTAACA	CAAGTCCATA	CGAAGTTAAA	CAAAACATGT	TTTCCCCAAA	41520
AGGACTATAC	ATATATAATA	AAAAAATGAT	TTCAAAACAA	ATAAATAACT	ACGGAGAGAT	41580
TGTAATAAAG	CACAACAAAA	TTATATTAAA	TCCAAGGAA	GACGAAATAG	AAAACGCGA	41640

TTATGGATTT AGCGGATTTT TTGTTTTAAT CAAAAACGGA AAGTATAAAA AAAATTTTAA	41700
AGAAACAAGG CACCCAAGAA CAATAATAGG AACTGATAAA AATAACAAGC ATTTATTTCT	41760
TGTTACAATA GAAGGAAGGG GTGTCAATAA TAGCAAAGGG GCCTCTCTTA ATGAAGCTAT	41820
TGATTTTGCA TTAAGCTACG GCATGACTAA CGCTATTAAT CTAGACGGGG GGGGCTCAAG	41880
CACTCTTGTT GTAAATCAA ATAACGCTCC TTACAAATTA AACTTCACAG CAAACATCTT	41940
TGGACAGGAA AGACCTGTCC CATTTTCATTT AGGAATAAAA CTCCTAATT GAAAAATCTC	42000
CAACCGATAT TAAATCCAAG CATAATCTCA GTTGTTAACC CAGAAAAATT TTTATAATTA	42060
GAAATGGAG AAATAGAAAG CATAAACAAA GGCCTAATAT ATAAACCATC AAGATCGGGA	42120
ATAAAAAGAT CAGCAGCAAG CCCCATGCTT AAAAAAAGA GATTGAAGTT ATTAGAGCTT	42180
AAATCAAAAG CATATTTAAA CCCAATTAAT GGGAAAAGCA TTCTAACCTG CTCTTTGAAA	42240
ACCATTGGAT ATGTTCCATA AAGCCCAAGC GAGAAATATC TCCCATTTGTG AGTAACAACA	42300
AAAGCCTCTT TGTAAGACAT TTCAAAAAGT ACATAATTTG CATCAAAAAA TAAATTCAAA	42360
TTAATCCCAT GATCTGCTCT GGTAAATTT GGAGCAAATT TAGTGGCGCC TGTTTTATCA	42420
GTATAATTAG TAAATTGATA AGAAAAACCT CCACCAAAG AAAGTGGATA AGAAACAATT	42480
AAATTATTAG AAGAGATGAG AAATAAAATA AAAAAAGAT ATTTCTTCAT TAACAATCCT	42540
TAAAAATTCT AAAAAATACT ATATTATTAT AGTAACACAC TAAAGTAGTA TATAAAAAAT	42600
CTGGGAAATT ATGAATACAA AAACATTATA TTTAATATCC TTAATTCTTT TAGCTTGCAA	42660
TAAAAATAAC AAAATTCCTC TCATTCAAAA ATTAGATTTG CCCAAAAGCA GCATTCTTGG	42720
CTTTAGCAAT AAAATGGGCA TAATAATAAA AGATTATGCT TTTCTTAGTA AAAGCACTAA	42780
GAAAAATAGC GAATTGGATT ATGATTACGC AATTCTACTC AGAAAAGACG AAGTCGTAAA	42840
AATTGAAAAA AACTAGAAA AAACAGAGCG CTATGGAATT GAAGGAAATT GGATCCTAGT	42900
CAATTACAAG GGAACATAAA GATACATCTT TAGCAAAGAC ATCAATATAG TCAACAATTT	42960
AATAATTGAT CATTCTAAAT AGCTTTACTA CATAACCGGA CAAAAGTCCG ATCAATGTAA	43020
TAAATTAATT ATTTTTTTTC TTATGTCTAT TTTTCTTCT TTTTCTTCT CTTTTATGGG	43080
TAGAAATTTT TTTTAATTTT CTTTTTCTT CGCAAGGCAC TCCCTAAATC TCCTTATCAA	43140
CCTTAAAAAT TAAATTCAAA ATGTTATCTA AATCATCCTC TGGATGAAGC CATAAACAT	43200
CAGAAATTTT GGCAAAAAAG GTCATTTGCC TTTTGCATA TAAAAACGAA TTTTGTTTA	43260
TTAAACCTAT TATATCATTT AAACCATAGC AAGGTCTACT TTTCCATAAC AAAAATCAT	43320
TATAGCCTAT TCCTTTAAAA GCCGGAGTAT TTTCATTGTA ACCCTTGCTA AATAAACCTT	43380
TAATCTCGGA AAGTAGTCCA CTATTAAGCA TTTCATTAAT TCTTATTGAT ATTCTGGTTT	43440

TCAAATCTTC	AAAAGATCTC	TTAAGGCCTA	TAATCACAAT	ATTTTAAAT	TCGCTACTTT	43500
GTTTTTTTTG	AAATTGGCTA	ATAGGAATTC	CTGTTTGATA	GTAAACCTCA	AGCGATCTTT	43560
TAATGCGATA	AATATCATTC	TTATTTAACA	TATTAAATCT	GATGGGATCT	ACATTTTTTA	43620
ATTCTTTTAA	AAGATAAGAT	TTACCCTTAA	GCTCTAAAAG	ATTGTTTACA	TAAATTCTTA	43680
TTTTAGAAGT	AACCAAGGGT	GTTGAAGGAA	ATCCATCCTT	TAAATGCTTA	AAATAAAAAG	43740
CAGTACCTCC	TACAAATATA	GGAATTTTTT	TTTCTGTCT	TATTTCTTTT	ACTATTTTTA	43800
AAGCTTGTTT	GTAAAAAATT	CCAATAGTAT	AATCCTTTTC	GGGATCTAAA	AAATCTACTA	43860
AATGATGCTT	TATATGTTTC	ATTAAATTTT	TACTTGCTT	TGAAGAAGCT	ATATTAAACT	43920
CTTTATAAAC	TTGAATAGAG	TCAACATTAA	TAATTTCTGC	TTTATTTTTT	GGAAAATGAA	43980
ATAAAATATT	GCTTTTGCCC	ACAGCTGTAG	GGCCAAAAAT	AAAACTACT	CTATCTTCCT	44040
TCAATTGAAT	ATCTAAATTT	ACCAGTCAAA	ACGTCATTAA	AAGCTTGCCC	TAATATTTTA	44100
TCATCAAAAA	TAGCGTGTTT	TGCTAAAGAA	ATATTGTCTA	TAATTTGCTC	AGTGCGCATT	44160
ATAGTTGCAA	CAACAAGTTC	ATAAAAAATTT	CCATCAAAAT	CTTGATTTTT	TTTTAAAGGC	44220
ACTTTAGTCA	TTTAATCTCC	TTATAAACCA	AACATATTAA	ATAAGTTTAG	CTATTTTTTT	44280
TCAAGTTTCT	TTTATCAATT	TCATCTCTAA	TTAATTCAAA	AACTTCATTT	GGATTAATAT	44340
TTGTAACATC	AATCACTAAA	TCGGTCTCTG	AAAAATAATC	ATCAATATCT	ATATTGTAAA	44400
TAGCTAAATA	TCTTTTTTTG	TCATTTTCAT	CTCTAATAAA	AGTACTGCTT	AAAACGTCAG	44460
AATACATGCC	CCCCTCTCTA	GTCATTATTC	TCTCAGCTCT	AACTTCCATT	TTAGCATAAA	44520
GATATATTTT	TAAATCAGCA	CTCTTAGAAA	TCCAAATAGC	AAGACGAGAT	GCAAGCACTG	44580
TATTATTTTT	TCTAGAAAGC	ACAGACAATC	TATTATCAAG	GATTTATCC	CAATAATAAT	44640
CATTTCTGCC	TATTATCTCT	TTTTCATAAA	ACTCTGAAAA	AGGAATATTA	TGCTCTCTTG	44700
CAATATCATG	AAAAGTATAA	TTAATAAACT	CAAGACCGTA	ATGTTTGGCA	ATCATCCCGC	44760
TTACAGTAGT	ATTGCCACAA	CCACTCTTAC	CAGAAAGTGC	TATTTTCATT	CAACATTCCT	44820
TATTTGCTCT	TTTATTTTTT	CTAAATTTAA	CTTCATATTC	AAAATCAAAT	TCTTAATATC	44880
AAGATCAACC	GCCTTATTAC	TCATGGTTGT	TATTTCTCTG	TGCATTTCTT	GAGAAATAAA	44940
TTCAAGAGCT	TTACCACATA	TCTCATATTC	AAGATTTTTA	TAAAAAGTTT	CTATATGAGA	45000
ATCTAAGCGC	ATGATCTCTT	CATTAATGTC	TAGACGAATT	GCCATTTTAG	CTGCCCTCTC	45060
TGCAATATTT	AAATCTCTAA	ATTCATCCAT	TAATTTAGAA	ATATTTTCTT	TAATACTTGC	45120
AAATAATTTG	ACATTTATAT	CACTGCAAGC	ATCTTTAACA	ATTTTAAGGT	CCCGCTCTAT	45180

TAACACAAGG GTTGACACTA TGTCTGACTT GGTATTTTCT CCTTCAAAAC TTCTTCCATT	45240
ATTGTAATGT AATAAAGCTT CTTCTAGAAC ACCTTTTAAAC AACCCATAAA TCTCTTCTTG	45300
ATGTTCACTA TCCTCATCAA TTATCAAAGC TCCTTTTAAT GATAAAAAAT CGCCCAAAC	45360
TAGTTCGTTT TTAATATTAA GATTGGTATG TGCCAAAGAA TCTCTAAGCC TAGAAATAGC	45420
CTCAATATAA TTGGGATTAA TCGTAAAATT CACACTAGGA ACCAATTCTT TATATCCTAC	45480
ATTTAAAAAA ACATTGCCTC TGCTAATATA TTTTGAAATC AAATTTCTTA TATCAAGATC	45540
ATAGCCAGAA AAAATTTCTG GTAACCTAAA TTAAATTCT AAAAAGTTTC CATTATAAGA	45600
TTTCAAATTA AACTAAACA TATAGTTACC AATTATCTTT TCCAAATAAA AAAATCCCGT	45660
CATGCTTTTC AATATAACAC CCTTACAGAA AATCGTGTA AATAAAATTA TTTCCAGCGC	45720
CCATTGTAAT AAACAAGTCT CCAGATATTA ATAACTTTT TATAAAATTA ATAGAGTCTT	45780
TAACATCCTT AAAAAAATAA GTATTCTTAT TTATTTTTTT AATATTTAAA AACAATTTAA	45840
CAGAAAGTTC ATCTGGATTA AAATTTTCCC TATTTGAAAG ATATATATTG TGCAAAATTA	45900
ATATATCGGC AGCACTTAGA ACTTCAACAA AATCGGCAA AAATTCCTTT GTTCTTGTA	45960
AGGTATGAGG CATAAAATCC AAAATTATAC GTTTATTCTT ATAAAAATTT TTAATACCAA	46020
AAAGAGTATT TTAAATTTCC CTAGGATGAT GAGCATAATC GTCCATGTAA ATCACTCCAT	46080
TTTCCTCTTT AACAACTTCA ACCCTTCTTT TTATACCGCT ATAATTTTTT GCAATTCTCT	46140
TTATTGCTTC TTCAAAATCA AAAATTGATT TCCCATTACT TTCTAAGAAA AGATTTAAAG	46200
CCAAAAGCGC TGCTGAAAAA TTAAATACAT TATGAAATAA AACAGTCTTA AGCTCAACAT	46260
TTACAAGCC TAAAAAGAA AAACAAAAAT ATTCACTCCT AACTGCAATA TTACTTATTT	46320
GAAAATCAGA TAAATCTCCA GACCCATAGC TAAAAATACT TATATCTTTT CTGTTGATTT	46380
GCCTTTTAAT TTAAAGCAA TTATTATCAT CGGAATTAAT TATCAATATT CCATTTTCT	46440
TTAAATTATT AATATACTGT AAAAAAGCCT CTTCAAGAGC CTCATAATTT TTAAAAAAAT	46500
CAACATGCTC GTAGTCAACA TTGGTTAAAA TAAGCATATT AGGGCTAAAA TTCAAAAAAT	46560
GTTTCTTATA TTCACAAGTT TCAACAATAA AAATATTGCT AATACCTGCT ATTGCAGAAT	46620
TATCTTTAAA ATCTTTAACA CTTGACCCCA CAATAACATT GGGATTTAAT CCTAATTTAT	46680
TAAAAAGAAC ACCTAAAAAC GCCGTAGTGG TAGTTTTACC ATGAGAACCT GCAATTCCAA	46740
TGCTATAGTA CTTTCTAGAA AGCTCTCCAA GAGCCTCAGG ATAAGATAAA ATAGGTATAT	46800
TTAATTCTTT TGCTCAAGT AAAACTTGCA AACCATCCTT ATTATAGGCT GAAGAATATA	46860
CTATTAAATC AAAAGACCTA TCAAGCTGTT TTAATGAAAA CTCATAAATA TTATCATAAT	46920
AAGATATTTT ATTATTACTT AAAATTTTCT CGGTATAAAA TTTATCAGAA ACATCTACCC	46980

CTTCTACACA ATACCCTTTT GAATTTAAAA AACAAGCCAG AGAACAAGCC CCACTTCCCT	47040
TTATTCCCTAC AAAAAAATA TTATTCAAAT CGTCAAAATC AACCTTCATA GCTCTCTTCT	47100
AAATAATCTT TTTTGTGATA AAATTTATGT ATAACTATAT CGATAGATAA TATATTAATT	47160
ATTGTATACT TAAGTACGTT CGTAATAATA TAGGTTCTAA GCATTTCTGT ATTATTAAGC	47220
AAGTTATTTT CAAGAGGAAT ATTTAAAAAC AGTTTAAAAA GGTAATTGTT TCCATCTTTT	47280
TTGATTTTAA GATCATAAAC AATATAATTT CTATCATACT CAGAAACACA ATGTTCAATA	47340
ATTTGCCTTA CAGCTCTCTT AGAAATAGAT AAAACCCCTT CTTCATAAAA ATGGGGCCTT	47400
ACAACAGATC GAATATAATT TTTCTTCCTA GCAAAGAACC ATCCGCTTTT AAAAAAACT	47460
TTAATTGAGT TTAATAGCAA ATTGGGCCTA ATAGACGTTA TTTCAAAAGC AGCTGCTGGT	47520
ACAACATGCT CCCCCATTG CCTTGAAATT CTGCTTTTTT CTATTTCTTG CCTGGTTGAA	47580
ACATCTGTTA TGTAATAAAT CTTAAAAACA TTTGGCAACA AAAGTTTTGA AATTATTTTA	47640
TCTATCATTT TAAGACTTGT TCCTAATATT AATATTTTAT TAAATTCTTC TTTTGCAAGC	47700
ACTTCAAGCA TTTCTCTGCA ATGAGCATCA TCTTCAAATA CAGATCGCCT TACCGCTTTA	47760
AAAACATTAT CTTCAAACCTT AGCAGAACTT CCGGCAATAA TTTTCATATT TTTAATTAAA	47820
ACACCATCAT CAATTATTAA AGGTATTGAA TATTTATCTG CTACCAAATG CGATCTAAAG	47880
CTCTTGCCAG TTCCAGCAGA TCCTACTAAT GCATACACCT TAACCCTAAC AAATTTATGC	47940
TTAATGCTAA TTGCAAAGTC TTAAACCTTG CTTAATATTT TTTTAAAAA AAAATCACTT	48000
GAAAAATTCT GAAAATTCAT AGACATCAAA AATATCTTTT ACTTGCTTTA AAAATCTAAA	48060
CTAGGCTTAG AGCAAAATTC ATTCTTTTTA AAGAATGTTT CATTAAATTT TACCAAAAAA	48120
GCATGTAAAA AGTAATCGCT TTTCTTGAAT TTATTACAAT ATTTCTTGTC ATTAATTAAA	48180
GGATGATTGT TAAAGGAACA CTGAGACCTT ATTTGATGGG TAAAGCCTGT TTCAATAACA	48240
ATCTCGACAA GAGTAGCTCT TTTGCAAGAT AATATTGGAT TAACCTTTGT AATTGCATTA	48300
ACAAAATTTT TATCTTCTAA AACAAAAGTT TTTCTCAACC TTTTATTTCT AAATAAATGA	48360
TTTTTATAAA CAACAGGAGA CTTAACCTCG CCTAAAAGTA TTGCAAAATA TTTTTTAATT	48420
ATAGATCCAC CACTAAATGC CTCACCTAGC TTTCTTGCAG TATTTATATT TTTTGCAAAA	48480
ATAATAATAC CAGAAGTATT TCTGTCAAGC CTGTGAACTG CCGAAGGCTT AAAGCTTAGG	48540
GATCTTAAAT TTTGACTTAA AAGATAAGAA TTTACTAAAA AATCAAGAGA ATTTTTACCT	48600
CCATGAACATA AAATACCTTT TTGCTTATCT AAAACAAGTA AGTCACTGTC TTCATAAATT	48660
ATTCTTTTTT GAATATATTG AAAATCAATA TTGCTTTTAA AGCATTTATC CGTGGTTAAG	48720

TTCAAATTTT	GGGCTAAAGA	TTTGTACAAA	TAAATTTTAT	CACCTTTGCA	AACTCTGCAT	48780
GAAAAATGTG	ATTTTAAACC	ATTTAGCCTA	ATGTCACCTT	TTCTAATATG	TTTTATTATA	48840
CTCGCTTTAG	AAAAATTTAA	AATTTTAATT	AAAATTGAAT	CTAGTCGCTT	GCCATTATCA	48900
TTAGCAAGCA	CTTCTAAAAA	AATATATTTA	TCCAAACGCA	AAAAATACCC	CTAACAAACC	48960
TTACTATTTT	TTTTACAAAA	AAAATTAACT	ACTAAAAATG	TAAATATAGA	AACAAAAAAT	49020
GATGGAAAAA	CGGGGTGAAA	AAACCAAATA	TTTAAACCAA	AGAATAAAAT	GGACAAATAA	49080
AATATTAACC	CTAAAAACAT	AGAAGCAAAA	GCCGCTATTT	TGCTTACAAA	ATTTAAATAA	49140
AGTCCAAAAA	CAATAATAGG	GAAAAACGAA	ACTTCCAAAG	CTCCAAAGGC	AAAAATATTA	49200
ATAAAGAATA	AAAAATTGGG	AGGAAAGAGA	GAAAATATAA	GTATTATTAA	AATAAAAAAA	49260
ATATTAGAAA	TCATTATTAT	TCTGCCAATC	TTTACATCTT	CTTTTAAATC	TTCTTTATAA	49320
ATAAATATTG	ACTTTATTAA	AACAGATGTT	ATTAATAGCA	AATTTGAATC	CACTGTAGAC	49380
ATTATTGCAG	ATAAAAGACC	TATAAAAAAC	ATAAAACAAG	AAAAAGGATT	TAAAACTTTT	49440
AAAGCCACAT	TTAAAACAAC	TTTATCATTT	GGACTTAAAT	CTGGAAAAAG	AATAATAGCA	49500
AAAAACCCTA	TTAAATGCAT	CAAACAATT	AAAAAGCTAA	TAATAAAAGT	AGAAATGGGA	49560
AGAGAAAATT	TTATAGCATT	CTCATCTTTA	AATGCTATAA	AATTATTAAT	AATCTGAGGC	49620
TGCCCTAGTA	TTCTATTCC	TATTAATATC	CAAAAAGAAA	TTATATATTG	TGGCTTTAAG	49680
TCAGCATTTG	AAGGAAGTAA	AAGGCTTTTA	TCTAAGCTAG	ACGTTGCTGT	TTTGAATAAA	49740
TTATTAATAC	CCCCTCCCAA	ATCTAGCATC	TTGGAAAACA	AAATAACGGA	TGAAACTAGC	49800
ATTAAAAATC	CTTGAATCAA	ATCCGTATAA	GCTACTGCCT	TAAAGCCGCC	AAAAAATACA	49860
TAAATAAAAA	CCAAGAAGGC	AAAAAAAGTA	AGACCAACTA	CGTAATCAAT	ACCCCAAAAA	49920
ACTTCTATAA	GTTTGGCACC	ACCTATTAAT	TGGGCAGAAA	TCAAAAACAT	TGAAAAAATA	49980
ATCAATACAA	ATCCACTCAT	TAACGCCAAA	AAATCACTTT	CATATCTATG	CCTAATATAA	50040
TCAATAATAT	TAATTGCATT	AATTTTTTTT	GATTTCGCGAT	TTAATCTCTG	ACCAACAATA	50100
ATAAAAAACAA	TTAAAGTTGT	AGGAATTTGT	ATGGTAGCTA	ATAATATAAA	AGATAATCCA	50160
TACTTATAAA	CAGCAGAGGG	ACCGGAAATA	AACTACTAG	CACTAATATA	GCTAGAAGAA	50220
AATAACAAAG	CCATAACAAT	AAAATTAATA	TTTCGATTTG	CAAGAAAATA	TTTATTTAAT	50280
AACAAAAACC	TACCTCTATT	TCTTTTTTTT	AGAAAATCTA	AAAATAAAAA	AATATCAATA	50340
ATGTATCAAG	TTTTACTAAT	TACTAAAATA	AAAAAACAAA	CCAAAAAATA	ATTATACTGG	50400
GGAATAAAAT	TCCTGACAAA	AAAAACCACA	AAGGAATATT	AAATATAGTA	GTTGATGTGT	50460
CAATAAAATA	GGCAAAACAA	AACCACAATA	CAAACATAAA	AACATACAAT	AATATAGCGT	50520

ACAAAATCCC ATTTCTCATT TAAAACAACC TTAACAAAAG GACATCAAAA TTTATAAATT	50580
CAAATATAAT GTATATTATA TAATATATAT TATATGGATA AAAATAAACA TATATTAATT	50640
GGTATATGTG GGGGCATAGC CTCTTACAAG TCAGTTTACA TAGTTTCCAG TTTAGTTAAA	50700
TTAGGATACA AAGTTAAAGT TATAATGACA CAAAATGCAA CTAAATTTAT TACTCCATTA	50760
ACTTTAGAAA CCATTTCTAA GAACAAAATA ATTACTAATT TATGGGATTT AGACCACAAT	50820
GAGGTGGAGC ATATAAAAAAT TGCAAAATGG GCACACCTAA TTCTTGTTAT TCCTGCTACC	50880
TACAACACAA TATCTAAAAAT TGCATCAGGA ATTGCTGATG ATGCATTAAC TACAATAATA	50940
TCTGCAAGCA CGGCTCCTAC TTATTTTGCA ATAGCAATGA ATAATATAAT GTATTCAAAC	51000
CCTATTTTAA AAGAAAATAT AAAAAAGCTT AAAACTTATA ATTATAAATT CATTGAACCT	51060
GATAAAGGAT TTTTAGCTTG CTCATCAAAT GCTTTAGGGC GCCTTAAAAA TGAAGACAAA	51120
ATTATAAAAA TAATATTGAA TGAATTTAAT CAAAAAGACT ACCTAAAAAA TAAAAAATA	51180
CTTATAACAG CATCCAGAAC TGAAGAATTA ATAGATCCAA TTCGCTATTT CTCAAATACA	51240
TCAACGGGAA AAATGGGGTT TTGCTTAGCA CAAGAGGCTG TCAAAC TAGG AGCTCAAGTT	51300
ACAATTATTA CAGGACCAAC CAATGAAAAT GATCCTGAAG GGGTCAACAT TATAAAAATA	51360
AAAACTGCAA TGGAAATGTA CAAGGAAGCT CTCAAAATAT ATAATAAATT TGAAATAATA	51420
ATTGGAGCCG CAGCTGTTGC CGATTTTAAA CCCAAACACA TTTTCAATAG TAAATTTAAA	51480
AAAAATAAAA TCAATAGATT ATATATAAAA TTAGTAAAAA ATCCCGACAT AATCCAACAC	51540
ATAGGACACA ATAAGCTTAA AAACCAAATT GTTATTGGAT TTTGCGCTGA GAATTCTAAA	51600
AATTTAATTC AAAAAGCTAA AGAAAAATTA AAAAAGAAAA ACTTGGA CTT TATCATTTGCA	51660
AATGAACTTA AATATTTTGG TTCAAAATTA AACAAAGTTT ATATAATAAA TAAACAAAGC	51720
ATAAAAGAAC TGCCAGAAAT GGAAAAATCA GAAGTAGCTA AAGAAATTTT AAAAATTTTA	51780
TACTAATATG CTTAATAGTT TATTAATAAT CAATAATCTT TTAAAAGCAT TTTAATATAT	51840
TCGGAGTTCG TTTCACTTTT AATTTTTTTT AGCTTATCAG AAAGCGATGA AGATTTATTA	51900
TAAACAGCTC CTTTTAATGC TAAATGCCTT AAATCAATAT TTTTGCTGTC AATGATTTTA	51960
GAATAAAAAAT TATCAAAATT ACCCTTTTTT CCAGCCAACA TTGAAGCAAC GCCCCTTAAA	52020
ACATTTGAGG GTCTATTAAT ATTTTCTTTA TTAACAATTT CTAAAGCAAT TGACAATGCT	52080
TTTAGAGAAT CCTTATCTAA AAGGTA ACTA AACATTGAAA TTTTAA AATT ATTGTCAATC	52140
TTAAAATCAA ACATAATGTT TTTTATCTCA ATATCCCAA GATCCATATC AATTAAGGCC	52200
TTAGCAGAAG CCTCCCTAAC TTTAAGAGAT GGATCGCTTT TAAGCTTATA AATCAAAATA	52260

TCCTTTGCAG AAGAGTCCCT ATGTCCTTTG ATTGCATTAA TAGCTTTAAA CCTAATATTA	52320
TCATCAGAAT CTCTTAAAAA TCCTTGTAAG ATCTCTTTAG ACTTTAAAGA AGGATCTTTG	52380
GACAAAGAAG CAATAATAGC TAATTTAACA TTAAATTAT TGTATTACT CTGAAGATAC	52440
AAATCAGCAT TTTCAGTTAC TTTATCTGAA GCAAGATATG ACAACGCTTC GATTGCAGCA	52500
GCCTTAATTG ATGGGCCCTC GTAATTATCT AGCGAAATTT CATAAATTCT ATCCTGATAA	52560
TCAACAGCGG ACATTTTTC AAGAGCAATA AGTATTTCTC TTCTAGCCCC ATCATTTCCA	52620
GAATATTTTT CAAAACTTC CATCATGTTT TTAGAATACT CAAGAGAATT AAGCTCTCCT	52680
AAATAATAAG CTGCAATAGA TACCACATTG CCCTCTTTAT TTTCAAGAAT GTCAATAAGA	52740
GTTTTTTTTT ATTTTCTTT ATCATCAAAC TCCTTAAGAT ACGAAATTGC CAAGCCAAAT	52800
AAAGCGTTTG AATATCTTTT ACTCTCATAA TTTTCAAGAA TATAATTTGC TGTATCAATG	52860
CCCCCGAAT ACTTAAGAGA AATAACAAT TCAAGTATTT CCCTTTTAAG CTCAGCATTA	52920
AAAGTTTCT CAAGTCTTTT TTTAAGAGAA AAATTATATT GACTATCGCT TGATTTTTTA	52980
AGAGCTTTTA TAATGCTTGT CACTTGACTA TCAAGCCCAT AAAGAATTGT ATCGTTAACA	53040
TACTTACCAT CTAAACCAAC ATTAGAAAAA TTCTCTCCCT TAGAAGAATT TTCTCTCTCA	53100
ACAGGCTTAT TTTCTGTAAT TTCGGGCAAC AAAGGCGGAC TAGGAAGAGC TGGAGAATTA	53160
ACATTTTGAG CATAACATT AAAAAAAGT AAAAAAATA AAAAAAATA GTATTTTATA	53220
AAGCATCCCT TCTAATATAT CTAAAAAGCT TATTTATTCC TAAAACAGAA TAACAAATAA	53280
ACAAAACAAA AATACTAACA ATTCCAGCTG CCATTAAAAA ATAAAGATTT TTAATACTAA	53340
ACCCACATC CCACTGAAAC TTTTCAAAAA AGAAATAAAT TGCATATAAA GGAAAAAGTG	53400
TAATAATTGA CTTTAAAAGA ACAAATAAAA TTTCAATTAA ATCAATTTTA ACTCCTCTTT	53460
TCAATATTAT AAAATAAAAA ACAATTACAC AAATCATAAA AGAAATAGAT TGAGCTAATG	53520
CTAAAGCGTT CAAACCATAA TAATTAATAC CAAAAACAGA TATTGCAATA TCAAGAATAG	53580
AAAATAAAAC ACTCAAATAA AACGGTGTTT TTGCATCACG AATAGAAAAA TAATATTTTT	53640
GGAAAAAACC AAACATTGAA TAAAAAGCA GACCTAAAAG AAAACATTTT AAAACACTCG	53700
CTGTTTTTTG AGTATCATAA ATAGAAACT TGCCTCCCAT AAGAAATAAA TTTAAAATAT	53760
AATCAGACCA AATAACATT AAAAAAGACA CTGGAATAAA AATTAACAAT AAAATTTTAA	53820
TTCCATCTAC TAAAAGGGCA TTTAATTTTA TATTATTCCC CAAAACAGCA TGCTCTGCCA	53880
TTTTGGGGAA AATCACTGTT GCAATAGAAA TATAAAAAAT TCCTACAGGA AGCTGATAAT	53940
AAACTACAGC ATTACTAAGG ATAGAAACAC TTCCTATCTC AAGAGTAGAT GCTAATGCAA	54000
ATGAAATCTG CTGAGTAATA ATTGAAATGG GAAATCCAA GAATCATACG AAGCCATCTG	54060

GTAAAAAATT TAAAACCTTT TCTCTGAAAT AAAATGTTGG CTTCCAGGCA AAACCAATCA	54120
TAAGGCAATT TGCAAACGGA ATTAAAAATT GTAAAAACCC CCCAAAAATT ACGCCAATAA	54180
CAGCACTATA TATTCCAAAA CGACCATAAA ATAAGAATAT GCTCAATATT ATTCCAAAAG	54240
AAAGCATAAT GGGCGAAAAC GAAGGAATGA AAAAAATTTT ATATGAATTT AGAACAGACA	54300
CGAAGATTGA TGATAGGCTT ATTAGTAAAA TATATAATAC CAAATAACCA AATACAGAAC	54360
TTGCAAAAAT TAAGTTTTCT CCCCTATAAT AAGATATAAA ATACATAATA GGCTTTGCAA	54420
AAATAATCAT AACTAAAACA ATTAACCCAA TAGAAATAAT GTTAAAGGTT ATGACAGTTC	54480
TGAAAAAAGA AACAGCTTTT TCGTGCATGTT TGTTTTTTTC ATGTGTAAAT TCAGGCAAAA	54540
AAGCCGAGGT CATCGCGCCC TCTGAAAGAA TTTTGCAGCA ATTATTAGGA ATATTGAAAA	54600
CATAGTTAAA AATATCAGCA TCAAGATTTG CACCAAAATA ATAAGAGAAA ATCTTTATCT	54660
TTACAAAGCC CATTATTCTT GAAAAAAAAG TGGAAATCAT GACCAAAATT GTAGAAACAA	54720
CATATTTATT CATCGAAATT TTCCTCTTCA TACTTTTTTA AATATGAAGT TCTAAAATTT	54780
AAAAAATCAT CATTTAGAAT TGCGGCTCTG ATCTTTGAAA TCAATCGAAA CATATAGTGG	54840
ATATTATGTT CACTTGCCAA AACTATTCCA AAAAGCTCTT TCGATTTTAT TAAATGTCTT	54900
AAATATCCTC TTGAATACCT TTTACATAAA GTACAGATGC AATTTTTCTC TACCTTAGAA	54960
GTATCATCCT TATACTCCTT TCTACCAATG CACATAATCC CATTATCTGT CAAAAGAGAC	55020
CCATGCCTAG TAATTCTTGC GGGATTAAAG CAATCAAAAA TATCAATGCC ATAATATATG	55080
GCATTAAGTA TGTAATGGGG AGTGCCAATA CCCATTACAT ACCTTGTTTT TTCTTTTGGT	55140
ATCAACAAAA AACTATATTC AAGGATTTCT AAATATTTCT CCCTTGTTTC TCCAACAGAA	55200
ATGCCTCCAA TGGCAATACC TGGGCTGTCT AATTCCAATA TATCATTGAT ACTTCTTTTC	55260
CTTAAATCTT TAAAAAATT TCCTTGAGTT ATTAAAAATA AAAGCCCGTT GTATCCCTCT	55320
TTTCTGTTTT TAGAAGATTT GAACGTGCTG CTAGCCCAAT TGGTTGTAAT ATTTGTATAT	55380
AAATTGGCTT CATTATAATC AATCCCATAA GAACTGCAAA TGTCAAGTGG CATAATAATA	55440
TCCTGCCAA AAATTTCTTG CATAGCAAAT ATTCCCTCGG AAGTAAAATA ATGGTACGAT	55500
CCATCTATAT GAGATTTAAA ATGCACACCT TTTAGATCAA TTTTCTCAG ATCAGAAAAA	55560
GAAAACACCC GAAATCCGCC CGAATCGGTT AAAAAATTTT TATTCCAAAT TGTAATAATTA	55620
TGAAGACCAA CATATTTTTC AACAGTTTTA ATTCCCAGCC TTAAATATAA ATGATAAGTA	55680
TTTGCAAGCA TCAAATTACA TTCTAACTTC TCAAGAACAG CATGTTTTAA CCCTTTCATT	55740
GCCCCCAAAG TACCAACTGG CATAAACAA GGAATATCTA CTCTACCATG AGGAAGATTT	55800

AAAAATCCAA	CCCTTGCAAT	AAAATGCTTA	TCATTCTTGA	TTACACTAAA	CATATAAATA	55860
TCCCAAATAA	TTATATATAT	TATTTCTTAA	CAATCCTATA	AACAAAAAAA	TTGATAATCA	55920
AAAAAAATAT	AGTTGTAAAA	GAACTTGCTA	TATATATATG	CAAATAGCCT	AGATCCGCTA	55980
AAAAATTAAA	AATTACAATA	GAAATAACAT	AAACAACAGC	AAAAGCAATG	CTATTTAATA	56040
GGCTGAGTAT	AAAAATATTT	TTTTTAAGAG	CAAGAGCAAT	AAACCCAACA	GTAAAGCTAA	56100
GAAGAATCAA	TCTAAATGAA	AAGAATATCC	TATTTAATAA	ATCAAAAAAT	GCATCAGAAT	56160
AATTTAAACG	TTCAGCTTTG	AGAAACTTA	TCCAATTAAT	AAGTTTAGTA	AAATTTAACG	56220
CCTTTGATGA	GAGCATCACA	GTTCTTATGT	AATCGGGCGC	CAGCTTAATA	ATTCCTGTCC	56280
CATCAAGAAC	ATCGTAGGCG	TTCTCCTTAA	TTTTTTTACC	AACCTTAACA	AACTCTCTAA	56340
TACCATAAAG	CCTCCATTTA	TTATCTTTCC	ATTGGGCTTT	ATTTATATCG	TACCTTGTTC	56400
GAAACTCATC	TTTATTGTCT	TTAATTATAA	TCATCAAGTT	AGCAAAAAGTA	TTCTCATCAA	56460
TATCATAAGA	TTTGATATTA	TAAATTTCTC	TAGCAAAATC	CCTTATTATT	ATAGTTTTAT	56520
CCCCAGATCT	ACTGTCGCCA	ATGCTATTCT	TAATAAGAAC	ATCTCTTCTT	GCTATAGTAT	56580
CTATTACCAA	ATAATTATCA	AAAAAGAAAA	GAACAACTGA	AATAAATATA	CTAATTAAAA	56640
TAATTGGTTT	TAATATCCTG	GTAAGTGGAA	CTCCACAAC	AAAAAGACCT	ATTATTTTCAT	56700
TTCTCATAGA	AAGATTGCCA	ATAAGATTCT	AAATAGCAAA	AAGAAAAGAT	AAAGCCACCC	56760
CATCTGAGAA	TGCCTTTGGC	AAATATAAAT	AATAAATATA	AAGAATATCC	TTAAGGCCAA	56820
TATTCCTTTC	AAGATAGTTA	AGAAGATTAA	CAAACAAATC	ACCAAGCATA	ATTAAAATCA	56880
TGAAAAGCAG	GTTTCATGGAC	AAAAAAGTAA	GAATGATGCT	TTTTATAAAA	AGCTTATCTA	56940
TTTTCATTTT	TTTAACAATC	TCAAAAAGAG	AATTGCTCCT	GCAATAATTA	AAATTAAATT	57000
AGGCAAAATA	GTAACAATAA	TAGGACTTGG	TGCATACTGC	ACAGTATAAA	CTTTTCCACC	57060
AATAAACATT	ACCCAATAAA	AAACACAAAC	AATAATTGAA	ATTACAAGTT	CAAGAATAAT	57120
GGAATATTTT	CTATTAGAAT	ACATTCCCAT	TGAAAAAGCT	AAAAAATAA	AAAATAAAAC	57180
TGAAAGTGGT	AAACTAATTT	TTTGATAAAA	TTCAAGATTA	AACAGAGCCA	AATTTTGCTT	57240
CATGCTTCTA	TCTTGATAAG	GTTTGAAATT	TAAATTTAAA	TTATACATAT	AGTTTAAATT	57300
TTCAAAAACA	TAAGATTCAT	CCACATAATA	GTTTTGATTG	TATAAATAAT	TTAAATAAAG	57360
ATTTGAAAAA	TTTAACTTA	AAAAGTCTCC	TTCTAGATTA	TTTTTTATAT	TTGAATCTGC	57420
AATTAAATTA	TTTTGCTTTT	TAATTAATTT	TATAACATCT	CTCATGCTCA	TTTGTGAAGG	57480
AGTTACATAA	TTTAATAAAA	AACTATCACT	AAATGTAACC	TGATCGATTG	AATATTTTCAT	57540
CTTATCTGCA	TAAAAATAAT	CATAAAATCC	ACTCTCACTG	TCTGTTAAGG	CAATAGATAG	57600

AACATCATTT AAAATAAAAT ACACCTTGAAA ATTTTCTTTT CTAATATCAA GATTTTTTGC	57660
CATAAATATT CTATCAAAAC CCTTAAGCCC AGTGTTATCA AAAAAAGTTA CATTTTTATA	57720
ACCATTTTCC GATTTCTCAC CAGAAACAAA AATCAAATCT CCATATTGTT TGCTTGAATA	57780
AGGCTTTAAT ACCAAATGGG GAACTTCTTC TTTTATTTCA TTAAAAATTT TTAATCTGCC	57840
AATAGATCCA AGTGGAAGTA AAATATCATT GGATATAAAA GATACAAAAG CAATAACTAT	57900
TCCCAATTTA AAAAATGGGA CAAGTAAATC AAAAATTGAT ATGCCAATTG AACGAAAAGC	57960
TAAAATTTCA TTGTGAAGCT TGAATTTATG AATAGTAAGA ATTACTGAAA TCAAAGAAGC	58020
AAAAGGGGGA GAAAGCGCAA TAACCATAGG AAGAGAATAT ATAATAAAAA TAAAAGCCTT	58080
AAAAAGGGA ACATAATTTT GAAGAAGTAT TCTCATAAAG AATAAAATTT GATTTATAAA	58140
AAATACGAAA AAGAAAAATA AAAACGTAAT TAAAAAATAT TTAAAAAATT CAGCAATTAT	58200
GTAAGACTCA TAACTGTTTT TTAATATTTT CATCTACAAA AACCAAACCG TTATTAATAG	58260
TGCCCAGTAT GACATAATTT TCAAATCTAG AAACTTTAT TAAATTCAA TTAAGAAGCC	58320
CATTATTGGG TCCAAAATAA TCCCAGTTGT CATTTTCAGA ATCATAAATC AATAACCCAT	58380
GATCAAAGGT TGCAAACAAT AGCTTTTTAT CTTTAATCTC CATATCCATA AAATAATTAA	58440
CATCAATATT ATTTGGCAATA ACGTGCTTTT TGTAACTATT TTTATTTAAA TTTAATTCAA	58500
AAAGACCCCC ACCATATGTT CCAACAAAAT AACTATCTTT ATATTCTTTT ATAAAATTAA	58560
TATTTTTTTC ATTATCATTT TTGCTAAAAA AATCCAAATG TTCAATCTTT TTCAAATTAT	58620
CGACATTAAC ACTATAAATA GCCTTGTCAC CTGTTCCAAC TAATAATAAA TTTTTTAAAC	58680
TATCAAAGCA GAGTGAAGAA ATTTTATTAG ATCCAAGCGG TATATTTTTT CAATTTTTTA	58740
AATCATAAAA CCATAATCCA GAATTTAGAG TGCCAACAAA TATTCCATTT TTAACAGCAA	58800
GCAAACTTG TACATTGCTA AAATCAGCAT TACCGGGAAC ATTTATTTGC TTTAAATCCC	58860
CATCAACATC ATCTATATAA TAAACAACAT TTTTACCACC AATATAAATT GTTCCATTAT	58920
AATCCGCAAA ACCCCTAATG CCATTTAAAA AAATGCTTTT TTTATCCTTA AGATAGACTC	58980
TACAATCATT TTTTTTAATA TTATATCTTA AAAGCCCTCC CAATATATTA GTTACAAATA	59040
TATTGTCATT AAAGACAAAT GTATCAAAAA CGCTGTTGTC AAGAAATCCT AAAGACTCTA	59100
AGTTTAAATG ACTTACTCCA AGTTTATTAC TTAAAAAGCC ATAAATCTCT CTATCATAAC	59160
CTGAGATAGA AAATTCATTA ATCTCTTTAA ATGCAGAAAT TGCATCAGAT TTTTCTTTAA	59220
CAAGATATTT TAATTCAGCT AATCTTAAAC TAGCATGAGA ATATTTATAG TCTTTTAAAA	59280
ATAGATCAAA ATTATATTCG GAAAGATCAT AAAAACCATT CTCATAATTT ACATATCCAA	59340

AAAACAAATT CGCTTTAGCT AGCAATTCTC TGCTGTGCTG ATTCTCATTA GTTACTATTT	59400
TATTCAAATA ATAATTTGTC AAGCCAATAT TTTTTTTAGC ATAACCTTCC CTGGCTTTTT	59460
TAAAATAAAA ATTATTTTCT TTTAAAAAAG CATCACTAAG AAAAAAAGAT TCATTATCTT	59520
TTAATCCTAT CAAATAGTCT CTTTTAAATT TACCCTCATT ACTCCCAAGA ACAACATTAT	59580
TATCATCAAT AATGACTGCT TCTTTTTTCT TCTCTACAAT ATCACTAATA TGAGAATCTT	59640
GAATAGATCT ATCTGTAGTA AGGCAGGAAA AAAACAAGAA AAAACATATA AGACAACCTT	59700
TAAATAAATT ATTCAAAACA AATTTCATAT TATTTTAATA ATCTTTATCT CTAACAATTT	59760
CAAGATCAAT TTTTCCAAAC TTGTCTATAT CAATTATTTT GACCTTAATT CGCTGACCTT	59820
CTTCTAATTT TGGGGGTCGA ACTAACCCCG CATTACCTCT TATATTCTCT CCACCGCCAC	59880
CAAATCTAGA ATATCTATTA CTATTCCCAA ATCTTCCAGA ACCATACTTA CTGTCTCTGG	59940
GTTTCAAACG AGTACTTAAA AATCCTTCCT TTGCAGGAGT AAGTTCAATA AAAGCCCCAA	60000
AGCTATTAAT CTTTTTGACA GTTCCTTCAT AAATTTGCGC TACCTTTGGC TCTCTTACAA	60060
TACTCTCTAT TCTTTCTTTA GCTTTTTGCA TCTTAAAATC ATCATCCCCG AAAAGAATGA	60120
TTTTTCCATT CTGCTCAATT TGAACCTTAA CTTCAAATTC ATCTGTTATA GCCTTAACAG	60180
TTTTTCCAGT AGATCCTATC ACAAGAGATA TCTTGTCAAT GTCAATTTGA AGTTGAACAA	60240
TTTTAGGAGC ATACTTAGAT ATACCAACTC TTGAATTAGA AATTACAGTA TTCATAATAG	60300
ATAATATATG TATTCTACCT ATTCTTGCTT GCTCAAGAGC ATCTCTCATT AAATCTTTAG	60360
TAACATTTTC AATCTTAATA TCCATTTGAA ATCCAGTAAT TCCATTTTTT GTACCGGCCA	60420
CTTTAAAGTC CATATCACCT AGATGATCTT CTTCTCCAAG AATATCACTT AAAACTACAT	60480
ATTTATCCCC TTCGCTAATA AGCCCCATGG CTATCCCCGC AACCTGCCCT TTAACAGGAA	60540
CCCCTGCTGA CATTAAAGAC ATGCTCCCAG CACAAACAGT AGCCATTGAA GAAGATCCGT	60600
TAGACTCTAA AACCTCAGAA ACTACCCTAA TGGTATAAGG AAAATCATTT TTTCCAGGAA	60660
CCATTGATTC TAAAGCTCTT TGAGCTAAAT GACCATGGCC AATCTCGCGC CTGCCAGTCA	60720
TTAGTCTACC GGTCTCACCA ACTGAAAATG GGGGAAAATT GTAGTGGAGC ATAAAATTAA	60780
GGCGTTTATC GCCATCAATA TCATCCATTA TTTGTTTCATC AATGCTTGTA CCAAGAGTAG	60840
TTACCGCTAA AGCTTGCGTC TCTCCCCTTG TAAAAAGCGC AGATCCATGC GTTCTACTTA	60900
AAATATCAAC TTCTGAGATA ATATCTCTTA TCTCATTAGG AGTTCTGCCA TCTGTTCTAA	60960
TATTATCGTT AAGAATAGAG CTTCTAACAA TCTCCTTCTC AAAATCATCA AAAGCCTTAT	61020
GAAAAAGAGA TTCATTGCTA TCAGTCAATT TCTCAAGAGA AGAAAAGTAC TCATAAGATT	61080
TATTTGCGAG CAAAGTTATG GCTTTATCTC TATTAAGCTT TCCCTTAACA AAACAAGCTT	61140

CTTTAAGATC AGCATAAACA AAATCCCTAA GCTCATCTTT AAATTCAAAT ATTTTTTCTT	61200
CAAAAGCTAA AGGAAGTTTT TCCTTCTTGC CTACAATATC TAAAAATTCT TTTTGAGCAT	61260
TACAAATTTG CTTAATATAT TCATGAGCAC CATCTATTGC TGAGAGCAAA ATATCCTCAC	61320
CAACCTCATT AGCACCACCT TCTACCATAG TAATTCCATT TAAACTTCCG GCAACAACAA	61380
TATCAAGATC AGAATCATGA ATCTCTTCAA ACGAAGGGTT TACTATAAAC TTACCATTCA	61440
AATAAACCAT TCTAACAGCT GCAATTGGAC CATTAAACGG AATATCTGAC AAAAAACTG	61500
CCGTAAAGC AGCATTCAAT CCAACAATAT CAGGAGGATT AAGCTGATCT GTAGCTAAAG	61560
TTGTAGGAAT TACTTGAATT TCTCGACCAA ATCTTTTATC AAAAAGAGGT CTCATCGGCC	61620
TGTCTATTAG TCTGGAAACA AGTATTCTT TATCCTTTGG CTTTCCTTCT CTTTGTATAA	61680
ATCCTCCCGG AATTTTACCG GCTGCATAAT ATTTCTCATT ATATTCAACA GAAAGCGGAA	61740
CAAAATCTAA ATCTTCTCTC ACGTTACTCG AGCAACAAAC AGTTGCAAGA ACCGAAGATC	61800
CACCATAAGT TGCAAGAACC GATCCATTAG CCTGTTTAGC CATAAATCCG GTCTCAAACA	61860
CTAACTCGTC TCTGCCTATT TTCAACTTTA ATATTTTCCT CAAAATTCAA CCTCTTTTTA	61920
TTTTCTAAGA CCAAGTTTAG ATATCAACAT CCTATAAGCT TCTAAATCTT TTTTCTGGTA	61980
ATACCGCAAT AAAC TTCGCC TTTGCCCTAC TAACTTTAAC AAGCCTCTTT TTGAACTATG	62040
ATCTTTTTTA TTTATCTTTA AATGTT CAGT TAAATACTTT ATTCTACCTG TAATAAGTGC	62100
AATCTGAACC CCAACAGAAC CAGTATCACT TTCATTTTTT CCAAATTCAG AAAC TATTTT	62160
TTGCTTTTGC TTTTATCTA TCATAAAGCA ACTCCTATAC CATTATAGCA AAGCTCTAAC	62220
AAACCTCTTG CCATAATTTA AAATAACTAC TACGATAGAT TATAATATTT TTTCTTAAAA	62280
ATAACAAAAG CAATTTATCC TTTTCGGGTT ATTTTAAATA ATAAAT TATT AAATTGTTTA	62340
AAAAAACAAA TATAAAATTA AAATGTCATA ATATATTTAT AATTAAAATA TAATGACATA	62400
TTTATATTTA TTCAAACCCA CTCCTTGAAT TACTGCTAAT ATTTTCTCTT CTCTGGATTT	62460
TAAATTTTAA AATTCATTAA TATTGATTTT AATTTCAAAA TAAACACCAT TTTTAACAAG	62520
ATTTATCTTA TTAGAATCAA TGTAACCTT TTCAAAACTT TTAAAGATT CTAGACTAAT	62580
TAAGGAAGCT TTA CTCAAAT TTTCACACAA TGTGGAATCT TTTAATCTAA ACATACCTAC	62640
TTTAGTCCTT TTAAATTAC TAACATACGC GCAAGAATTT AGAGAATATG CCAAATCTCT	62700
TGCAATACTC CTAATATAAG TACCTTTTGA ACAGCTAATT TTCAA ACTAA GCAAAGAAGA	62760
ACTAAATCA TAACTTAATC TTTGAATATT ATAAACAGTG ACTTTTCGTT TTTTAATTTT	62820
AAAAA ACTTT CCATTCAAAG CAAGTTTATA GGCTCTGCTG CCATCAATAT GAACAGAAGA	62880

AAATCTAGGA	GGACTTTGAT	AAATCTCTCC	TACAAAATCT	TTAAGCTTTA	AATCTATATC	62940
CTCTACATTA	GGAATATAAT	CTGTTTTACT	AACATATCTT	CCATTCGGAT	CAAGGGTATC	63000
TGTTTCTAAT	CCAAATCTGA	ATTCTGCTAC	ATACTCTTTA	TCTAAAGAAG	TAAAATAACC	63060
TGAAAGCTTT	GTGTATTTTC	CCACAAGACA	AACCAAAATT	CCACTTGCAA	ATTTATCAAG	63120
TGTGCCAGCA	TGCCCAACAC	GATTTGTATT	AAAATATTTT	TTTATAGGGA	AAAGAGTTTC	63180
AAAAGAAGTT	TTACCTTGTT	CTTTATTAAT	TAAAAGGAAT	CCATTTTCCA	AATTTAATTC	63240
TCTCTTGTAG	TATTTAATCC	TTCAATTAAC	TTATTAACAT	AAAATGATTT	GGAAAGAGAA	63300
TCATCCTTAA	CAAATAATAA	TTTGGGAGTG	CTTCTAACTT	TAATTCGCTT	AATAATTTGA	63360
CTTTGAATAA	ATCCCTTAGC	ATTATTTAAA	GCTTTAACTG	CATTGTCCAA	AGAAGCACCT	63420
TCCTTAATAG	AGCCCATAAA	CACTTTAGCA	TTTATTAAAT	CTTTTGAAAA	TTCTACTTTA	63480
ACCACGGTTA	AAAATGAATG	AATTCTGGGA	TCTTTAATCC	CCCCACTTAC	TATTAAATTG	63540
CCGATTTCTT	GAGCAATAAA	ACTTTCAAGT	TTAAACTTTT	TAATATCTTT	ATACATAAAC	63600
ACATATAAAT	AAAACAATAC	TAAGTTTTAA	AAGATTTTTT	AACCTTTTTT	ACCTCAAATG	63660
CTTCAATTAT	ATCTCCTTCT	TTAATATTAG	CATAATTATC	AATCATAATA	CCACACTCAT	63720
ATTGCTCAGC	AACTTCTTTA	ACATCATCTT	TAAATCGCTT	TAAAGATGAA	ATTTTGCCGG	63780
AATGAATCTG	TAAACCATCT	CTCATTACAT	TAGTAATCGC	ATCTCGCTTT	ATTAGCCCCC	63840
GAGAAACATA	ACAACCGGCT	ATTACCCCTA	TTTTAGGAAC	ATTTATTACA	GCTCTCACTT	63900
CAGCAAAGCC	AATAAACTGC	TGCTCAACAT	CTGGCTCAAG	CATTCCTTCA	AGAACTGACC	63960
TAAACATCATT	TATAGCATCA	TAAATAACAT	TGTACTTTCT	AATCTCAACT	TTTTCCTGAT	64020
CTGCTAGTAC	CTGAGCTTTT	GCAGTAGGCC	TTACATGAAA	TCCAATAACA	ATAGCATCGC	64080
TTGCTGAAGC	AAAGCTAATA	TCTGTTTCGG	TTATTACCCC	TGCTGATGAA	TGCACAACTC	64140
TTACTCGAAC	CTCATCGTTT	GTTAATTTTT	CAAGAGAATT	CTTTAAAGCT	TCCACTGAGC	64200
CTTGAACATC	TGCTTTTAAA	ATTATTTTAA	GCTCTTTAAG	CGCTCCTTCT	TTAATTGAAT	64260
CATAAAGATT	CAACATAGTA	ACTTTCCTTA	CATTTTTGGA	AGATTCATAT	TTTTTAAGAT	64320
CTTGTCTTTT	AGAACTGATC	AATTTTGCTT	CTTTTTCAGT	TTTAGTTACT	TGAAAAGGAT	64380
CCCCGGCTTG	AGGCATTGAA	GAAAATCCCTA	AAACACTAAT	GGCTTTAGCG	GGTCCAACGC	64440
TCTTAACAGA	AACACCCTTT	TCGCTAATTA	ATGCCTTAAC	TTTACCATAG	CACGCTCCAC	64500
CCACAAAAGA	ATCTCCCACA	TAAAGCGTTC	CATCCTCAAT	AATAACAGAA	CAAACATATC	64560
CGCGCCCCAA	ATCAATCTTG	GCATCAAGCA	CTTTTCCAAT	AGCTCTTTTG	GATGGATTTG	64620
CCTTTAACAA	CATCATATCT	GACTGTAAAA	GAATCATATC	AAGTAGTTCA	GAAATTCCTA	64680

TATTTTAAAG AGCAGAAATC ATCACAAAAA TAGTATCTCC CCCCCAATCC TCAGATACTA	64740
AACCGTATTC TGAAAGCTGG TGTTTAATCT TATCGGGATT TGAATCTGGT AAATCAATCT	64800
TATTTATAGC AACATAATT GGAACATTTG CCTCTTTTGC ATGATTGATA GCCTCAATGG	64860
TTTGGGGCAT AACACCATCA ATTGCTGACA CAACAAGAAC AACAAATATCT GTAACCTGAG	64920
CCCCACGACT TCTCATCATA GTAAAAGCTT CATGACCAGG AGTATCTAAA AATGTTATTT	64980
CTCGATCATT ATAAACAATA GTATAAGCTC CAATATGCTG AGTAATACCA CCGGACTCTG	65040
TTTGATTTAT ATCTATATTT TGAAGCACAG AAAGTAGTTT GGTTTTGCCA TGATCAACAT	65100
GACCCATTAT TGTAATAACA GGAGGCTTTT CAACTCTTTT GCTTTGATCT TCCACTTCTT	65160
CTTCTATAAC CGTTTCATCA TAAATAGAGA CAACATTAAC TTTTGAACCA TATTCTTCAA	65220
CTAAAATAGT TGCAGTATCA GAATCTATCT TTTCATTAAT AGTAACCATT ACGCCCCAAG	65280
CCATTAATTT AGCAATCAAA TCAGAAGATT TTAAATTCAT CTTTCTTGCA AGATCAGAAA	65340
CAGTAATGCT ACCCATAATG TCAATTGACT TTGGAATAGG GTTGGCTAAA TTTTCTCTCT	65400
TCTTTTCTG AAGTTGTTCA AAAACTTTTT GTTCAATTGT TTTGCTCTCA GTTTCTGCTT	65460
TTTTTCTCTT ATAGCTTTTT TGAATCTCTT GTTGCTGTTT TTTTTTCTCG CCAAGCTTAC	65520
GATTTAACTC TTTACTATTC TCAGAATCCG CTGCAGGTGT GCTGCTAACA ATAGCGGGAA	65580
CTTTAGTTTT TATAAGTCTT CTAAAAGACA TAGAAGTAGT AGTATATTTA TTTTGAGAAT	65640
TATTTTGGC AACATATGTT TTCTTTACTG AACCTTGATA TTGAAAGGAT AAGCTGTCTC	65700
TGTTTTGTGA ATATCCACCA GTTCTGTTAT CTCTGTTTTG TGAATATCCA CCAGTTCTAT	65760
TGTCTCTGTT TTGTGAATAT CCACCAGTTC TATTGTCCCT GTTTTGTGAA TATCCACCAG	65820
TTCTATTGTC CCTGCTTTGT GAATATCCAC CAGTTCTGTT GTCTCTGCCT TGTGAATATC	65880
CACCTCTATT ATCCCTATTT TGTGAATACC CACCAGTTCT GTTGTCTCTG TTTTGTGAAT	65940
ACCCACCAGT TCTGTTGTCT CTGTTTTGTG AATACCCACC AGTTCTGTTG TCTCTGTTTT	66000
GGGAATATCC ACCAGCTCTA TTGTCCCTAT TTTGTGAATA TCCACCAGCT CTATTGTCCC	66060
TATTTTGTGA ATACCCGCCA GTTCTATTGT CTCTACTTTG CGAATATTCA GCCTTATTGC	66120
TGTTATTATG CAAATCAACA AAGCTATTTG AATCATTTTT AACGCTTAAA TCATTATATG	66180
TTACAATTTT TACTACCTTC TTTTCAACT TAATAATCTT AACTTTTTTG CCATCTTCAT	66240
TTTAAATATC ATCAATATTT TTCGACAAAC CTACTCCTCC TCAAACCTCAA AACTAAGCCC	66300
TATTTTACAA CCCGGACAGG AGGTCATATT TTCATTAATA ACAACACCGC ATTCAGGACA	66360
AAGAAGCTCT TCATCTTCTT CTACCTTTTC CATAGACTCA TCATTGTCAT TAGCAATTAT	66420

TATCATCCCC	TCTTTTAATA	TTTTGTAAAT	TTCTTCTTGT	TTTTCATAAC	TTACACCAAG	66480
ATTAAAAAGC	ACTCCCTCAT	CTGCTTGTA	AAAATTGTGA	ATATCATCAA	ACCCCTCTTT	66540
TGATAAATTA	GAAATCACAG	AAGGATCAAG	CAATTTAAGA	TCACTTATTT	TACTAATCTC	66600
TTCAAATTGC	TCCTCCTCAA	CAACATCTTG	CATAACTTTA	TCAAACATTT	CGAGTGTTTC	66660
TTGCTTAAAC	TCCGAATTAG	CCTTCATTTT	TGCAAATTGA	CTGCTAGTTT	TAACATCAAT	66720
AGCCCAGTCA	AGAAGTCTAT	TAGCAAGTCT	AACATTTTGA	CCCATTTTAC	CTATAGCAAG	66780
AGAAAGCTGG	TCATCACTAA	CAACCACTAA	AGCTTTATGT	AAATCCTCGT	CAAGAATATA	66840
AACATGTTCT	ATCTTTGAAG	GAGTCAAAGA	ATCCTTTATA	AATTCTTTAA	TATCTTTACT	66900
ATAGGGAATA	ATATCAATTT	TTTCTCCTTC	AAGTTCCTTA	ATTATAGATT	GAATTCTGAC	66960
TCCTTTTTGT	CCTATACAAG	GACCAACAGG	ATCAATCTCT	TCTTTTTCAG	AATAAACAGC	67020
GACTTTGATT	CTGTAACCAG	GATCGCGAAC	TATTTTATGA	ATCTTAATAA	TACCTTCTTC	67080
AATTTCTGGA	ATTCAAGCG	CTAAAAGCTC	TTCAATAAAC	TTTGGATGGG	TCCTAGAAAG	67140
AATAACTTCA	ATACCATTTT	TACCCTTTTT	GACATTATAA	ACTAAAACTC	TAATCTTATC	67200
ATTAAGGTTA	TAAACTTCTC	TTGGCGATTG	ATATTTCTTG	GGAATTATAC	CATCCGTATT	67260
ACCAAGATTA	ACATAAAGAT	CACCATTCTT	ATTTTGTTGA	ACGTACCCAA	TAACAACCTT	67320
ATTCAACTTG	CTTTTAAATT	CTGATAAAAT	CTCATTATCC	TCAATTCCTT	GCAGGTCATT	67380
TTTGGTTCTT	TGTTTTGCAA	CCTGAATAGA	AAGCCTATCA	AAAACCTTGG	GATTAATTTT	67440
AATGTAAGCA	TAATCACCTT	CTACAATATT	TTCTTTTGAG	ATATCTTTTT	CTAATATTTT	67500
AAGCAAAGAA	TCTTTTACCT	CTTTTACAAT	TTCTTTTTTT	GCATAAACAG	ACAAATCTCC	67560
CGTATCATCA	TCAAACCTAA	TAAAAGCATT	CTCATTGCTT	CCAAAATACT	TCTTATAAGC	67620
TATTAATACT	GATTCTTTAA	TTGTTTTTCT	AATAGAATCT	ATACTCATGC	CACGATCATT	67680
TGCAATATTT	ACAATCATAT	GCCCCGTGCC	CTTTATCATC	CAAACCTCCT	CCTTAAACTA	67740
ATCTAGCCTT	TTTAACATCA	CTATAAAAAA	CATTTACTTC	TTTGCTATCT	GTTTTAAAAA	67800
TAAAACCTTT	TGGCTTTGAC	TCTAATATAA	AACCCTCTTC	AAATTCATTA	TCCAACATCA	67860
ACTTAATCTT	TTTACCTTCA	AAAATTTTAA	ACTCTCTGTC	ACTTTTTATT	TTTCTATCTA	67920
TTCTGAGAGT	AGAAAGCTCT	AAAGTAAAAC	CATATTTAAG	ATTTGCTTCT	AAAATTAATA	67980
AAATCATTTT	ATGCAAAATCA	GTCAAAAAAT	CAATATCTAA	GGAAAAATTT	TTACTATAAA	68040
GAATATTTG	AATTTTTTCCA	TTATTTTTAT	TTCTAAAGAT	ATTAATTTCT	AATATCTCAA	68100
CATTTAACCG	CCCTGTTAAA	TCTTTTATCA	AATTAAAAAC	TTCATTATTT	TTGTCAAAAT	68160
ACTTAATCAA	CTGTATTCCT	AAAAATAATA	AGGTTCTTTT	AAAGAACCTT	ATTAAATACA	68220

TAAACTAAAC	CTTAAGTCAA	GGTTAACT	TAGCAAAAT	AATGTCAACA	TTAAACCAA	68280
TTATAAGATT	TGGCCAAAGA	AAGCTTTATC	ACCTTATAAG	CTCCCAATTG	CATAATAAGA	68340
TCTTCACAAA	TGCACATAGA	TGCTCCTGTG	GTAACAATAT	CATCAAGTAA	AACAATCTTT	68400
TTAAACTGAA	AATTTTTATA	TTTTGATCTT	AATTTAATCT	TATTTTCAAG	ATTTTAAAT	68460
CTAAGATTCC	CTTTCATTAA	CTTCTGGCTT	TTCCATACT	TTCTTGAAAA	AATATTTATA	68520
TAATTAAAC	CAAAACGGCT	TAACAAAATA	CCAATGTATT	CCATATGATC	AAAACCATAA	68580
AATAATTTTC	TTTTAAACT	ACAAGGAACA	GTTACTATTT	GATCAAAATC	AATATTATTT	68640
AAACATTCAG	CAATTCCTCT	TGCCAAAAAT	CTACCAATTG	ACTTTTGAGC	ATCCCTTTTA	68700
TAAGACAAAA	TTAAAGATTT	GTAATGCTCT	TTATATTCAA	AAAAATAAAT	CAAATCTCTCA	68760
TCAAATTTAA	TGTTAAAATT	AAAAAGTGAC	TTACATTGGT	CACAAAGAGC	ATTAGAAGAT	68820
ACATACCTTT	TTCCACAAAA	GACACAAAAA	GGCAAAAATA	TACTCTTTAA	AACATTTAAA	68880
TAGCTCATAC	TAAC TGGACT	GAGAAATAAC	CTTTAAAACA	ATTTGATTTA	ACAGCTCAAT	68940
TGATTGAAAA	GGAGTAATAT	TATTAATATC	TATGTTAGAA	ATAAAATTTT	TTAACTCTAA	69000
ATACTCATTT	AATTTAATAT	GAATATCAGT	GTCATTTTTT	AAGATCTCTT	TATCATTACC	69060
ATCAGAAGAA	ACATGGGGAA	GAAACTCTAA	ACAAGAGTTG	CCCTCTCGGC	CCACCAAACT	69120
TTCTAGAATA	ACATTAGCTC	TATCTATTAC	CCTTAAGGGA	AGTCCTGCTA	TGCGAGCAAC	69180
ATAAATACCA	TAAGAATTAA	GAGATGGCTT	TTCTTCAACT	TCTCTTAAGA	AAACAAGATC	69240
GTTGCCCTGC	TTTTCAATTT	TCATTGAAAG	ATTAATAAAA	GCCTGATGAT	TAATAGACGA	69300
CAATTCATGA	AAATGTGTGG	CAAACAACT	TCTAGCTTTA	ATATACTCTA	AAATATACTC	69360
TATAATAGAA	TAAGCAATAG	CAAGCCCATC	ATTTGTGCTA	GTACCTCTTC	CAACTTCATC	69420
CATAATTATT	AAACTCTTTT	CTGTTGCATT	CCTTAAAATG	TTGGCTGTTT	CATTCATTTT	69480
AACTAAAAAA	GTGGATTCCC	CTTTGGCAAT	GTTATCACTT	GCTCCAATCC	TGCAAAAAAT	69540
TTTATCTGTA	ATACCTATTA	AAGCTTTAGA	AGCTGGCACA	AAAGAGCCTA	TATGCGCCAT	69600
TAAAGTAATT	AAAGCCACCT	GACGCAAATA	GGTTGATTTA	CCTGCCATAT	TAGGTCCAGT	69660
AATTAAACAA	AAATACTTTT	CTTTATTAAT	TCTTACAAAA	TTTTCAGTAA	AGATTTTCAGT	69720
ATTTTTAGTG	TAGTGCTCAA	CAACAGGATG	CCGAGACTTT	TCAAGAAGAA	TTTCTTTACC	69780
AGATGTCAAT	ACAGGCCTTT	TATATTCATT	TTTTTTTGCC	AAATAACCAA	AGTTAACAAC	69840
TAAATCAATA	TATGCAAAAA	ATTCTGCAAC	CTTTTAAAGA	ACTTTATTAT	GCATAACAAC	69900
ATTTGATGCT	ATTTTCATCA	AAATTTCCCTG	TTCAAAAGCA	ACCACATTAT	CTTCAGCATT	69960

ATTAATATCC	ACCTCAAGAG	AAATAAGTTT	TTCTGTTTTA	TATCTTTTTG	AAGAATTAA	70020
AGCTTGGCTT	TCCATAAAAT	GTGGTGGCAC	TTGAGCATAA	TTACTCTTTG	TAACTTCAAA	70080
AAATAACCCC	CTATTATTAG	TTTTTCTAAT	CTTTAGGTTA	TTAATCTTGC	TAAGCAATCT	70140
CTCTGATTCA	AGATATTGAT	CAATATATTT	ATTTGCATTA	ATCTTTAAAT	CTTTTAAGTT	70200
ATCAAGCTTT	AAGTCATAAC	CTCTTTTAAT	AAGTTCATCA	GGTGCACTTG	AAATTGCACT	70260
ATTTATCAAA	AAATAAACTT	TAGAAATACT	ATCCTCTTCA	AATTTATCAA	AATTCCAATA	70320
ATCAAAATTA	TGCTTGTCAA	ATAACTTTTT	TACCGTAAAA	AATACAGAAA	GAGCTTTTTTC	70380
AATAAATAAA	AAATCTTTTT	TAATATATCT	TTTCATTTGA	ATCCTAGATA	TTATTCTCTC	70440
AATATCCCAT	ATATTAATAA	AAGTTTCTCT	TAAAGTCACA	GTCAAGCTAA	TATTTTTGCA	70500
AAAAAATTCA	ACATGATCTA	GCCTGGTATT	AATCTCAGAA	ATATTTAAAA	TTGGATTAA	70560
AATAAATTCT	CTTAAAGTC	TCTTTCCCAT	TGCAGTTTTG	CAATCATTTA	ACACAGAATA	70620
TAATGAATAT	TGAGAAGAAA	AATCATTATT	ATTTTTTACA	AGTTCAAGAT	TAAC'TTGAGT	70680
TACGTCATCA	AGAAACATGT	ACGAAGAATC	ATTATTGATA	TCTATTTTAT	CAATATTACT	70740
TAATAAATTT	TTTAAATTAT	TTTTTATATG	ATTTATAATA	AGAAAAATTG	AAATGTAATA	70800
GGGCTTTTCC	TCATCAAATC	CAAGAGAGCT	CAATCCAAGT	ATGTTAAAT	GCTCCTTTAT	70860
TGTTTTTATT	GCAATATCCT	TATCAAGATG	CCAAGTAGGA	ACTCTGTTAA	TTAAAAATCT	70920
ACTAAGATTA	AGCTTCTCTG	AGTATTCATA	ATAAAAATTT	TCAGAAACTA	TTATCTCTTT	70980
AGGAGAGTAT	TTCTCAAGAT	CCCTTTTAAG	TTTTTCAAAA	AAACCATTCT	CATAAAACAT	71040
TATTCCAAGA	CTGGAAGTAG	ATAAATCTAT	ATAAGAAAAC	GAATAATAAT	CTTTATAATC	71100
ACTAATAGCA	ACTAAATAGT	TATTAATATC	ATCATTTAAA	AAATCTTCAT	CAATAATAAC	71160
GCCTGGGGTT	ATTACCTCAA	CAACCTCTCT	TTCTAAAGGC	CCCCCAGAAG	TAGAATTGGA	71220
CGCTTGTTCA	CAAATGCAA	CTTTTTTATC	AAATAAAATT	AATTTCTTA	TATATTCTTT	71280
ACTGGTATGA	TAAGGAACCC	CACACATTGG	AACATTTTCT	CTTTTTGTCA	ACGTAAATT	71340
AAGAAGCTTG	CTTACCTCAA	TTGCATCATC	AAAAAACATT	TCATAAAAAC	TTCTACTCT	71400
GAAAAAAGA	ACAGCATCTT	TATATTTTTT	CTTGATATCT	AAATACTGCC	TTATCATTTG	71460
GGTAACATTT	TTTTCCATAT	GCTTCCTAAA	TAATATTGAA	TTACAATTGA	TATTATAAAA	71520
TAAATATAAT	TCAATTAAAA	AGAAAGAATA	TAAAATAATA	AAAAGACCAT	AAAAAAAATA	71580
TTTTACGCAA	TTAAACGCTA	TTTAATTATT	AAAAAGCCTA	ATGTTTTTAA	TTTAATTAAC	71640
TTTAAGGGTT	TTTATTGTCC	TTTTCTAAAA	GATGCTTAAC	AACATCGTTT	GTTATATCAA	71700
CAGTGCTATT	GTGGTAAAGA	ATATATGGAT	TATTTTTTTT	CATAATCAAA	GAAAACCCAT	71760

TAATTTCTGC AACATATTGA ATACCACGAA GTATTTTACT TAAAGATTCA CTATTATTAT	71820
TTAAACTATT AATATTGGCC AATCTCTGCT GTTCTAAATT ATTCTTTGCT AAAC TAGACA	71880
CTCTCTTTAG CTCATCAACT TTCAAATTAT ATTGATTTC AAAAGATCTT GCATTATCTA	71940
AATCATTATC AGCAATCGAT TTATCATACA TATGTTTTAA ATTCTTAAGC TCTAAATTTA	72000
ACGTATTTAT TTGTTCTTGA TACCGATTTT TTATTTGATC AAGATTAGCT TTCAATTGAG	72060
GATTTAAAAC TTCAATCACA ATTCTATCAA AATCAACAAT TCCTATCTTA ATAACATCTA	72120
TCGAAAAAAC ATTAAGAT AATAAAAAA ACAATGGTAA AATCAAAAA AACACAAATT	72180
TCTCCATAGC ATTAATCAAT ATCTCATCTC AATTCCTAAG AAAAATTTAA ATCCAGAATA	72240
ATATTTGTAA TAGCTGTTAA CTTTATCATT GTCAAAATAA AAAGGATAAG CTATTACAAA	72300
AGACAGCGGC AATTGAGGTA AAAGACTTCT AATTCCAGTT CCCAGCTAA AAGCAAACT	72360
ACTAAAAGGT CTAAACAAAG AATTTTCTTG CCCTTCTAAA GAATAGGAAG CAAAATCTAT	72420
AAAAAAGCA TCCCAAATA AAATATTTTT TAACAAAGGA ATAGATATCT GCACAGTATT	72480
TACAAAAGAA CTGTAAATAT TTTTCAAAT CCCCCAACCT CTAGCCTGCA TAAATTTTC	72540
ACTAAGAATT ATGTGGTGAT GGGGTTGAAT TTCAATTTCA AAACCATTAC CAAGAGGAGG	72600
TAATATATTT GAATAGACAC TCCTTAAGGT CAAAATAATA TCAAATAAG GAGTAAACAC	72660
ATCCTCATAT CCCAAAGAG AAAAATATCT CTCAAAGTT GTAGAAGATT TAATAAAATG	72720
GCTCTGACCA AATAAAAATC CACCAAAAA ATCAAAGTGT TGCTTAAGTA AAAATCCATT	72780
ATTAGATAAA GAGGTAGAAT TTCTTGATC CCAAGCCGCG CTCAAATAA GAGAATTTTC	72840
AAATCTAAAA GTTTTATAAT TGTCTCTTAA ATAATAATTT GAAGGTCTGT TAACCTCATT	72900
ATCATAAAA ACATATTTTA AAGCAGTTTG CAAAGTGCCA AGAAGGGTTT GTTTGCCAAG	72960
ATAATTAGAA AAAGTATACC CGGTAAACGC TCCAAATA AGTTTaAGCA AAGAATAATT	73020
CATAGCATTAA AAATCGGAAA AGCTTTTAGC ATCTCGATAT TCTTCCCAAC TTGTAAATGG	73080
ATCAGGAACT TCCCTCTTGC CAGAAAAAAT AGGCCCATTA ATATCCTGAT AAGCAGTATT	73140
AACGGAATGT GAAAAATCTA TAAATCCACC TACGGTCCAT CTTTTTTGAA AAAACCAATT	73200
ATCTCTAAAT GTCAAATAA GACTTTGCTC TAAAAAGAT AAATTTAGTC TTGCTGCAAA	73260
ATAATAGCCT TCGCCTAAAA AATTAGAAAG CTCCCACTGC CCAAATACTG AGAATGGAAA	73320
TGAAGAATTT GAATTGCCTC CAAAATTCAT ACCAAATCCA AAATTACTTG TTGCTCGCTC	73380
CTCAATGTTT AAATTTATTT TCATAAGCCC TTCTGTATTG CCTGGAACAA TATCAGGAAT	73440
TACATTTGAA AAATAACCAA GCTGCTGTAA ATTTGCCATA CCCATCTTAA ACTTGTCCAA	73500

ACTAAAAACA	TCTCCCTCTT	GAAGAGGAAT	CTCTCTAAGT	ATTACATGCG	AAGCTGTATT	73560
TTTATTTT	TAAACAGTAA	TAGACTCAAT	ATGAGCTTTA	TCCTTTTCTA	AAATTTTAAT	73620
TAACAAATCA	ACAAATTCCC	CTCTTATCTT	TTGCGAAGGA	ATAATTTCTG	TAAAAATATA	73680
CCCTTCTCTA	AAATAACTTT	CCTTAATTTT	GACAAAATCC	TGCTCAAATT	TAGAATCATT	73740
AAAAATATCA	CCTTCGCTAA	AGGTAATAAA	ACTTTTTAAT	TCTTCCAAAC	TAAAAACTGA	73800
ATTACCAGAA	ATTTCAAGCT	TTCCAAATCT	AAAAACATTG	CCTTCTGAAA	GAAAATATTT	73860
CAAAAAA	ACT TCCTTTTCTA	GTCTTTTAGA	ATCTTTAAGG	GAATCTTTAA	TATCAACAGT	73920
GCTATTGATA	ATCTTAACAT	CAATATATCC	ATTATTTT	TAAAAAGACT	CTAATTGACG	73980
CTTGCTTT	TCAACATTAC	TTTTTAAATA	TTTACCATCT	GAGAAAAGAG	ACACTACTCT	74040
TGATGCTAAA	GATTCCTCA	AGGTACTGCT	TTTAAAGCTT	AAATTTCCCT	CAAAGTCAAT	74100
CCCCTTAACA	ACATATTTGG	GTCCAGCTAC	TATATTAAAA	ATAATATCAA	CTAAATTTCC	74160
TTCTTCTTTG	ATTTCAAAAT	TTGCAGAAAC	CTCAAGATAT	CCCATGTCTT	TATACATCTC	74220
TTCAAGCTTG	CCAATACCTT	TATTAACACT	TGCAAGATTT	AAAGGCTCAT	TGGTTTTAAT	74280
ATTCACCTTC	TCAACAAGTT	CGCTATTCCA	AAAAACTCTA	CTGCTATCAG	AAAAACAAC	74340
AGAATTA	AAAGATTTT	CTTTTACAAT	AAATGTAATA	AAAAGATCCT	CACCATCTAT	74400
TTTAAATATA	GGCTTAATAA	GCCCAGAAAA	ATAATCAAGA	GAATAAAGAT	CAATTTGCAA	74460
TTTATCAAAA	ATTTCATTAG	AATATGACAC	GCCAATGTAA	GGTTTAAAA	TATTAATAAA	74520
ATCTCTCTCC	TTCTTATTCT	TAAGTCCTTC	AAAATTAATA	CCCTTTATTA	TTTTCCCTT	74580
GTAATTTTCA	ACTTGACCAA	AACTAAAAAC	AACAAAAAAT	ATTAAAAAAC	TTACAAAAAA	74640
CAAACCTCTA	ATTGAACCCA	TCTTAACCTC	TTAACAATTT	AATATTTAAA	TTTCCAAGAA	74700
ATGCCTATAT	TATTTCCCTAT	TCCATCTAAA	CCTTTTTTCA	TAAAATTGTA	ATCAA	74760
TAATTAACCA	AAAAAAATGG	AGAATCAAAC	TCAATACCCa	AATTGACAAC	aAAATTTAAA	74820
TCTTTTGAAA	AAGGAGACAT	TTGTTCTTTC	AAAAAACCAA	AGCCCCCACT	AATAAAAACA	74880
CCCTCAACAA	GATATTTGCC	TACCTTAACA	CTTGATTGT	CAAGAACATC	AACAAAAGTA	74940
GGATTCCCGA	TTTTGAAAAA	ATTACTATTA	ATAGAATTTT	TCAATATATC	TGTCTTTATA	75000
CTCAACAAGT	CTAAGTTTAA	TACAGAACGC	ATATAATCTT	CAATGGGTTG	AATTAAAAAA	75060
TCAAGAGCAA	TGTCACCTAC	TATTCCAATT	GCCATTT	CAGCATTAGT	CCCTGCCGAT	75120
CGCAATCCTC	CCTCATACCC	TCCTATTGTT	GAGCCTGAAA	GCAAATATTT	AATTTCTG	75180
TCATTTCTAG	AAGGATAAGA	CATAAACTCA	ATTTTCCATA	AACTTAAAGG	ACTATCAATG	75240
CTTATTGTAA	CAAGCAGTTT	ATCATTTCTA	TCCTTAATAG	TATTTGTAGC	CTCCGCTTTT	75300

ATCCATGGAT CAAATTTAGC CCTACTCTCA TTAAAGGATA TATAAGAGCC GCTTTTAAAA	75360
ATAAATTTTT TATTATTATA ATTAACAAAA CCACTTGCAA TATTCAAATC TCCCTTAATA	75420
ATAAAATCAT CTGTTTTTGT GTCAGATTTT ATTACAAGTT TATCCCCTCT TGAAATAGTA	75480
GCTTGTA AAAA AAGAAATATT ACTATCTGGC CAAtGAAAAG TAACACCGCT GTCAAAATTT	75540
ATCTCAAGAT CAGTTAAAAT ATCAAAATCT AGAAGATTAA TATCAGTTTG CAATCTTTTTT	75600
GCTCGTTTGA AAGGATTAT TAATAAATCA ACAACAGAAC TTTCAAGAGA ATAAACCCAA	75660
GCATTTGAAA TATTTAAAAT GCCTTTAAAC ATAATTTTCA CAGCATTTCC TTCAATTGAA	75720
AAATCGCCTA AAGCATAGCC TGTAAGCTT AAGGCAATTT TTTCAAATTT AATAGGAACT	75780
CCCGTTCTAC CAGTCACATT AATATCTATT TTGTAATAAT CAATAATAGT ATCACTTAAA	75840
AAATTTAAAT TTAAACTAGT AGAAACAAAA ATCTTGGAAT ATCGATCTAG GTTAAACTCA	75900
TTACTAAAAA TGATTTTATT ATCCTGAATT GCAACTGGCA TATCAAATAT TTCTAAAGCT	75960
CTATCACCAC CAAATTTTCT AGAAGCTCTT AAATACTCAG TGCTAATTGA TCCTTTTTGA	76020
ATATTTAAAC TTCCATTAAT ATTAGGATTA TACAAATCCC CATCAATATC GAATTCACCA	76080
TTTAAACAA GATCGTAAAG AATAAAATGA TTGTCAACAT TAAATAAAGA ATGTGAATCC	76140
AAAAATCTT TGGTGATTAT TTTTGAATCA AATTTAATAT CTCTCACATT TCCAAGAATT	76200
TTATTTTAA TTATTTTGCC TGACGAATTA AACTAAGGG GCAAATAATC TTTTAAATA	76260
AAGCTATATT CCCCCTGCT ATAATGATAT AAAACATTAA CAAGGTCATA ATCAATTGAA	76320
GCCATATTAA ATTTTTCAAA ATCATTGCTA AATTCAATCG TAAGATTGGA TAAAGATTCA	76380
TTTTTATACT TAATGTCTCT AAAGAAAAAT TCGCCCTCTG TTTTGGTTTT CAAACTCCA	76440
AATTGCTCTT CAACTCCACT TTGGAAATTT CTAAAATTTG CATTAACCT GTAAGAAAA	76500
AAGTCGCTAT TAAAACTAT ATTAGATACC CCTATAGAAC TGCTTAGGTC ATATCTTAAG	76560
CTCCGGTAA GAACTCTTT TTTATTGCGC TTGGCTTTTA TGTCATATAT GTTAAGCTTA	76620
TTATCCAATA ATCCTAAATT CATAGAAAAC TGAACGGGAA CGCCCAAAAA AGTTAATTTA	76680
TmTGCCTCAA GATATCCACT CAAAGAATAA TTTTAAAAAT CATTCTTTTT AAAATTTAGC	76740
AAAAAATTAC CATTAACCTT TCCCTCTAAA AGGGAGAAAG AATTAAAATT GTAAAAATCT	76800
AAGCTTGAA ATTTAAGCAA AAAATAACTT CCATATTCAT CGGAATTAAC CCCTAAAAAA	76860
TATCTCTCTG AATTTAAGCT AGAAAATAGA TTCAAACCTC CATTAAAATT ATCTTTTAAA	76920
TTAAATTGTC CATATCCTTG CAAATTTGAA AGTTTGTTTA TAAGTTTAAC ATCAGAAATG	76980
TACAATTTAT CATATTCATA TAAGCCCTTA AAACCAAAGT TGAAATTATA GGCAGGTGTT	77040

TTAGAACTT TTATTATATT AAACCTCGTCT ATTTTAAATT TCAAATCTTC ATTAAGGCCT	77100
AAATAGTTCC CATTAAATTT TATATTTATT AAAAGATCAG AGGTTTATT GTAAACCTTA	77160
AAATCATTAA CATTAGGGT ATAACTACT TTAGAATCAA AATAATTAAA ATCTAATTTA	77220
ATACCAAGAG GAGATTCGGC AACAATAAAC TTATCTTTAA GATTAACATT AAAATGCAAA	77280
GGATAAACTT TATTCAAATA AGAAAAATTC GTGCTAATAT TAAACCCACT TTCAAATAGT	77340
TCAACAAACA AGTTAGAATG CAAATTGTGA TCATTGTACT GCAAATCAAA ATTGTTTGAT	77400
TTGTAAAAAT TTTTTTCTCC ACTGGCATCA AGCACAAATT TGAAATTGTC TAACTTTGAA	77460
AATACCATGA AATTGAATTT TTTTAATTTA TTTTATGAT AATTAAATTT ATTAAAATTA	77520
AAATCAGAAA CCAAATTTAA ATATTTACCT GAAAATAAAG TCTTGGGAAA AAAATTTATC	77580
AAGTGAGAAC TGGGAATAAC TTCTTTTAAA AAAAGCAAAG GAAATTCTTT AATACCTAAG	77640
CTTAAAGAAA ATTCTTCATC ATTAAGATCT CCTTTTAAAG AAATTTGAGA GTTTTTATTT	77700
TCTAAATAAA TCAAATAGTC AACAAAAATT TTATCCTTTA AAAATAAGT TTTTAAATTT	77760
AAATTTTGAA AACTAAGATT TCCAAGACTA AAATTATCAG ACTTAACCGA AAAAATATCT	77820
TTATCTTTAT TAAAATCTAA ATACCCATTT AGGTCGTAA AGTTTAAAT TTTTGCAGAC	77880
TTAAAGTTAA GACGTCCCAT TGGAAGCAAA TCTTTCAAAG AATAATAACC TTTATAGTTT	77940
ACAACCCCC TTTTAAGCTT TAAAAAAGCA TTCTTAACAC TTACAATTCT ATCATCCCC	78000
TTGATTTCAA GCTGCAAGCC TTGAACTTCT TTTCTATAG TATCTACATT TAAAGATGAA	78060
TCTATTATTC CTGCATATCT TAAATCTTTG TCCTTAAAT CATAAGAAA TGCCAATTGC	78120
CCATTTAAAC TTATATCAA ATAATCTTTA TAAATTTCAA AGCCTTTGTT TAGCTTAATC	78180
CAATCTAAAA GACTAACATT GAAAAATAAA GCATCTAATC GAACAAAACC ATTAGCCTTG	78240
TCATAACTTA AATTAAAATC AAAATTCTCT CTTCTGTAAT TAAAAATTTT TAAATTTCT	78300
TTTGAATAAT TTATTTGGAA CCCCTGCTCA AGTAAAGAAA AATAACTTGT TTTAAATTCA	78360
AAAAAGCTAA AATTAACATA GCCATCTTCA AAGCCTTTTT TGAATTTCCC CTCAAATAG	78420
AAAGTTGAAT CCAAATTC ATCATCAACT CTTTCAAAGG GTAAATTAAT TTCTAAATTT	78480
TTAACAGCAC TAAATCAAC TACAGAGCTA AATAAAAAAT CTCATCTAC GGTACTTAAG	78540
GAAAAATTTT TAACCTGAAA ATTAAGCCAA CTATTATCAT TAAGCTTGAT ATTAATATTG	78600
ATATTTTCTA AATTAATATT TAATCTATAA AGGTAGTTTA AAATTTTATT AAAACTGTA	78660
TTTTCATTGT CAGAATAGGC ATTGCTAGGA TTTAAATCGC CAGATAAACT AAAGTCGTTT	78720
ATATCAAAAT TGAAATTACT TCCTTTAACA TAAACATTTA AAATAATATT TTCATCACCC	78780
AAAATTAATT TAAACAGATT TAAATCTATC CTAACAATAT CTATTAATAT TTTATCTTTT	78840

CCATCCAAGC	TTAACTCTAA	ACCGTCTATC	TTGATTGATG	ATAAGAAATA	CGGTGAAATT	78900
TTATCATATT	TAATCTTAAA	GCCAAATTTT	GATTCAAGAT	ATTTTATAGC	AAAAAACTTT	78960
GCAGAATAAA	TTTGAGCTTG	AACAAATAGA	TTAATGGAAA	AAATTATTAA	AACAAAAATA	79020
AAAAATGGCA	AAATCAACAA	TATAAATGTC	TTACTTCTCA	AAAACAACAA	ATTCATACAC	79080
TCTATCGATA	ATTATTATTA	TATAATAATT	ATCGATAACC	TAATTATTGA	CACCAAAAGA	79140
AAGGAAGAAA	AAATATTTGT	GATTAAAATA	TTGAAAAACT	TTTATTGCAT	AGAAGGAATT	79200
GATGGAAGCG	GGAAAACAAG	CATCACTAAT	AACTAAAAG	CTCTTTGCAA	CGATGAATCA	79260
AGGTATTATT	TTACAAAAGA	ACCATCAAGT	GGAATAATTG	GAGAAATGAT	AAGAAAGCAA	79320
TTAATGAATT	TTGAAAATCC	TTTAGAAGAA	TCAACATTTG	CATATCTTTA	TGCTGCAGAC	79380
CGACACGATC	ATTTATATAA	AAAAGGTGGA	ATACTGGAAA	TTTTTAAACAC	AAAATCTAGA	79440
AAAATAATAA	CTGATCGCTA	TTTATTCTCA	TCGATTGCAT	ATCAAGGAAA	ATTAGGATAT	79500
GAATTAAATA	AAAATTTCCC	ATTGCCTGAA	AAAGTATTCT	TTATCGAAAC	AGACCCAAAC	79560
ATAGCTTATG	AAAGAATACA	GAAAAATAGA	ACACAAAGTG	ATCTTTTTTGA	ACTTGAAAAA	79620
TATAAACTTT	TTGAACAAAT	TGCTCTAAAA	TATTTAAAAA	TATTTAAAAA	ACTAGAAAAA	79680
AAAATTAATG	TGATTTACAT	CAACAATTCA	ATAAAAGATA	ATTTAGATAA	AAACGCAAAA	79740
AAAATTTTCA	ATCTAATAAA	ATTCTAATAT	AATTAATCAT	ATGCATATTT	TCAAAAATGT	79800
CCCCTTCCAA	ATAAATTTAA	TTTTATTTCT	TTTAGTATCA	GTTGCAAAGA	TAAATGCATC	79860
GTCCAAATTT	TATTACGCAG	AACAATGGTA	TGTAATTTTT	AATTCTCAAA	TGAAAAAAA	79920
ACCTGAAAAC	TATAAAAAAA	ATATATTTTT	TCTTCAAAAA	GCCTTAAAT	ACCCATTTGG	79980
AAATCCAAAA	TATTCTCTAA	CTAAATAGA	AACCAAGAA	CAGTGGGAAA	AATATAAACT	80040
TCTTTTCAAA	ATGCATGTAA	ACTTGCTTCT	AGTTAGGCAA	AATTTACATT	TAGGAGATTT	80100
ATTCGACACA	AGAAATTTAT	ATTTTTTCAA	AACTCCAGAA	AAAGATGGAA	TTATTTCCAA	80160
TCTAGAAAAA	TCAAAAAAAT	TATATAAACT	AGCTATTAAT	TACTACAGCG	AAGCACTAAA	80220
ATACCACAAA	AACTTGAAA	ATTACACAAC	TGTTAAACTA	GAAAACGATG	GAATAACAAA	80280
CTGGGAAGAT	GAATATCATA	AAATTTCTCT	TAAAGAGCTT	AATTACTATG	ACATTATTAA	80340
AAAAGAACTA	CTAAGAATTG	ACGAACTAA	AGCATTTTTT	GAACAAGGGC	CAAACATTA	80400
TTAAAAAAAC	TCTTTGCCCT	CTTTGGAAAA	AAAAATTTTA	TTTATATAAT	CCTTATTTAA	80460
AGAAAACTTA	AAAACAAGAT	CTTTAAATTT	ATCCTTACTC	AAAATACTAT	ATTCTGAGAA	80520
AAGAGTTATT	AAGGCTCTTT	CTGCTAAAAA	AGGCAATTCT	AAAATATTTT	TTAAAATTTT	80580

GGCTCTAAAT TCACGCGCTT TTTCACATATC TAAAGAATTT AAAAAATTAG AATTTTCAAC	80640
ATCAGTGCTT AGTGCTACAA TTTCATTTTC AAGAAATTTT TTATCTCCTT GTGAATATAG	80700
CAAAGCAAAT GGCTTTAAAA AAGAAAAAAA ATATTCCTTA CCTATAAGAT AATGGTGCAT	80760
TGAACATCTT GTAGAGTAAT TTGGGTAAAT AGCAGATTCA ATCTCTTCAT CGCCACCAAC	80820
AATAAGCAAA GGATCAAAAT AAGGAGCTGG AATTTCTTTA TTGTTGTAAA AATAATACCT	80880
ATACGAAAAA AAAGATTCTT CCATGCAATC AATGTGCCCA CAATAAGCTC CAAGCTTATA	80940
AATCTTATCT GAATATTCTA CTAAAAGTTT GGCAGTATCA TTGAAAGATT CTTTTCTAAA	81000
ATTATAAAGC AGTGTAGGTA ATATAAATAA AATATTCTCA TTTGATGAAA TTTTATTTAA	81060
AACAAAAATT AAACGTTTCAT CATAAAAAACA TGCCTCATCA ATAATAAAG TGCCACAAC	81120
AGGATTAGAG GCTATTAAAT TTTCAATATC AAAAGAGTTG CTAGCATAAC CAATCTCATC	81180
AATTTTATCT TTTCCACCGC CTCTATATGG TATTACGTTT TCTGGATAAT CTTGAAACCT	81240
CCTCTTGTCG AGAAAATTTT TAATAAAAAA TACATTAACC CTACTTCTAT TTCCTTTAAT	81300
AATATTGCCC AATACCTTGA AAGATTTTTT TCTTACAACA AGCGAATCTT TATAAATTTT	81360
TGCAGCATAT TCTGTTTTTC CACTTCCCAT GGGTCCAAC	81420
ACAAGAATTA AGTTTATTTT	
TACCCTAAAA TCAAAATGAC TAACAGAGAC AATGTTATTT AATTTAGTAT CTTCTTTATT	81480
AGCAAAGTCT AAACAAAAAC CCAAAAATCC TCCCTAAAGT AAATCAAATT CAATTATATA	81540
AATAAAAAACA ACAAAAAACA TTAACATTAA AAGCCTAAAA ATTAATAATT TAGGATCTTA	81600
TTAAAGCTAT TATTCAAAAG AATAATAGCT TTCAAACTA TCATCATCTA ACAAAGCTTT	81660
CTTTATTTTT AGTTTATTCT TCTCATAAAT TTCAATATAA TTAAATTTTT TAGAACTATT	81720
AACTTTTTTA TAAATTGAAA CCAAACTTCC AACCACATAA TTTTTAATTT CTACCAAATT	81780
AGATCCAAAA TATTTTTTTT TACTTATCAA GCTTGATCTA ATATCCAAAA CAGAAGTTTT	81840
TTCAAAAAAT AAATTAAAG CATTTGGAAT AAAAAATCC CTAATATCAA TCAAGAACAA	81900
CTCTCTGATC CCAAACTAT TAAAATTGCA GCCCAAATTG TTAAAAAGAT TAACTTAAA	81960
AGCATGTAAA GCAAAGGTAT AAACATCTCT TTTATCAGGA TATTGAACCT CAATCATATC	82020
AACATAAGGA TAAACAGAAT AATTTATTTT ATAACCAAGC AAATATTCT CATAATAAAC	82080
TGGAGACTTA TCTTTAAAAT AAATTTTATT AAAATATTTG CTATTTAAAC TAAATTTGCT	82140
GTCAAAATCT ACTATTCCTG AAAAAATGCC TACTAAACT CCATCTTTTA GTATGGCAAC	82200
ATTATTTTTA TTATCAATGC AATAAATTC TGACAACTT TTATAATCTT CTAAAAATTT	82260
ACTCTTCATG TCGGGATCCT CTAAAAGATC ATAAAACATT TTATATTCAT TTATTGTCTC	82320
AGGAGGAAAT TTTTTAAAA TCCTATAAGC TTCATCAGGA TCTAAAAGTT TGTATTTTAA	82380

AAAATAAATA CCGTGAATTC CATTATATTC TTTAATTTTG CCCTTAAGAA AAGAAAACAA	82440
AGAAACAGAA TTGTCATAAT TAAAATTTGA ATTTCTAAAT ATATAATTAA TGTTTTCGGT	82500
TGTAAAGAAA AAATCTTCTT TTGATCTAAT AGTATTAAAG ATGCTAAAAA AAAACCTATC	82560
TTCTTTTAAA AACCATTTAA AAAATAAAAA ATCATTACCA TATAAAGAAA AAGCCTTAAA	82620
TAAAATTTTT TTGAAATCAT CTCCAAAAC TCAAGTCTT CCAGAAGCTT CAAGCCTCAT	82680
GCAAATTTAA TCTTTGTCTA TTTGCAATTC TTCATTCAAG TTTCTATACA AAGTAATAAT	82740
TTCTTCATAC ATATTCTTAT TTTCATTTTG TCTTAAAAGC AACGAAAAAT AATAAGTGTA	82800
TACTTCTTTA AGGGTACTG CTTTAAAGTT ATTAATATTA ATTGCTTCTT TTAATAAATA	82860
AATTTTATCC GTTAAAGCAA CATTCTCTTT TAATGAAAGC TCATAAGAG CATCTGAAGC	82920
TAGCAAATTG AAATCAAGAG ATCCATAAAT TAAATCATTT CCTTTTGTGA AATTGGAAAA	82980
ATTTTGTAGC TCATTGAAAA GAATACTTGA AATATCTTCA TCTTCTTTGA CTGAAATTGC	83040
ATATAGGTTT ATAGAAATAA AAAGAATGAA ACCCATCTTC AAATAAAACA TAAACACTTG	83100
CCTAACCTTT TACATCCTCC CCCTTACTT CTTTGTAGT AGAGTCTGAT GAAAATAAAT	83160
CGTATTCATC CTTATTAGCT TCAAAACCCA AAAGCTCTCT CACTTCTTTG TCTGTCAAAG	83220
TTTCTTTTAA AACAAGTTCT TTTGCAAGCT TAACAAGTTG ATCCTTATGC TTTAAAAGAA	83280
TATCCGATGC CTCTTTTAAA CATTCTTCAA GTATTCTTTT TACCTCTCTG TCAACTTTAT	83340
CGGCAGTGTT CTCAGAATAA GCTTTAGCCT TTGAAAACTC TTTCGGAAGG AAAATAGGTG	83400
CTTCATCGTC TACTAAAAAT ATTGGACCAA CTTCTTCACC CATTCCCCAC TCCGTAACCA	83460
TTTTTTTAGC CAAACTAGTA GCTTGCATTA AATCATTTTG AACACCCGCT GTTGTAACAC	83520
CCAAATTTAT TTGCTCGCTA GCATAACCAC CATAGCATAT CTTTATTTTG TCAAGAATTT	83580
GGTGTTTGTT TATTGAAAGT CTATCTTCCC TTGGAAGAGA AAATGCAACA CCAAGTGCCC	83640
TGCCCCTTGG AATAATGGTA ACTTTGTGAA GTGGATCAGC ATGTTCAAGA TAATAGTGAA	83700
GCAAAGCATG GCCTGCCTCA TGATAAGCCG TCTCAAGCTT TTGCCTATCA GTAATAGTCA	83760
TGGATTTTTT TGCAACTCCC ATCAATATTT TATCTCTGGC TTCTTCCATA TCCTTCATTA	83820
AAATTTTCATC TTGATTATTC CTTGCAGCTA TTAAGGCTCC TTCATTAATT AAATTGCAA	83880
GATCAGCACC ACTAGCTCCA GGAGTAGCTC TTGCTATTAC TTGTAAATTA ATATCTTTTG	83940
AAAGCTTCGT TTTTAAAGAA TGAATATTTA ATATTGCCTC TCTTTCCTTA ATATCAGGCA	84000
AAGAACTGT TACTTGCCCTG TCAAATCGTC CAGGCCTAAG CAAAGCAGAG TCAAGAACAT	84060
CGGGACGATT TGTAGCGGCC ATAACAATTA CATTGGTATG CGTTCCAAAT CCATCCATTT	84120

CAACTAACAG	CTGATTAAGA	GTTTGCTCTC	TTTCATCATG	ACCACCGCCA	AGCCCCGCAC	84180
CACGACTTCG	ACCAACAGCA	TCAAGCTCAT	CAATAAAAAT	AATACATGGA	GAATTTTTTC	84240
TAGCATTATC	AAATAAATCT	CTAACACGAC	TTGCTCCAAC	CCCAACAAAC	ATTTCAACAA	84300
AATCTGAGCC	TGACATGTGA	AAGAAACTAA	CCCCAGCCTC	ACCGGCAACG	GCTTTGGCAA	84360
GCAAAGTCTT	GCCAGTACCC	GGAGAGCCCA	CTAAAAGCAC	TCCTTTGGGG	ATTTTTGCAC	84420
CTATTTTTTC	AAATTTTTTT	GGATTTTTAA	GAAATTCGAC	AACTTCTCGA	AGCTCTTGCT	84480
TAACCTCTTC	TTGACCAGCC	ACATCTTTAA	AGGTGATTTT	ATTCTTTCCA	GCTTCATACT	84540
TTTGAGCATT	ACTTTTCCCA	AATGTAAAAA	CCTTCCCACC	GCCACCTTGA	GTTTGACGAA	84600
ATATAAAGAA	AAAGAAAATA	AAAAACAAAA	TCCATGGCAA	AGTTTGTAAT	AAAACCCCAA	84660
TCAGAGAAGC	TTGACTTTTC	CCTGAGCTAA	GCTCAACTTT	TTTATTTTTT	AGTTCTGAAA	84720
GTAAATTTAT	ATCAAGATAG	GGAATGCTGG	TAGAAAAATA	AGACTTTGCA	AAGTTAGAAC	84780
CCTTGACGAC	AAATTGAATC	AAATTTTTAT	CAATTATTAC	TACAGACTCA	ACTAGACCAT	84840
TGTCTAAATA	ACTCTGAAAA	GTGCTATAAG	GAACATTTTT	ATAGCTTTCC	CCCCCCTTA	84900
TAAAATATGA	CATAAATATT	GCTGAAATTA	GAAAAACAAC	AACAAGTCCT	AAAATCCAAT	84960
TTTTATTCTT	TTTTTTGTTG	TTAGATTTTC	CATTGTTATT	CATATTATTA	TTGCCATTCA	85020
TTCCTTTAAA	AGCCCTCCAA	TCAAAGATAT	ATTAATTTTT	TTAAGAATGC	TTTTTTCACT	85080
CCATACTAAG	TTTAAAGTAT	TTAAATCAAT	AATCCCAATT	AACCTGTTAT	CTAATGCTAA	85140
CAACATTAAA	TAAGCCGGAT	TACACCTTAT	AACTTAGAA	AAAAATTTTT	TTGCTTTCAA	85200
TCTATCCTTA	AAAAATTTAT	ACCTAAACTC	ATAAGAACAA	CATTTTAATC	TTGATACAGA	85260
AGCTGCATTA	CACTCTAAAT	ATTTTAGCAA	AATCTTACCT	AAAGATAAAC	TATGCCATTT	85320
ACCAACTTCC	AAAATAAAAT	CAAAAGGTTT	GTAAATTTTT	TCATCCCTTT	TAAAAATTAA	85380
ATTAATTTTA	TTATGCCTTT	TTTCTAAAAA	AAAATCATTG	GTTTTTAACA	AAACATTATT	85440
TTTTTTCCTA	TTAATCTCTA	CTTTAAACGC	TTCATTAAGA	GCTTTATAAG	AACTTTGGC	85500
TGCAATTCCT	TCTGAATTTA	AAATTTTAAA	AATCAATCTA	AATACCAAAT	ACTTAGGAAA	85560
ATCTAAGAAA	GTTTTTCAGAT	CAAAAGAATA	ATAATATTTA	CCTTTCTCAA	CAGGAAAAAA	85620
TTCATCTTTT	CCAAAATAAT	CCGCAAATTC	CTTTGAAAAT	TCAGATATTC	TTTAAAGACA	85680
TTTTTTCATAT	CCTTTAAAAA	CCTTTTTTAT	AGCGGGTAGC	AAATTATTTT	TAACCCTATT	85740
TCTTAGATAT	AAATTTTGAG	CATTTGTACT	ATCAACAAAA	AACCCAATAT	TATTCAAAGA	85800
TAAAAAATTT	TCAATTTCTA	GTCTTGAAAC	CTCAAGCAAG	GGCCTTATAA	TGTTTCTATT	85860
GACACTAGGA	ATACCTGAAA	GACCATCCAA	AAAAGATCCT	TGAAAAAATC	TCATAATTAT	85920

TGTTTCAATT TGATCGTTTT CGTTATGAGC AAGTGCAATA TAATTGCGC CATTTTCTTT	85980
AAGAGCATTT TCTAAAGCAA TATATCTAAA TTTCCTTGCA AGCTCCTCAA TAGATACTCC	86040
CAACCTAGCT GATTCACTTT TTATATCTAT ATCACATTTT TTAATTTGTA AAGCAATATT	86100
GTAAAGATCG CAAAACCCCT TTACATGCTC TATCTCTTGA TTTTGCTCAT TATCAGATCT	86160
AATAAAATGA GCAAAATAAA ATGCAATAAC ATTATTGCTC AGGTAATATT TTAAATTCAA	86220
TAATAAAGCC GTAGAATCAG CCCC GCCAGA AAAAGCAACA ATAACCCGAT TTTTATCTAA	86280
AGAATTTTTT TTATAAAAT TATCTATTTT AATTTGTATA TTTTCGTCTA AAAAATGCAT	86340
TAAAAATTAC TAGAATTAAT TTTTGAACC TTATTTTAA AATTTGCTTC GCTAATATCA	86400
ATCAGCTCAT CACTTAAAA ATCATACAAT TTTTCAAGTC TATCCATTTT ATCCTTGCAA	86460
AATCTAGAAA GAACAAAAC CTTTATATCA CGCATAAGAT TGCTTCCAAC CCCAATATAA	86520
AGTCTACTAT AGTTAGAGCT TCCAAGAACA CTTGAAATCG ATCTAAGACC ATTATGAGTA	86580
GACACACCAC CTCGCTCTTT AAGCCTGCAT TTTCCAGGG GAAGATCAAC ATTGTCAAGA	86640
ACCACTAATA AATTCTTTAT ACACATATAA AAATCTGAAA ATATTGAAGG AAATAGAGAG	86700
CCACTTAGAT TCATATAGGT CAATGGCTTA ACCAAAATTA CTCTTCCGGA AATCATTTTT	86760
AATTCTGAAT ATTCATACTT TTTTTTCTC TTTAAAAAA GGCCGTTTTT AGAAACAATT	86820
TTATCCAAA GAGAAAAACC AACATTATGC CTAGTTAAAG AAAATTCTAA TCCAGGGTTT	86880
CCTAATCCAA GTATCAACAA CCCCATAAAA TCACTTTATA ATAACAACCT CCAAATTCTC	86940
GTCATTTTCT GCAAGCCTAA CATTAGAAG CAACACAAGA TCTTTAAGAA GAACGCTATC	87000
TCCTTTATTA ACAGGAGTTA AATCAAGCTC TATGAATTCT GGCAAATCCA AGGGCAAAGA	87060
CCTTACCTTA ACCTGCTCTT TTAAACAGT CAAAATTCCA CCTTCTTTAA CCCCAATAGA	87120
AGCTCCAATA AGCTTAATAG GAACATATTT TTCAAGCTCA ACATTCCTAT CTACTTCGTA	87180
AAAATCAATA TGATAAATGA GCTTGCTGGC AATATTTTCT GCAGCATCTT TAACAAAAAC	87240
ACATCTTTCA AGCTTGCCAT CATCTAATAT TAAGACAGTA TTATCCGTAA ATTTTGCAAA	87300
TTTCTTATTA AATTCAC TCTTAATTCT CAAGTGTGAA ACATCCTTAC CTGCCCCGTA	87360
AACAACAGCT GGTATTTTCAG ACTTAGCTCT TATTCTGCGA GCATTAGAAG ATCCAAAGCT	87420
TGATCTATAT TGGCAACTTA AAACCCTGCT ATTTTCCACC AAAAAACTCC TAATGTAAAA	87480
TACTGGGACG GAAGGATTCG AACCTCGAA TGACTGGACC AAAACCAGTT GACTTACCAC	87540
TTGTCGACGT CCCAAATACC TTATTAATAC TTACAATTGA CAAGCATACA AGATACAACG	87600
AGCTTTGTCA ACAATTATCT AAAAATCTAA TTCAAGTTCA AGATCGGCTG GATTTTCTCT	87660

TATATATTCC	TTAAAAATAG	AAGTTTGCAA	AGCTTTTCTA	AAATCCTGAC	TAATAGGATG	87720
TACAATGTCT	TTATATTAC	CGACTCTAGT	TCTTCTGTTA	GGCATCGCAA	TAAATACTCC	87780
CTTTTGCCCT	TTAATAACTC	TAATATTGTG	AAGAACCAAA	CAGTTATCAA	AAGTAACTGC	87840
AACATATGCT	AATAATTTAG	AACCAGAATT	TTTACTATCA	ACTTTCTTAA	TCCTTATGTC	87900
TGTAATATCC	ACTTATAAGC	CTCCCGCAA	AAGTACATAA	CTTAAATCTA	AAATATTTTC	87960
TATTTTTTGT	AAACACGTTT	TTATGATATT	TTTAGTTTTT	TTAATTAATT	TTAATTAAAC	88020
TAAGTAATTA	GGGATAAATA	ATGGTTCCTT	TGGACCATAT	TTTTTCAAGC	TCATAGTATT	88080
CCCTAGATTT	TTCCTCATT	AAATGAATTA	CCAAATTTGC	ACCAGAAACA	ACAGTCCAGT	88140
CATAAACCAA	CCCTTTTCCT	TCAGCATTA	GATTAATTTT	TTTTTCTTTA	AAGAATTTAA	88200
TTATCTTGTC	AATATATAAA	GCTTCCATTT	GCTTAAATGA	TACAAAAGTG	GCTATTATAA	88260
AAAAATCAGT	CCAATTACAA	ATATCGCTAA	CATTAATGCC	TATAACATCA	ATTCCATTAA	88320
AATCACTTAT	TATTTTACAT	AAATCATTA	TATCATTTAC	TTTAAACATA	CCTTCCATCA	88380
AAATCATCTC	CTAAAATAAC	TATTACATCA	GGATTAATAT	CAAGATTATC	AAGCTCTAAC	88440
AATCTTTTAG	CTTGAACCTC	AGAAATTGGC	TTAATATTTG	AAGTTTTAAT	TACCTCTCCA	88500
ACCCTAACAG	CCATTTCTAA	ATTATCCGAA	TTATTTATAA	TCAGGGTATT	TTTATAAGAA	88560
TTTTTATCTG	CATTACCAA	TTTTAAACT	TTAAATTTTA	AAGAATTAAA	AATATTTGCT	88620
GTTTTTTTTG	CAAGCCCAAC	AACTTTGT	CCATTTAAAA	CAACAATCTT	TACTATCTCT	88680
TCTGCACCTT	CATTAACCAA	CTCTTTGTTT	AATTTATCCA	CCGATTCTTT	TAAAATAGCA	88740
CCCCCATAAT	AAGGAAAAAC	CACCTTTATC	AAATTATTAT	CATTATCCTT	AAAAATCTCT	88800
TCTTGTCCCT	TAATATTAAT	AGAAATAATT	TTATCATTAT	TTATTTTATA	ATTTTAAACA	88860
ATATACTTAA	AAACAACCTC	TGAAAGGTTA	GTATCTAACA	TGGAATATAT	TTTAAAAAAA	88920
CTGTCATTTT	CAATGCCAAA	ATCTGAAATT	TGAAAAAGAA	GTCTTTTAAA	AAATTCTTTA	88980
AAAAATTC	CTCTCTCTC	AACTGATTA	ACATCATTA	AATATCTCA	ATAATCATA	89040
GCCTTATCAC	CATCAAAATT	AGAAGTGCCA	GAGGGTATTA	AAATAGAATC	CTCGAAACTA	89100
TAACTTTTCA	CTGGGTTTTT	AACAAGAAGT	CTAACTCCCC	CTAAGTAATC	AATAAGCCTA	89160
ACAAAATTTT	CTTTTTGAAA	ACGAATATA	TAATCTGATT	CATGAGATA	TTGTGTATA	89220
ATTTTAGATA	AAAATTTATT	AAAAGAATTT	TTTTTATAAA	GATCTTTAAA	CCAAGATATA	89280
TTCCCTTTTA	AATCTTCATA	TCCAGTATGA	ATTGGAATAT	CAAAAACCC	AATATTTTCT	89340
GTTTTCATAT	TAATAAAAAT	TTCTTGCATA	CTTACAAGGT	TTTTGTTAAG	ATCTTCTATT	89400
AGAAACAAAA	AACTAATATT	ACTCTTTGTA	TTAAGCTCGA	AGTAAACCAA	CTCTTTTTTC	89460

GAACCTCTAA	TAAAAAAAT	TACTACACTT	GCTATTATTA	AAACAATTAA	AAATAAAAAA	89520
ATTAAATCCT	TTCTCAAACA	TTTACCTTTT	TAACATATAA	ATTATTATCT	TTAATGTATT	89580
TTAACACACC	AAAAGGCAAT	AAATAGCTGA	CGGGCAATCC	ATTTACAATT	CTATTTCTAA	89640
TCTCTGATGA	GGAAATCGGT	ATTATTTTAT	TATCTATATA	AATATGCTTA	AAAGAACTTT	89700
TAAGTCTCTC	TTTGTAGATT	CTATGAGCAA	CAACAAGTTC	AACAGAACTT	ACAATACTTT	89760
GAGGATCTTT	CCATGAATCA	AAATTTTGAA	AAAGATCATC	GCCAATAATT	AAAAAAAGTT	89820
TATCGTTTTT	GTATTTTTTT	TTAACACAAG	AAATAGTATC	AACAGTATAA	GTTATACCAC	89880
CATTTATTAT	GTCGCAATCA	TCTATGAACA	TTTTATCTTC	ATTCTCTAAT	GCAAGCTTGA	89940
GCATATCTAT	TCTATTGCTA	ACACTAACAT	TCTCATCAAT	CAATTTATGA	GCTGGATTGC	90000
AAGTAGGAAT	AAATATTACT	CTATCAATAT	TTAATAAATA	CTCTATTTCT	TTAGCCAAAA	90060
AAATATGTCC	AATATGAACT	GGATTATAAG	TGCCCCCTAA	TATTGCAATT	CTCACGATTT	90120
CTTTCCTAAA	TAAAATCTGA	TATCCAAAAA	CCAAGTCTTA	AAAATAAAAA	GCCCACAATA	90180
AAAATCAATT	TTATTAAAAA	GTTTTAGCCA	AAATAAAAAA	TTCTTTAATA	AGTTCATCAA	90240
TTCTCTTATT	CTCATAAATA	GAGATGCCAA	CAACCTTTTC	TTTTCCTAAG	GCTTTTATCA	90300
GGCAATCAAA	ATTTTTCTCA	GAACCGTCCA	AATCAAGCTT	GTTGGCAATA	ATAATTTTTT	90360
TTTTATTAAA	AAGCTTATGG	CTATAAGATT	TTAATTCATT	TAAAAGAATG	TTATATGACT	90420
CCAAAAAATT	TGCTTCAGAA	ATATCAATAA	CCAAAGCTAA	AATTTTAGTT	TTAGCAATAT	90480
GCTTTAAAAA	TTTAGTCCCG	AGCCCTACTC	CAAAACTAGC	ACCTTTAATT	ATTCCGGGAA	90540
TATCTGCAAT	AATCAAATCA	TCATAAGAAC	GCCTGAGCAT	ACCAAGATGA	GGAATCTTTG	90600
TTGTAAAAGG	ATAATTTGCG	ACCCTAGATT	TTGCTGAGGT	TATCCTATTA	AGAAGAGAAG	90660
ATTTACCAGC	ATTGGGTAAT	CCAACAAGCC	CAATATCCGC	CACCAAAAAA	AGTTCAAGAC	90720
GCACGCTCAA	ACTATTACCC	GATTCTCCAG	GTTGAGCAAA	CCTTGGAACC	CTTCTAACTG	90780
AAGTTTTAAA	ATTCCAATTA	CCAAGACCCC	CTCTGCCACC	TTTTAAAACA	ACAAATTTCGT	90840
CATTTAAATT	TTTAAGCCTA	TACAAAAGAG	TTCCATCATT	TTCATTATAA	ACTTCTGTAT	90900
TTGGAGGAAC	AAAAAGAGTT	AAATCTTTAC	CATTAGCACC	ACTTCTTTTA	AAACCCATTC	90960
CAGGTTTACC	ATTTTCAGCA	CAAAGCACAT	GACCATTTTT	GTAAAAAGAT	AAAGTGCTAA	91020
GATTTTCCCT	CACCTTGAAA	ATTACACTCC	CACCACTCCC	ACCGTTTCCG	CCATCTGGAC	91080
CACCTTTTGC	ATTAACTTTT	TCTCTTAAAA	AAGAAACACA	CCCAGAACCA	CCATTGCCCG	91140
AAACTACCGT	TATATTTACA	GAGTCCTTAA	AGTTATACAA	ACTTTCTCCA	ATTTTTCAAT	91200

TAAAACCAAA	AATCTCCAAT	CTTTTCAATT	AAAACATAAC	AATACTTACG	TATTTTCGCC	91260
CCTTTAAAGT	TTTAAACTCT	ACCTTACCAG	ATGAAAGCGC	AAATATTGTA	TAATCTCTTC	91320
CAAGACCAAC	GTTTTTACCT	TTATGAAACT	TTGTACCTCT	TTGTCTAACA	ATTATCTCTC	91380
CAGCTTTAAC	AAACTGACCA	CCACTTCTTT	TAACCTCAAG	TCGCTTGGAT	ATAGAATCTC	91440
GTCCATTTTT	TGAACTACCA	CCACTTTTAC	TTGTTGCCAT	TAATTTTCCT	CCAAAATAA	91500
TTTAATATCA	TTAGGATACT	CAAAGCACAA	ATCATTTATG	CCTCTAATTA	AAAACCTACT	91560
ATAGTAAAAA	AGACTTTCTT	TGTTCAAATC	CTTAAAAAAG	GGCTTAAATT	CTAAATAACC	91620
TCTTTTTGAA	TTTTTACAAA	CAAAAGCCTC	ACCCTCAAGA	TCAAGAACAC	TAAAAAAGGT	91680
TCTCAAAATA	AAAGAAAAAG	AAGAACAGAC	AACGTTAACA	TTATTCTTAC	CTATAGCATG	91740
ACCATTGGCT	AAAAGATAAA	TAATTACATC	GTCTTTTACT	TTTACCAAAA	CATTAATCAA	91800
TATACTTAAA	AAACTATTTT	ATCAACCAAA	ATATAAGAAT	AGGTTTGCCT	GTGCCCAACT	91860
TTTCTCTCAC	TTGATTTTCT	TCTTCTGTAT	CTGTAAGAAA	CAACCTTTTT	ATCTTTTSTA	91920
TCTTCTTTAT	AGGTACATCT	AATAAGAGAA	TTTACGACAT	AAGGCTTTCC	TATTTTAACC	91980
TCTCCGTCTT	TATTAATAAG	CAAAACACTA	TTAAATTCCA	ACTTATCTTT	TTCAACAGGA	92040
GAAATTTTGT	CTATTTTSTA	AAATTCACCC	TCAATAGCCT	TATATTGCTT	GCCATTTATT	92100
TCTACCAGTG	CATACATATA	TTACCTCAAC	TAAACATTGT	AAATTTAATA	AAAAAGAAAA	92160
GTCAAGCATT	AAATTAATTA	TACCTTACAA	GGGAATTGAC	TTTATAACTT	TCAAGACTTT	92220
GTCTACCATT	AATAGCGCAA	AGCTCAATAA	AACAAAAAAT	ATCCTTAACC	TTGCCCCCGG	92280
CTCTCTCTAG	CAAAATTGCA	GACGACTTTA	AAGTTCCACC	GGTAGCTAAT	ATGTCATCTA	92340
TTAAAAGAAT	ATTGGAATAC	GTCCTAACAT	CGTCTTTGTG	CACCTCTATT	CTCCCAAAAC	92400
CATATTCAAG	CTCATACTCT	TCACTAAAAA	CCTCTCTGGG	CAATTTACCC	TCTTTTCGAA	92460
TTAAAACAAG	GGGTAGCTGC	ATTTTTTAAAG	ACAAAGGAGC	ACCTATTAAA	TATCCCCTAG	92520
ACTCAACAAC	TGCAATGCAA	TCGATCTTTT	TAAAATTATA	AAAAGAATAT	ACTTCATTTA	92580
TTAATGAACT	ATAAACTTCG	GGTTTTAGCA	AAACGCTAGT	AATATCATAA	AAAAGAACAC	92640
CCTTTTTAGG	AAAATTGGGT	ATTTTTTGAA	TAAACTGATC	ATAATACTCT	GTCTTATTTT	92700
TCATAACCTA	CTTATCCCAT	CTATATGTTT	ATATATTTTT	CAAATATCAA	GACCAAAAGC	92760
CAAATTTATT	TTTTTACAGG	GGGCGCTGGA	ACAAGATTAT	GCAAATCTAA	TTTTGGTATT	92820
TCATCATCTT	TAGCTCTTGT	CCAAATTTTA	CTTCTACCAA	AAATCCAAAC	TTTCCCCTTG	92880
GTAATAAGAT	TTCCGGTTTT	ACTATCAACA	CGCATCTCAG	AATTATAAAT	TTTACCGTTT	92940
TTAGGATCTA	TTATTTTGCC	CCTATCCCAC	TTTTTAGAAG	AAGAAGAATA	CTTAAGACCC	93000

CACATAAAAT	CAAGACCCTC	TATTGCAAGA	TTTTCAAACC	CAACTACAGT	ATCTCCTGAA	93060
GGATTTTTAG	CATCATACTT	TTTGCCATCT	TTTATTATAG	TTAAAAATCG	GCCATAAACT	93120
TCCCCATTAT	ATTTATAAAT	ATAGATAATA	GAATTCTTTA	TGTTACTTAC	ATCATTATAA	93180
CCAACCCAAT	ATCCTAAAAC	TTCATTTTCA	AAAACAGGGT	TTTCATCCTT	GCTAACAATG	93240
TCCTTTTCAT	TTGAATCTTC	TGAATTTGCA	AATAAAAGCA	TTGAAAAACA	AAAAAAAAGA	93300
AAAAACTTTG	AAAAAACTCT	AGTCATCAAT	CCTCCTTAAA	ACCAAATTAT	AGCTCTTTTT	93360
TTAAATTACT	CATGTAAGGC	AGCTAATTTA	AAAATTAGCC	ACAAACATCA	TTATACAAC	93420
TATTTTATAA	TTTAAATTAT	TAAGATAAAA	ACCTAGACAA	AAAAATATAA	AATTAAGCAA	93480
AAACACAACA	GGCCAATTAA	TTGTTATATG	GGACAATTAA	TGCTAATATT	AATAAAGTTA	93540
ATTGTCTTTA	AGGATTTAAC	CGTGGTAAGA	GGAATTTATA	CAGCTGCCAG	CGGAATGATG	93600
GCAGAAAGGC	GCAAGCTTGA	TACCGTGTCA	AATAATTTGG	CAAACATAGA	TCTTATTGGA	93660
TACAAAAAAG	ATTTGTCTAT	TCAAAAAGCA	TTTCCAGAAA	TGCTAATAAG	AAGACTAAAT	93720
GATGATGGTC	TTTATAAATT	TCCCAAAGGA	CATCTTGAAA	CAGCTCCGGT	TGTGGGCAAA	93780
ATAGGAACAG	GGGTGAAGA	AAATGAGATA	TACACAGTAT	TTGAACAGGG	CCCATTAATA	93840
ACTACTGGCA	ATCCATTAGA	TTTAGCACTC	ACCGATCAAG	GATTTTTCGT	AATACAACT	93900
TCAGATGGAG	AAAGATATAC	AAGAAACGGT	TCTTTTACTA	TTGGAAAAGA	AGGAATCCTT	93960
GTTACAAAAA	GCGGATTTCC	CGTTC TAGGA	GAAAAAGGAT	ACATATATCT	TAAGAAAAAT	94020
AATTTTAAAA	TAACACCTCA	AGGACAAGTC	TTTCACAATT	CAAACCTTGA	ATCAGACCCC	94080
AAAAGACTTG	TTAGCGAGTA	TGAAAATTCT	TGGGAAAATT	ATGAGCTGCT	TGATACCATT	94140
AGAATTGTAA	ATTTTGAAAA	TCCCAGATTT	CTCAAAAAAC	AGGGAAATTC	TTTATGGATC	94200
GATACAAAAA	CATCTGGCAA	AGCACAAGAA	ATTGATATAT	CATTAAGGCC	TAAAATAGAA	94260
ACAGAAACAC	TTGAGGCTTC	CAATGTTAAT	GCTGTTAAAG	AAATGGTTTT	AATGATTGAA	94320
ATTAACAGAG	CTTATGAAGC	TAATCAAAAA	ACAATACAGA	CTGAAGATAG	TCTATTGGGA	94380
AAATTAATAA	ATGAAATTGG	AAAATATTAA	GGAGCATGTT	TTATGATGAG	AGCATTATGG	94440
ACAGCAGCAA	GTGGAATGAC	TGCACAACAA	TACAATGTAG	ATACAATTGC	CAATAACCTT	94500
TCAAATGTAA	ATACTACAGG	ATTTAAAAAA	ATAAGAGCAG	AATTTGAGGA	TCTAATTTAT	94560
CAAACCCATA	ACAGAGCAGG	AACCCCTGCA	ACTGAAAATA	CTTTAAGACC	ACTTGGAAT	94620
CAAGTTGGTC	ACGGAACAAA	AATTGCTGCC	ACCCAGAGAA	TATTTGAACA	AGGAAAAATG	94680
CAATCCACAA	ATTTACTCAC	TGACGTTGCC	ATTGAAGGAG	ATGGATTTTA	CAAAATTCTT	94740

CTACCTGATG	GAAC TTATGC	ATATACTAGA	GATGGGTCAT	TTAAAATCGA	TTCTAATCGA	94800
GAGCTTGTA	CAAGCCAAGG	ATACAAAGTA	TTGCCTAATA	TACTCTTCCC	AGAAGAATAT	94860
ATCCAAAAC	CAATTACAAT	ATCTGAAGAG	GGAATAGTAT	CGGTAAAAAT	TGATACCAGC	94920
AACGAACCA	TAGAGCTTGG	GCAAATTGAA	ATATCAAGAT	TTATCAATCC	TGCAGGACTA	94980
AGTGCCATTG	GAAGCAATTT	ATTTAAAGAA	ACAGCTGGAT	CAGGCCAAGA	AATAGCAGGA	95040
ATACCAGGAA	GTGAAGGCAT	GGGAAGACTA	AGGCAAGGCA	TACTTGAAAT	GTCAAATGTA	95100
TCTATTGCTG	AAGAAATGGT	AACAATGATA	GTAGCTCAAA	GGGCTTATGA	AATAAACTCA	95160
AAAGCTATTC	AAACTTCTGA	CAATATGTTA	GGAATTGCAA	ATAACTTAAA	AAGGCAATAA	95220
AATAAAAAA	AGATTATTTA	TTTTTATTTT	ATTTTTCACA	ACAAGCTCAA	TTATAAGAGC	95280
TTCTCATGAT	TTATGTTTCA	ACATTGCGCC	TAGTAAAACA	TATTTCTTTT	CAAAGAAGTA	95340
TTCAAAAAA	TGTAACAATC	AAAGCTTATC	AAAAATATAT	ATCCCCCAC	ATTTAACAAA	95400
AAAATCAATA	ATTTTGTAAA	TGATTTATTA	CATTACAAAA	AATTTATCAA	ATGAAAATAT	95460
CTATATACTT	CAATTTAACT	TTGATGAATC	TGAAATAAAC	ATAGAAGATA	AATTTTTCAA	95520
AAAAGTAAAA	TTTAAGGTAA	AAAGCAACAA	TTCATACAAA	AATATTCCAA	TTGAAAAAAC	95580
TCTTGTTTAT	TATGCAAAAA	ACTTTGAAAG	CTACAAAAGA	CACAATTACA	TCAATATGTA	95640
CATTGATGTA	ATCGAGCCAA	TTGTATTTGC	AAAAGAAAAT	CTAAAAAAA	ATGAAATCCT	95700
TAATGAGTAC	AATACATACT	TTAAATACAA	AATTAACACA	ACAAGAATAA	ATGATGTTTT	95760
AAGTCTAAAT	GAATTAAACA	ATAGCAAATA	CAAAGTTATA	CGCAACACAA	TCAAAAATGA	95820
AGAGATAAGA	TTAAATAAGG	TGCAAAAAGA	ATAATACCTA	ATTTTATCTT	CCTTTTCTAA	95880
AAATTATTAT	TTTAATCTCC	CTTAATGCAG	CTAATATTTA	ACAAATCAAG	GATTAATTAG	95940
TAATTTAACG	AAAAAAGTTT	CATTAATTGC	AATAATTGAT	ATAAAATAAT	AGATATTAAA	96000
GAAATACAAT	AAATAAGGTA	AAGAATGAAC	AACTAATGT	TGATGTTAAT	TACATTTGCA	96060
ACGAGTCTAT	TAGCCCAAAC	AAACAAAGCT	TCAACAGGAC	TAAAAACAGA	TCAATCATTT	96120
AACAATAGCC	TATCTGAAAG	CGTAAAATTA	AAAGAAATTG	CGGATATTTA	TCCCACAAAT	96180
ACAAATTTTT	TAACAGGTAT	TGGAATAGTA	GCGGGACTTG	CTGGAAAAGG	AGACTCTATA	96240
AAACAAAAAG	ACCTTATAAT	TAAAATTTTA	GAAGAAAACA	ATATAATAAA	TGAAATAGGC	96300
TCTAATAACA	TAGAAAGTAA	AAATATTGCA	CTAGTAAATG	TCAGTCTCCA	AGTAAAAGGT	96360
AATACAATCA	AAGGTTCAAA	ACATAAAGCT	TGCGTTGCAT	CAATACTGGA	CTCAAAAGAT	96420
TTAACAAATG	GAATACTTTT	AAAAACAAAT	CTTAAAAATA	AAGAGGGGGA	AATAATAGCA	96480
ATTGCATCAG	GAATTACACA	GCCCAATAAT	AAATTAAAAG	GATCTGGATA	TACTATAGAT	96540

AGTGTAATAA	TAAATGAGAA	TCAAAATATT	AACCACAGTT	ATAATATAAT	TCTTAAAAAA	96600
GGAAATTATA	CATTAATAAA	TAGAATTCAT	AAAATATTAA	CCTCTAAAAA	AATCAACAAC	96660
AAAATTAAAT	CAGACAGCAC	AATAGAAATA	GAAGCAAAAA	ACATAAGCCT	ATTAGAAGAG	96720
ATTGAAAATA	TTAAAATAGA	AACCAACCCC	AAGATATTAA	TAGACAAAAA	AAATGGTATT	96780
ATTTTAGCAA	GTGAAAATGC	AAAAATAGGA	ACTTTTACAT	TTTCCATTGA	AAAAGACAAT	96840
CAAAACATTT	TTTTAAGTAA	AAATAACAAA	ACAACAATTC	AAGTAAACTC	AATGAAATTA	96900
AATGAATTTA	TATTAATAAA	TTCCAACAAT	CTTAGCAATA	AAGAATTAAT	TCAAATAATT	96960
CAAGCTGCGC	AAAAAATTAA	TAAATTAAAT	GGGGAACCTA	TCTTGAGGGA	AATTGATGGA	97020
AACCAAAATT	AATTCACAAA	ATCTAAAATT	TAAAAATCAA	ATAAATAATT	TTAAAAATTC	97080
TGTAGAAATA	AAAAAATCCT	TTCAAAAAAA	CGAAGATCTT	CGAAAAGCTT	CTTTAGAATT	97140
TGAAGCTATG	TTTATCAAGC	AAATGCTTGA	AAGCATGAAA	AAACTCTTA	ACAAAGATCA	97200
AAATTTGCTA	AACGGAGGCC	AAGTAGAAGA	AATTTTTGAA	GATATGCTTT	GCGAACAAAG	97260
AGCAAAACAA	ATGGCACAAG	CTCAAAGCTT	TGGCCTTGCC	GATTTAATTT	ACAATCAATT	97320
ACAAAAAAGT	AAATAATTCA	AAAAATACTC	CCCCTAAACT	CAAAATTATA	TCCTATTTAG	97380
TTTAAACCA	TTTTTAAATT	AAATTGGCAC	AGTTTTTGCA	TGGAAATTAA	GTAGTAAAAA	97440
CTTAATCACA	ATATTCAAGA	AAGGGGAGAA	AATATAATAA	CTATGAACAT	ATTTAGTAAT	97500
GAGGATTTAA	ACATATATTT	AAAATCAGTA	AGAGAACACA	AGCTAATTAC	TCACGAAGAA	97560
GAAATCAAAC	TTGCAGGACA	AATACAAAGA	GGCAATGCAA	AAGCAAAAAA	CAAGATGATA	97620
AATGCAAACT	TGCGACTTGT	TTTAAAAATA	ATAAAAAGAT	ATGCGGGTAA	AGGGTTAAAA	97680
ATTGAAGACT	TAATTCAAGA	AGGCAACTTG	GGATTAATAA	GAGCTGCTGA	AAAATATGAC	97740
CCGAATAAAA	ATACCAAATT	TTCAACTTAT	GCATCATTTT	GGATTAAGCA	ATCACTACAA	97800
AGAGCATTAA	ACACTAAAC	CAGATTGGTA	AAAGTCCCAT	ACAGAAAAGA	AAATCTAATA	97860
CTACAAATAA	ATAAATATTT	AACAGAAGAA	GAAAAATCGC	CCAAAAAAGA	AGAAATAATG	97920
AAAAGATTCA	ACCTATCTCC	TGCTCAGTAT	ATAAAAATTA	TTCCCTATCT	TGAAAAAGAA	97980
TATTCTCTGG	ACAAAGAAAT	AGAGGGATCT	GAAAATTCAA	CACTCTTGAA	TCTATACGAG	98040
GATAATTCTT	TTAACCCTGA	AATTACCCTT	GAACAAGATT	CAACTCTAAA	ACATTTGAAT	98100
TATATACTTG	AAACAAAATT	AAATGAAAAG	GAAAGATACA	TAATTAAAAA	AAGATATAAC	98160
CTGGACAATA	GTCCCAAAAA	AAGCACCTTA	AAAGATATTT	CAACAGAACT	TGGAATATCA	98220
TCAGAAACTG	TAAGACAGAT	TGAAAAAAGA	GTTCTTAAAA	AATTAAAAGA	AGAAATAAAT	98280

TAACATTGAC	ATTCATGACA	TGTTCTGGTC	TACTTGTAAG	TCAGTGGTCA	TGAATGTTTG	98340
TATTTTATAT	TAAAAAAAC	AAGTTTATTA	TTGTAATTTT	TATTATAATT	TCTATTGTTA	98400
TTGCAATAAC	TCAGGCATTT	GCAAGTTTTT	TATATTTTAA	TGACAATTCA	AAAATTGCAA	98460
ATGCCCCACT	TAAAAATAGG	TTTGAAAAAA	CACAAAAAGA	AAGCTTAATA	ATAAAAACA	98520
ACAACGAGGA	TAAAAAGCC	AAAAGCAAAC	CTAAGTTTTA	CTTAATCATT	GACGACGTGG	98580
GCTATGATGA	ATTTATGTTA	GAACAATTTA	TAAAACTTAA	TCTTAAAATA	ACTTATGCTA	98640
TTATTCCATT	TTTACCAAAA	TCAATGAGTT	TATACAAAAA	ACTAAAAAAT	GCTAACAAAA	98700
CAGTAATAAT	ACATTTCCCA	ATGCAATCAA	AACATAGAAA	TTCAATAGAA	AAATTTCATA	98760
TAAACATAAA	AGATAAAAAA	GAAGAAATAC	ACAAAAAAAT	CGAAAAAGCA	TTTAAAAAGT	98820
ATCCTGATGC	AAAAATAATG	AATAACCATA	TGGGAAGTTT	AATCACTTCA	AATAAAGATT	98880
TGATGAAAAT	CATTTTAGAA	AAGCTTAAAG	AGATTGACAG	ATATTTTTTC	GACAGCGTAA	98940
CTATTGCAGG	AAGCGTACCA	GAAATAATAG	GCAAAGAAAT	TGGAGTTAAA	GTAGAAAAAA	99000
GAGACGTATT	TCTTGATAGC	AAAGACACAG	AAGAGTCCGT	AACAAAGGAG	CTTGAAAAAG	99060
CAAAAAATAT	TGCTAGAAAA	AATGGAATGG	TAAAAGTAAT	AGGACACATT	TGGTCTAAAA	99120
ATACGCTAAA	AGTCCTTAAA	AAAGAAGGAC	CTGATTTAAA	CCAGGAATTC	GAATTCGACA	99180
ACTTATTAAA	TCTTTACGAG	GAAACAATCA	GATGAAAGTG	CTTGGAATAG	AAACCTCTTG	99240
TGACGACTGT	TGCGTAGCTG	TAGTAGAAAA	TGGAATTCAT	ATTTTAAGCA	ATATAAAATT	99300
AAATCAAACC	GAACACAAAA	AATATTACGG	CATAGTGCCT	GAGATTGCCT	CAAGACTTCA	99360
TACGGAAGCT	ATTATGTCTG	TTTGTATAAA	AGCACTAAAA	AAGGCAAATA	CTAAATATC	99420
TGAAATTGAC	TTAATAGCTG	TAACATCTAG	ACCTGGACTT	ATTGGATCTT	TAATAGTTGG	99480
ATTAAACTTT	GCCAAAGGTC	TAGCAATTTT	ATTAAAAAAG	CCCATTATTT	GCATTGATCA	99540
CATCTTGGGT	CATCTTTACG	CCCCTTTAAT	GCACTCAAAA	ATAGAATATC	CATTTATATC	99600
ATTATTATTA	AGTGGTGGAC	ATACATTGAT	TGCTAAACAA	AAAAATTTTC	ATGATGTTGA	99660
AATACTTGGA	AGAACTCTAG	ATGATGCTTG	TGGAGAGGCT	TTTGATAAAG	TGGCAAAACA	99720
TTATGATATG	GGATTTCCGG	GAGGTCCAAA	CATCGAACAA	ATATCTAAAA	ATGGAGATGA	99780
AAATACATTT	CAATTTCCAG	TTACCACCTT	TAAAAAATAA	GAAAACTGGT	ATGATTTTTT	99840
ATACTCTGGA	CTAAAAACAG	CTTGCAATCA	CCAACTCGAA	AAATTCAAAA	GCAAAGATAA	99900
CCCAACAACA	AAAAATAATA	TAGCTGCAAG	CTTCCAAAAA	GCTGCCTTTG	AAAATCTAAT	99960
CACCCCACTA	AAAAGGGCAA	TAAAAGATAC	TCAAATCAAC	AAATTGGTAA	TAGCAGGAGG	100020
TGTTGCAAGC	AATTTATATT	TAAGAGAAAA	AATAGATAAG	CTTAAAATAC	AAACTTACTA	100080

CCCTCCTCTT	GACCTTTGCA	CAGACAATGG	AGCAATGATT	GCGGGACTTG	GATTTAATAT	100140
GTATTTAAAA	TATGGAGAAA	GTCCAATTGA	AATTGATGCA	AATTCAAGAA	TAGAAAATTA	100200
TAAAAACCAG	TATAGGGGGA	AAAATAATGA	AAAGAATTTT	AGCAATGCAT	GATATTTCAA	100260
GCATGGGAAG	AACATCTCTT	ACAATATGCA	TACCAGTAAT	ATCTTCGTTT	AATATGCAAG	100320
TTTGTCTTTT	TGTGACAGCT	GTCTTTTCTG	CTTCCACAGC	TTATAAAAAA	TTTGAAATAG	100380
TGGATTTAAC	CGATCATTTA	GAAAAATTTA	TCAATATATG	GAAAGAACAA	AATGAGCACT	100440
TTGACATACT	CTATACCGGA	TTTCTGGGAA	GCGAAAAACA	ACAAATAACA	ATAGAGAAAA	100500
TAATTAAATT	AATAAAATTT	GAAAAAATTG	TAATTGATCC	TGTGTTTGCT	GACGATGGAG	100560
AAATTTACCC	TATATTTGAT	AATAAAATAA	TTAGTGGATT	TAGAAAAATC	ATAAAGTACG	100620
CAAACATAAT	AACACCCAAT	ATCACAGAAC	TTGAAATGCT	AAGCAAAAGC	TCAAAACTTA	100680
ACAACAAAGA	TGATATCATA	AAAGCAATAT	TAAATCTTGA	TACAAAAGCG	ACGGTAGTTG	100740
TTACAAGCGT	TAAAAGGGGA	AATCTCTTGG	GAAACATTTG	CTACAATCCT	AAAAACAAAG	100800
AATACTCGGA	GTTTTTTTTT	GAAGGATTAG	AACAAAATTT	CAGTGAACA	GGAGATTTAT	100860
TTACCAGCTT	ACTTATAGGA	TATTTGGAAA	AATTTGAAAC	AGAGCAAGCC	TTAGAAAAAA	100920
CAACAAAGGC	TATTCACCTA	ATAATAAAAG	AGTCAATTAA	AGAAAATGTT	TCAAAAAAAG	100980
AAGGGGTCCG	AATTGAAAT	TTCTTAAAAA	ATACATTTTG	AATTTAAATT	CCATTAAATT	101040
CAATTTTTTA	GATTGAATCA	ATTTCTTGGT	ACAAAGGAAA	TACTGATATT	GCAATATATT	101100
ATTAAAAATA	AATGTGAAAA	AATTTATTAC	AAAGTAAATG	CTTTATTGTT	TTCATGAGTA	101160
AATAAAAAATA	TGTCAAATAA	AAAAATAATA	TTTTTTACAG	GGGGAGGAAC	TGGGGGTCAC	101220
GTATTTCCAG	GAATTTCCAT	CATACAAAAA	TTAAAAGAAT	TTGATAATGA	AATTGAATTT	101280
TTTTGGATAG	GTAAAAAAA	TTCTATAGAA	GAAAACTAA	TAAAAGAACA	AGATAATATT	101340
AAATTTATTT	CGATTCCATG	CGGAAAACTT	AGACGCTATT	TTTCTTTTAA	AAATTTTACT	101400
GACTTTTTCA	AAGTAATACT	TGGAATAATA	AAAAGCTTTT	ACGTTTTAAA	AAAATATAAA	101460
CCTCAGCTTA	TTTACGCAAC	CGGAGGATTT	GTTTCAACTC	CTGCAATTAT	TGCATCCAGC	101520
TTGCTAAAAA	TAAAAGCAT	AACCCATGAA	ATGGATCTAG	ATCCCGGACT	TGCAACAAAA	101580
ATTAACCTTA	AATTGCAGAA	TAACATACAC	ATAAGCTTTA	AAGAAAGTGA	AAAATACTTC	101640
AAAAATTACA	AAAACATTAT	TTACACAGGA	TCTCCTATAA	GAAGAGAATT	TTTAAATCCA	101700
GATCCCAAAA	TAATCAAACA	ATTGACACAA	AACACTAACA	AACCAATTAT	TAGCATACTT	101760
GGGGGATCTC	TTGGCGCTAA	TGCTTTAAAC	AACCTTGCAC	TCTGCATTAA	AAAGGATGCT	101820

GAAATCTACT	TCATCCATCA	ATCGGGGAAA	AATTTTAAATG	ACCTAAGCGA	AAAGAATTAC	101880
CTTAGAAGGC	AATTTTTTTAA	CGCAGAAGAA	ATGGCAAGTA	TAGTTAAATT	TTCTAATCTA	101940
ATAATAAGCA	GAGCCGGAGC	TGGAGCAATA	AAGGAATTTG	CAAATGCTGG	TGCATGTGCA	102000
ATTTTGATTC	CATTTAAAAA	AGGCTCTAGA	GGAGATCAAA	TTAAAAATGC	AAAATTACTA	102060
ACAAATCAAA	ATGCCTGCAT	TTATATAGAT	GAAGATGAAA	TTTTAAATAT	AAATATTTTA	102120
AAAATTATAA	AAAAAACTTT	AAAAGATAGA	GAAAAAATCA	ACTCTCTCAA	AGAAAAATATC	102180
AAAAAATTCA	ATAATAAGCA	TTCTTCAACT	TTAATAGCCA	AATTGCTAAT	AAAAGATATT	102240
AAGGAGACAA	AATCTAAATG	ATAATAAACG	ATCCTGTAAA	AATAACTGGA	ATAGTAGACA	102300
TATTAATAAT	AATAATTTTT	ACATCTTTGG	GATTTAGAGG	ATTTTTAAGA	GGATTTATTA	102360
AAGAAATTAG	CGGATTTGCT	GAAGTTTTTG	TTTTAATCCT	ACTGCTTTAC	AAAAAACTG	102420
AAGAATTTAG	AAGGTTTGTT	GAACCTATTA	TTGAGCTATC	CTACATTCAA	GCACTACTTG	102480
TATTTTTTTT	GCTTATACAT	ATAGGATTTT	TAATACTACA	ATCCCTAATA	GAATCAATAA	102540
TAAGTCAACT	TAAATTGCTA	TTCTTCAATA	GAATACTAGG	CTTAGTGCTT	GGCCTACTTG	102600
AAGCTTTTGG	AATAATTGCA	ATCGTGGTTT	ACATAATACA	CTCACAACAA	ATATTTAAAC	102660
CTGAATATTT	CCTAAAAGAA	AGCAAACCTAC	TTGATTATTT	AAATCCTGGA	ATAAACTATC	102720
TCTTTAAAAAT	TTCAAAAACA	AAATAAGGGC	CAGCAATGAC	AATGCTTCCA	AAAATTGCAA	102780
AAGAGATAAT	AAACGAATAT	GATCAAAAAA	TACTGCCAAA	TGCAATTCTT	TTACTAGGAG	102840
AAAAATTTTC	TTCAAAAAAG	ATTAGCGCAA	TTGAGCTTGC	AAAAAAAATA	TTAAACGGAA	102900
AAAACTTAAC	AAACCCTAAT	TTGCTCATT	TCTCAAATCT	TGACACAGTA	GAAGCAAAAG	102960
CACATCTTTC	TACAAATTCG	CAAAAGATAG	CAAATAAATA	CCTAGAATAT	ATTAAAACTG	103020
TAATTTTAC	CAAATGTTAT	TTGAGCAATG	AAAAAAATTT	AAAAAAAATA	GAAAAAATA	103080
TCAACTACAT	TAATCTGT	TATTATGAAA	AAGAATACAA	TGAAAACATA	AAAAATGAGC	103140
TTATAAAAAA	TATAGAAAAT	ATAAACAAAG	AATTAAATCA	TAGCATTACT	GTTTATGATG	103200
TAAAAAAAT	TCAAACCTGG	ATTTTTTCTG	AAAAAGAAAA	ACCAAAGGTA	ATCTACATAA	103260
ACGAAATCGA	AAATTTATCA	TTTAATGTCC	ATAACTCACT	TTTAAAAATA	TTGGAAGAGC	103320
CTCCCTCAAA	TATTTACTTT	ATCTTGGCAG	CAAGAAATAA	AAACAAAATA	CCAAAAACAA	103380
TACTTTCAAG	ACTTAGAGTC	TACAATTTTCG	CAAAACTAGA	CAGAAGCTTA	GAAATTCAAA	103440
GATTTAAAGA	AAGCTTTCTA	ATAAATAAAG	ATATAACAAT	TGAAGAGTAT	TTGCGCTCAT	103500
TTTACAAAGA	AGAAAGCAAA	AAAATAAAAA	AAGAATTGGC	AAAAATTCTA	AATATAATAA	103560
AAGAAAAAAA	ATCCATATTT	AATCTTGAAG	AAGTCGACTT	TATAAAAAGAT	GAGCAAAGCT	103620

TTAAATATT	TTTAAACGAA	CTTACAATTA	ACATTAGAAA	AGATTTTTTA	GAAAACAAAA	103680
TAGATATTAA	TCAATATCTA	AAGTACACAG	AGCATTTGAA	AAATATTTAC	AAATATCGCC	103740
CCTATAATCA	AAATAAAAAA	TTAATAATAG	AAACTTAAT	GCTAAATTAT	GAGGAGATAT	103800
GAATAATTTT	TTCAAAAAAG	CTTTAACAAA	GCTAAACAAA	TTATCTAACG	AACAAAAAAC	103860
TAAATTTATT	GAACAAATTT	ACAAAAAAT	AGAAATATAT	GACGGAATAT	TTGCATCAAT	103920
TAATGAAGGA	ATCATTGTAC	TTGACAAACA	AAACAATATA	ATCTATGCAA	ACAAGATTTT	103980
ATACCAAATT	TTAGCTTTAA	CATCTAAATC	AAAAATAGAA	ATTCTTGATG	ACATTCAAAT	104040
TCCAAACTTA	ATAAATTTAA	TAAAAGAACT	AGTTAGAACA	GAAGATAAAA	TAATAGGATT	104100
AGAAGTTCCA	ATCTCAAACG	GCATATATAT	TAAATCTCA	TTTATGCCTT	ATGTAAAAGA	104160
AAAAAACTT	GAAGGCAACA	TTATTTTAAT	CGAAGACATT	AAAGAGAAAA	AAAAGAAAGA	104220
GGAACTATTT	AGAAGAGTTG	AGGCTTTGGC	CTCTTTTACA	AGGCATGCAA	GAAATATTGC	104280
CCATGAAATC	AAAAACCCAC	TTGGAGCAAT	CGATATAAAT	TTACAACTGC	TAAAAAAGGA	104340
AATTGAAAAA	CAAAAAATGA	AAAATGGTAA	AGCTGAAAAT	TATTTTAAAG	TAATAAAAGA	104400
AGAAATAAAC	AGAGTAGATA	AAATAGTAAC	AGAATTTTTA	CTAACTGTCA	GACCAATAAA	104460
AATTAECTTA	CAAGAAAAAG	ATATTAAACA	AGTAATAGGC	AGCGTATGTG	AATTGTTAAA	104520
TCCTGGATTA	GAAAAATAAC	ACATAAAACT	ATTGCTTAAT	TAAACAAAA	TAAGCAATAT	104580
TCTCATTGAT	GAAAAACTAT	TAAAACAAGT	TATTATAAAC	ATCGTTAAAA	ACGCAGAAGA	104640
AGCACTGCTT	GAAACAAAAA	AAGAAATAAA	AAAAATAGAA	ATTTTCTCT	TCGAAAAAGA	104700
CAATAAAATA	CATATCAACA	TAAAAGATAA	CGGAAACGGA	ATAAAAGATG	GGGTAAAAGA	104760
GGAAATATTT	AAGCCTCAAT	TTAGCACAAA	AGAAAAAGGA	AGTGGAATAG	GACTTACTAT	104820
TTCTTATAAA	ATAATAAAAG	AGCTTGGAGG	TGAAATTTTT	GTGGAAAGCA	AAGAGGGCAA	104880
AGGCACTATT	TTTACAATTA	CGCTGCCTAA	ACTAAATAAA	AAAAATATTT	TAATTGAAGG	104940
GTATTGAAAA	TGAGCAAAAT	ACTTGTAGCT	GATGATGAAA	AGAATATTAG	AGAAGGAATT	105000
GCTACTTATC	TTGAGGATGA	AGGATATTTT	GTTTTCACTG	CTAGTGACGG	AGAAGAAGCT	105060
CTTGAAACAA	TTGAAAATGA	AAATCTTGAT	GTAATAATAT	CTGACCTGAG	AATGCCCCAG	105120
ATATCTGGAG	AAAAATTGCT	CAAAATAGTT	AAAGAAAAAA	ACTTGGGAAT	ACCTTTTATT	105180
ATTCTAACAG	CCCACGGAAC	AGTTGATTCT	GCTGTAGATG	CCATGAGAGA	GGGTGCTTAT	105240
GATTTTTTTAA	CAAAGCCCTT	AGACCTTGAA	AGACTTTTGC	TAATAATAAA	AAGATCACTA	105300
AATAAAAAAG	AAAATAACGA	TAATGAAAAT	GCTAATTTAG	AAAATATACT	AATAAGAAAA	105360

GATCTAAAAT	ACTATGAAAA	AATCATGGGA	AAATCCCTAT	TAATGCAAAA	AATTTTTTGAA	105420
CTTGTAATAA	AAATAGCAAA	ATCAAATGCA	TCTATTCTTA	TAACGGGCGA	AAGCGGTGTT	105480
GGTAAAGAAA	TAATAGCAGA	TGCTATTTTT	GATCTTTCAA	ATAGAAATGA	CAAACCATTT	105540
ATAAAAGTAA	ATTGCGCAGC	ACTTTCTGAA	AGCATTCCTG	AAAGTGAAC	TTTTGGCCAT	105600
GAAAAAGGAG	CATTCACTGG	AGCAATTTCC	AAAAAAAAAG	GCAGATTGGA	ACTTGCAAAC	105660
AAAGGCACAA	TTTTTCTTGA	TGAGATAGCA	GAAATTTTAC	CTGAAATTCA	AGTCAAGCTT	105720
TTAAGAGTAC	TGCAAAACAA	AACTTTTGAA	CGTGTGGGG	GAGAAGCTAC	AATTAAAGTT	105780
GATATCAGGC	TTCTGGCTGC	AACAAACAAA	AACATTTGAAG	AGGAAATTAA	AAAGGAAAAA	105840
TTTAGAGAAG	ATTTATTTTA	TAGATTAAAT	ATCATTAATA	TAAACATACC	GCCTTTAAGA	105900
GAAAGAAAAG	ATGATATATC	TTATTTAACA	AACATACTAA	TAAAAGACGT	CGCAAAGGAA	105960
AACAATAGAG	AAGAAAAAAC	TCTTTCTAAT	GATGCAATGA	AAGCTCTCTA	TTATTACGAT	106020
TGGCCAGGAA	ATATTAGAGA	ATTAAAAAAT	GTGCTTGAAA	GTGCATTAAT	ATTATCAAAA	106080
GGCAAACAAA	TCATAAAGA	AGATTTGCCA	GCAAAAATCA	AAAATAATGA	AAATCTTATA	106140
TTTAAAATAA	CACTACCAAT	AGGAATTAGC	CTAAAAGAAG	CTGAAAAAGA	AATAATAAAA	106200
CAAACACTTT	TTCATTCCAA	AAACAACAAA	AGCAAATGCG	CCGAAATACT	AAAAATAGGA	106260
AGAAAACTT	TACACAATAA	AATAATCGAA	TATAATATTG	ATTAATAGGA	TTTATTTTAA	106320
ATTATTAAAT	TATAATGGGT	ACAAAAAAT	AATACTGCTT	TAAATTCCAT	GTATATTTTT	106380
GAAACCAAAA	AATTTTTTAA	TGCCAATAAT	TATATTAAAA	TGAAACACTT	TCTTTTAAAA	106440
TCATGGCGCA	AAAGTGTAAG	AATATTTTTA	TCAAACAAAT	AATTATACAC	CATTATTTGT	106500
TAATAATCAA	TACAATTTGA	TAATTTAATA	TATTTAGCTG	GCTACAGAGC	CTGACCTTAC	106560
TTTAAAACT	TTAAAGGGT	AATAGGAATA	TTTTTTTTTA	ATATTTCAA	GTGCAAATGA	106620
GGACCAGTTG	CGCGACCCGT	TTGCCCAACC	TTTCCAAGAA	ATTCTCCCGA	TTTAACAAAA	106680
TCACCTATCT	TTACAGAATA	TAAATTTAAA	TGCCCATAAA	GAGATTTAAT	ATTATTTTTG	106740
TGACCAACCA	CAACAAAATT	CCCATAAAGA	TCATTGTATC	CAGCTTCAAT	AACTATTCCA	106800
GAAGAAGAAG	ATACACTTCA	GCATTCATTG	GAGCTGCAAG	ATCTATTCCT	GTATGGAAAC	106860
TTTTGTTGCC	AGTGAAAGGG	TCATTTCTAA	ATCCAAAATC	AGAACTAACA	ATAAATTTTT	106920
TTAAAGGAAA	AATAAAATTG	GCATTTAAGA	AAAAAAGCAA	TTCTGTGCCT	GAAAAAAGTC	106980
CAAAATCTGG	ATTCTTAACA	AAATCAAAAA	AATAAAATTC	ATAAACTCTG	TCGTTCCCTT	107040
TAATTTTTAC	CTTTTCAGCT	TTAGCAAGAT	CCCTTGTTGC	TAAAAGCAAA	TTATTAAATC	107100
TATAATCTTT	ACTATCAAAA	ACAAAAACTC	CTTTTTTACT	GGGAATAAGA	ATCTCTTGCC	107160

CAACACTCAC	AGCAGGAGAA	TCTAATAAAT	TAATAGTAGC	AATGCCGGAC	TGCCATCCAT	107220
TTATTTTATT	GGCAATTTTA	AAAAAAGTAT	CCCCTTTTTT	AACTTTATAT	GAGTAAAAAA	107280
ACAGAGGAAT	ATGTTGTTTT	TTGTTATATT	TTAAAACTTT	AATTTTAAGA	TCAGAAAAAA	107340
CAGGATCTTG	CCTTGAGAAA	TTTTTTATTT	CTGGATAAGA	AAAAACATAA	ATTATTTTTA	107400
AAAAAAAGAA	ACCTGCATTA	AATAATAAAA	AAATTTTACT	CATACTATAA	ATTCTTTAAC	107460
GATTAATTAA	TCAAATATAA	TAAAAAACAT	AAAAAAAATA	AATCCTATTT	GGACTTGCAA	107520
ATAATAACAA	ACTGTAATAA	ACTGTCTCTC	AACATGGAGC	TAAACGAATA	CCAAGAAAAA	107580
GCAAAAAAAA	CTGCTAAATA	CAAAAATAAA	AAAGAAGAAT	TAATTTTAAC	AACACTTGGT	107640
CTTGCTGCTG	AAACTGGAGA	AGTTGTTGAA	AAAATAAAAA	AATTGGGAAG	AGATAAAAAAT	107700
TACATTATTG	ATGATGAGTA	TTTAATATCA	ATTAAAAAAG	AGCTTGGGGA	CGTATTATGG	107760
TACTTGTCAA	GTTTAAGCAA	TAATTTAGGC	ATTACGCTTG	AAGATGTTGC	CCTCACAAAC	107820
CTAAAAAAA	TACAAAACG	ACATGAAAAT	GGAACAATAA	ATGGCGAAGG	CGATGACAGA	107880
TAAGGCATTT	AAATTTAAAA	TACTCAAAGT	TTAAAAATAA	AAATGCTTAA	TATTTATATC	107940
AAGGGAATTT	TACTTGGAAT	TGCAAACATA	ATCCCAGGGG	TTTCTGGGGG	AACGCTGGCT	108000
TTAATATTAA	AAATTTATTA	CAAAATAATA	AACTCCATCT	CAGAAATCTT	AAAGCTCACA	108060
GAAATTAAAA	AAAATTTAAT	GTTTTTAACT	ATTTTGGCAA	CAGGAATGTT	AACCTCAATA	108120
TTATTAACTG	CAAAAATATT	TAAAAC TTAT	GCTTTTGACA	ATGGAATAAT	AGAAGCACTG	108180
CTAATAGTAT	TTTTCATAGG	ATTAGCATTT	GGAAATATAC	TAACACTAAA	AACAGAAATA	108240
TCTATAAAAG	AAATAAATAG	TAATACAAAA	ATATTAAATA	ATTTATTGTT	TTTCATTGGT	108300
ATGAGCATTA	TTGTACTCTT	CTTAATACTC	AAAGAATCTA	ATATACAATT	GCAAAGTACA	108360
ATACCTAAAG	ACAAAAACTC	AATAAAATAT	TACTTATTAT	TGATATCCTC	TGGAACAATA	108420
AGCGGAGCAT	CAATGATCTT	ACCGGGAATC	TCAGGATCTG	CAATGCTTTT	ACTGCTTGGC	108480
TTTTATAAAG	AAATAATACT	TATTGTGTCT	GAATTTAACA	TTATTCTTAT	TACAATATTT	108540
GCAGCTGCTG	CAACAATGGG	AATAATTACA	TCAATATTAA	TAATAAAGAA	AATAATAGAT	108600
AAGCACTTAA	ATAATTTTAT	TTATTTATCA	AAAGGCTTAA	TTTTTGGATC	AATTCTACAA	108660
ATGATATTAA	TTGTATTAAA	ATTGAACTTT	AAAATCGGCT	TTACATCTTT	TACATCTCTG	108720
GGAACATCAT	TCATACTGGG	AATCTTTATA	AACAAAAAAT	TGGCTGAGAA	ATATAAATAA	108780
AAAATTTAAA	AATACCGAAG	ACCGGACTTG	AACCGGTACG	AGCTTCCTCC	TCAGGATTTT	108840
AAGTCCTGTG	TGTCTACCAA	TTCCACCACT	TCGGCATAGA	ATAATATAAT	AAATAATAAT	108900

ATATTGCAAT	GTCAAGTTAA	ATAAGAAAAT	AAATATAAAA	ACTCAATTGA	TAAC TATTTT	108960
TTGAGGAAAA	TTCTCAACAA	CATAATTGCT	ATGCAAATAA	TCTGCAATTA	CAACATAAAA	109020
TGAATATAAA	GAAACCCTAG	CAAAAAAATT	AGAAAAAACT	CTAAAATCAA	TTTTATTTGC	109080
TAACATTGAA	GTGTAGTTTG	AATCATTTAT	TAAGCTAAAA	AATCCATTTT	TGATTAATAA	109140
ATCAAAAATA	ACAAATTCAG	ATTCATCTAA	AATAAACATC	AATTTATCCA	TTTGGGCTTT	109200
TAAATATAAA	ATTTGTTTAC	TAATTTGCAA	ATTGGCAATA	CTTTTAATAA	AATCCTTGCT	109260
TAAATTATAA	ATAACAATAC	CATAGTGATT	ATTCTCAAAAT	TTAAAATCCA	CAAGCAATCC	109320
TAATTTTAAA	TCGCAAGAAT	CTTGCATTAC	ACTTAAAACT	TTAATATTTA	TTTTGCGCTT	109380
AGAAAGAATG	CTAACAGAAA	GGCCACTACC	TTGATCAATA	AAATAAGCAT	TCTTAAAAGC	109440
TCTAAATAAA	ACTCTATTAT	TAATTAAATC	AAGAACATTT	TTATCTTAA	GATTCTTAAT	109500
AATTATTAAA	TCAAACTTC	GATTTAGAAT	ATTATAAGCA	GAATCAAGTA	ACCCTTGAGA	109560
AAAATCATCA	TTTAAATTAA	AATTTGCAAC	CTTAAACTCC	AAAACACTAA	AATCTGTATC	109620
TACAACATTA	CAGGAAAAAA	ATAAAACACT	AAGCGGAAAT	AACTCTTCA	AGTTGATACT	109680
TTGTCTCAAC	AACTTCAAAT	ACAAGCCCAT	ACTTTTTTGC	AGCACTACTA	TCCAACCAAA	109740
AATCTCTATC	AGTATCCTTT	TCTATTTTAG	AAATTTTTTG	ACCCGTTTCT	TTTGAAATAA	109800
TATTATTAAG	TTCTTTTTTA	ACTTTATTTA	ACTCATTAGT	GTAAATCTCA	ATATCTGTAG	109860
CAACTCCCTT	AAATCCACTC	AAGGGCTGGT	GCAATAAATA	TCTGGCAAAG	GGCAGTGAAA	109920
ATCTATTTTC	TAATTTTGCA	GCCAAAAAAA	TTAAAGCAGC	AGCGCTAGCA	ACAAGCCCTA	109980
CTCCAAGTGT	AAAAACTTTA	GGCTTAACAA	AGCGAATCAT	ATTAAAAATA	GCAAATCCAG	110040
CATCAATGTC	GCCTCCTTCT	GAATCAATAT	ACACAAATAT	AGGCTTTTTA	AAATCTAGAG	110100
CCTCTAGCAA	TAATATTTTT	TCCTGAAAAA	GCCTGGAAAC	ATCCTTGGTA	ATCTCACCAG	110160
CAATAACTAT	TGATCTGCTC	TTTAAAACTA	ACTTCAATGA	TTTATCATGC	AAAACACAAG	110220
CATCATTATC	TTCTTTCCCG	GTCATAAAAC	ATCCCTTATA	CAAAAACATA	ATGATATATT	110280
ATAATTGAAA	ATAAAAGGTT	TTTAAATGAT	AAAAAAGCAC	AAAAATTAAA	CAATTGCACT	110340
TAATTTCTGA	AAAGCAAAAG	ACTAATAAAT	CTTTAATCAA	GCTTCATTAA	AGTTAAAAAA	110400
TACTCTAAAT	TTTACAAATT	AAGTAAAATT	AAAAAGGAGT	TTATAATGCA	CCATGAATTT	110460
GCGGTATATCG	GAGGGGGAAT	AGCGGGAAGC	ACCGTTGCTT	ACGAAC TGCT	TAAAAGAAAT	110520
AAAAAAGTAA	TTCTTTTTGA	TAATGAAGAT	ACAAAAGCAA	CAATGGTAGC	GGGCGGGCTT	110580
ATTAATCCTA	TTATGGGTAG	AAAAATGAAC	ATTGCCTGGA	AAGAACCACA	TATTTTTGAA	110640
TTTGCAAAAA	ACTACTATCA	AGAAATTGAA	AAAACCATTA	AATCCAAATT	TTTTATAGAA	110700

AAAAATATCT	TTAGACCCTT	TACTACTGAA	AATCAAAAAA	ATGAACTGAT	TGATAAACTT	110760
GAAAATAATA	AAAACATAAC	AAACTTTATT	TTAAAAATAC	AAGATGGAAA	AACTTACAAT	110820
TTCTCAAACG	ACTCTAACGG	CGGAATGATA	ATAAAAGGCG	CCAGGGTTAA	TACAAAAACA	110880
TATATAAAAA	ATATTAAAAA	ATACTTAATC	GAAAAAAATT	CTTACATAAG	CAAAAATATA	110940
AACGAAAATA	AAATTAAACT	TGGAGAAAGT	TTTTTCAAAA	TAGAAGATTT	TAAATTTGAA	111000
AAATTAATAT	TTGCAAAGG	GTATAAAGAA	AAACTCAAAG	GATTTTTTTC	TTATCTCCCA	111060
TTTGAGCCTG	CAAAGGCGA	AATCATTATA	TTAGAATGCA	AAAAATTAAA	CTTTAAAGAG	111120
ATTTACAATA	GACACATATC	TTTAATTAC	TTAAAAGGCA	ATAAATTTTA	CCTTGGAGGC	111180
ACTTACGAAT	GGAACACTTG	GAATACACTT	ACAAATGAAT	GGGCAAAATT	AGAGCTATTG	111240
AAAAAATTTA	AAAAAATAAC	AAATCTAAAA	TGCAAGGTCA	TTGCTCAAAA	AGCACATATA	111300
AGGCCTTCAA	CTCTTGATAG	AGAACCTTTC	TTGGGAGAAC	ATCCTAAGCA	TAAAAATATC	111360
TTTATATTAA	ATGGTTTTGG	AACAAGGGGC	GTATCTATGG	CTCCATACTT	ATCTAATTTA	111420
TTAGTTAATA	ATATTGAAAA	AATTGACAAA	ATTCCAAATC	ATTACAATAT	TAAAAGATAT	111480
GCAAAATATT	ACAATATTTT	GGATCATTCT	TAAAATCAAA	ATTTTTAAAT	CCATACATAC	111540
TGACAAACGA	CTACTATTAA	TATTTCTAAA	TTCATAAAAA	AATAATATAA	TGTTTAAGTT	111600
AAGCTAAAAT	AATTCTTATC	CAAAGAGAAA	CTAAGAGTGA	AACAAGATTT	AACAAAGCAA	111660
ATAAAATTAA	TTGACACTTA	CAAAACAAAC	CAGGAGAATA	ATCTTTGGGA	TTTAATATTA	111720
ATATCATAGG	AACTGGAGGA	ACAAGGCCAC	TCCACAATAG	ATATTTGTCA	TCCGTACTAA	111780
TCGAATACGA	TGGAGATAAC	TTTTTGTTTCG	ATTGTGGTGA	AGGAACCCAA	ATGTCTTTAA	111840
GGAAACAAAA	AATATCCTGG	CAAAAAATAA	AAATGATTTG	CATTACACAC	TTACATGCTG	111900
ACCACATCAC	GGGACTACTT	GGAATAGTAA	TGCTAATGTC	ACAAAGTGGA	GAAACAAGAA	111960
AAGAACCATT	AATAATCGCT	GGACCTGTTG	GAATAAAAAA	CTATACACAA	GCTAATATAA	112020
ATATGCTTAA	AATATATAAA	AACTATGAAA	TAATTTATAA	AGAAATAATC	ATAGATAAAA	112080
CCGAAAAAAT	AATATATGAA	GATAAAACAA	AAAAAATTGA	ATACACTAAA	CTAAAACATT	112140
CAATAGAATG	TGTTGGATAT	TTATTTATAG	AAAAAGATAA	ACCCGGCAAA	TTCAACACAG	112200
AAAAAGCAGA	AGAGCTAAAT	ATTCCTAAAG	GGCCTATTAG	AAAAGCCCTA	CAAGATGGAA	112260
AAGAAATATT	GGTAAACGGA	AAAATTATAA	AGCCATCAGA	AATACTTGGA	AAATCTAAAA	112320
AAGGACTAAA	AGTTGCATAC	ATTACAGATA	CTGGTTATTT	TAAAGAAGTC	ATACAGCAAA	112380
TCAAAAATTT	TAACCTTGTA	ATAATTGAGA	GCACATTTAA	AAATGAGCTA	AAAAAGAAG	112440

CCGATAAAAA	ACTTCACTTA	ACAGCTGGCG	GGGCTGCAAA	TATTGTCAAG	CAAGCAAAAG	112500
TTTTACAAAC	AGGACTTATC	CATTTTAGTG	AAAGATATAC	ATTAAGAAAA	GATCTTGAAA	112560
ACTTACTAAA	GGAGGCAAAA	TTGGAACATC	CAGACGGAGA	AATTTTTTTT	ACAAGAGATG	112620
GAATGAGGCT	TGAAGCAAAC	AAAAATAACT	TTATTATTAA	ATAGGAGGGT	ATATGATAAA	112680
TGTAGAAAAA	GTTACTAAAA	TGTATGGGCC	ATTACAGCA	CTATTTAATG	TTAGCTTTAA	112740
GGTTGAAGAA	GGCGAAGTAC	TTGGTATACT	TGGCCCAAAC	GGAGCCGGAA	AGTCCACATT	112800
AATCAAAATC	TTAACATCAT	TTCATTATCC	AAGCAAAGGT	AATGTAAAAA	TTTTTGAAAA	112860
AGACATTGTA	GAGCATTCGA	AAGAAATACT	ACAGCAAATA	GGATATGTTC	CTGAAAAACT	112920
AGCTCTTTAT	CCAGAGCTTT	CTGTTAAAGA	ATATTAAAG	TTTATATCAG	AAATAAAGG	112980
TGTTAAAAAA	TTAAAAAAG	AAATTGACAG	AGTAATAAGC	ATATTCAAAT	TAAAAGAGGT	113040
TGAAGATAAG	CTGATTTCTC	AACTTTCAAA	AGGATTTAGA	CAAAGAGTAG	GAATAGCTGG	113100
CGCTTTAATA	AACAATCCTA	AACTTGTAAT	ACTTGATGAG	CCAACAAACG	GTCTTGATCC	113160
AAATCAAATA	ATTGAATTTA	AAGAATTTTT	AAGAGAACTT	GCAAAAGAAA	GTACAATATT	113220
ATTCTCTTCG	CACATACTAA	GCGAAGTAGA	ATCTATTTGT	AAAAGAATAA	TTATTGTCAA	113280
CAACGGAGTA	ATTGTTGCTG	ATGACACAAA	AGAAAATATT	ATTAAAAATA	AACTTAAAGA	113340
GATTGAAATA	GAATTAATAG	TTTCAAAAAA	ATCTGAAAAT	GAGAAAAAAA	TTTTCAACAG	113400
CAAAAATGAT	ATTTTTTCAT	TAATAAAGCT	TGAAGAACAC	GAAAAAGACT	TAAATATTTT	113460
ATTAAAACTA	TCTCAAGGCA	AAACAGAAGA	AGATCTCTTT	AGCTACATAG	TAAAAAATAA	113520
TATAATCTTA	AAAGCAATGA	TTCCAAAACA	TGAAAGCCTT	GAAAAGATAT	TTAGCAAATT	113580
AACCAAGGAG	AGAGAAAAAT	GAAAATAGAT	TTAAAGCAAT	CTTTATCGCT	TTCTAAAAAA	113640
GAACTAAAAA	TATTATTTGG	AACCCCAACT	GCATACGTTG	TGATGCTATT	TTTTTTAATA	113700
TTCATAAACT	TTTCATTAT	TTTTTTATCA	GGATTTTTTT	TTAAAGACAA	TGCATCTCTT	113760
ACCTCTTATT	TCTCTTCAAT	GCCTATTATT	TTAATGTTGG	TACTGCCAGC	ACTTAGCATG	113820
GGAGTATTCT	CAGAAGAACA	CAAAACAGGA	AGCATTGAAC	TTCTTTATGC	TCTACCGCTA	113880
AGTCCTCAAG	AGATAGTCTT	GGGCAAATTT	ATTACGCTTA	AAATATTTAC	CTTAATACTA	113940
TTCTCACTTA	CCCTACCTCT	TACAATAATG	ACAATTTTCA	TGGGCGAATT	TGATCTTGGG	114000
ATAATATTGC	TTCAATATCT	AGGAATAATT	CTTTATTCTC	TTTCTGTGCT	AAGCATGGGA	114060
ACATTTATAT	CCTCCATTAC	AAAAAGCCAA	ATAGTCTCTT	ACATTCTTAC	CGTATTTACA	114120
CTGATATTAA	TACTATTTTC	TGGGAAATTG	GTTATGATCT	TTGGAAAAGA	AAATATAATA	114180
GGAGAAATAC	TTAATTTTGT	TTCAATAACC	AATCACTTTA	GCTATTTTAA	TATGGGTATA	114240

TTAAACTTAT	CAGACTTTAT	TTATTTTATT	ACATTCACAG	TCACATTTCT	AATACTAAGC	114300
ACACACAGCA	TAACACTAAA	AAAATGGAGA	TAAATTTATG	AAAAACAAAG	AAAATGAAGT	114360
TTTAAACCTA	ACTTTGAACC	TTACAATAAT	CTTTTTGATT	TTTTGTAATA	TATCTATTTy	114420
CATTTTTTAAA	ATAGACTTTA	CAAAACACAA	AGCTTTTACA	ATATCTAAAG	TTACAAAAAA	114480
TTTGTTCTCA	AGTGCAAATG	AAACAATATA	TATAACATAT	TACAATTCAG	GAAGCCTTGA	114540
AAACTATTTT	GCTTTTCCAA	ACCAAATAAA	AAATTTTTTA	ATAAGTTTTT	CTGATGCTTC	114600
AAAATGTAAG	GTAATTTATA	AAGAAATTGA	CGCTGATAAA	ATTTCAACAC	CATTAGAGCA	114660
CATTGGTATT	CCCTCTCAGC	AAATCGACTT	AAGAGATATT	AATCAGCTTT	CAATACTCAA	114720
AATATACTCA	GGAATTGAGA	TTATTTACGA	GGGAAAAAGA	GAAGTAATAC	CGGTGTGAAC	114780
AGAAATCAGC	AATCTAGAAT	ATGACCTTGC	AAATGGACTT	GACAAACTAA	TAAATAATAC	114840
CAAAAAAGTT	TTAGGACTTG	CTTTTGGAGA	CAGCACTTTA	AAAGAAGCAC	ATAAAAACTT	114900
TTCCGAAATA	ATGAAAAAAG	CATTTGGAAT	TGAAATAAAA	GAAATAGATT	TAAAAACTGA	114960
AAAATTAGAA	GACATTAGAA	AAGATATAAA	TGGATTATTC	ATTATTGGCG	CTAAAGAAAT	115020
TGACGAAGAA	ATTGCAAAAA	AAATTGACGA	TTTTATTGTT	AATGATGGAA	AAATATTTGT	115080
TGCAACAAGC	ACAATTGACT	ACAATCCTCA	AAATCCATAT	GGCATAACTC	CTATTAAATC	115140
CAGCCTATTT	GATCTATTTG	AAAGTTATGG	GATAAAATAC	AACGATAATA	TTATTCTTGA	115200
TAAAAGAGCG	CCCACAATCT	TTTTGGGTGG	CAATTTCCAA	ACTTACTATC	CATGGATCTT	115260
AATAGACAAA	AGCAATATTG	TAAAAAAAAGA	CATGCCATTG	CTTAAAAATT	TTTATACCGC	115320
TACAATTCCT	TGGAGCAGCT	CATTAGAACT	TATAAAAAAA	GATGAAACAG	AAGTAAATT	115380
TTTACCTCTA	TTTGCAAGTT	CCAAACAATC	ATGGCAAGTT	AAAGAACCTA	ACCTTTCAAA	115440
CATATCTTTG	AATGCATTTG	AAGTTCCAAA	TAAATTTGAA	GAGAATAAAA	CTAAAATACT	115500
AGGATATGCA	ATTGAAGGAA	AAATTAAAAG	TCCTTATAAA	GATCAATATT	CCAAAAATTC	115560
TAAAATAATC	CTAACAGGAT	CAAGCATGAT	ATTTAGCGAT	TATATGTACA	ACGGGTCTCC	115620
ATCAAACCTT	GAACATCAG	GAAGAATTTT	GGATTATTTA	ATGCAAAAGG	AAGAATTTTT	115680
TAATATTAAG	TCCAGAGAGG	TACGAGCTAA	ATTAAAATTT	GCAAGCTCTT	CAAACGAAAT	115740
GGTCAATGCA	AAGTTTTTCAT	TAATAATTGT	TAACCTTAATT	ATTCTTCCAA	CAATAATATT	115800
AATATTTGGA	CTTGTTAGAT	TTACTAGAAA	AAGAAAAGCA	AATTAATAAG	AACAAAGGAG	115860
TGTTTATGAC	AAAACCAAAA	ATATTCTCAA	TCAATAAAGA	AAAAATAAAA	ATATTGATAA	115920
TAGTAGTGTT	AACATCTACA	TTCTTATTGG	GAATAATTTT	TTCAAATGAA	AATAAAGTAG	115980

CAAGGATCCT	TGAAGAAAA	TTTTTTGATT	TTGACTTTAA	TTTAATTTCT	AAAATTGAAA	116040
CAGAGCTTGA	AGGAACGCTA	ACAAAACCTG	GCAAAGATTG	GATTTTAACA	TACAATAAAC	116100
AAAATATTCC	TGTTGATAAC	AAAAAAGTCA	ACTCTCTAAT	CAAAGCATT	GACGAGCTTC	116160
AAAAAAACAA	GCTTGTAAGT	AGAGATCAAA	AAAAACACAA	GGAAC TAGGA	ATTGGAGAAA	116220
ATCCAAGCTT	TAAATTATTT	GACAATAATA	ATAAGCTGTT	AACAGAAATT	TTTGTTGGAA	116280
AATCAGGAGA	AGGCGATTCA	AGACTGGCAT	ACATTAAAGG	TAGTGACGAA	AATGTTTACT	116340
TAACAAAAAA	CATTTTCTTA	TCATACAAAG	GAAATTCTTA	CAATACATTT	TCAGATACTA	116400
CATTGTTCCA	AGAAAAAAC	ACAAAATTAG	AAAATTTATC	ATTCAAAATA	ATAAGAAAAT	116460
TAAACAAGGA	AAATGAAAAT	AACATAAATA	ATAACTATGA	GATTATCAGT	AAAGATGGCC	116520
TTTATTTTTT	AAATAACCAA	AAAATGACAA	AAGAAAGGCC	TTTAAATATT	ATTGCTGAAT	116580
TTAAAGCTGA	CGGACTTGAA	ATTGATAAAT	CTAAATAGA	TGATTATAAT	CTTCAATACA	116640
AAATTGAAGT	CAAATGGAGC	AATAAAAGTG	TCAATAATAT	TGAAGTTTAT	TTTAATAAAA	116700
ACGAAGAAAA	TGACAAAGAC	ATATTAATCA	AAAAAGATAA	AGATGAATAT	TACTACACGA	116760
CTAGCAAATG	GACTTTTTTT	GATGTATTCG	ACTTAGAAAA	AAAATTAACA	GAAAAAGATG	116820
ATATTTCTAG	CAACGATAAT	CAAGAAGATC	ATCATGAACA	TCACAACAAT	GCAGATTAAT	116880
CTTGCTATAT	ATAAAAAGCA	TTAAAAGAAA	AACATATAAA	AATAAATATA	ATTAAAATAT	116940
ACCATGACAA	AGACAACATT	TTATCAAAAG	ATAAGATGTT	GTTTGGCTTT	ACTGATATAT	117000
CTTTTAAATT	AAAATTAATA	TCAAACAAAC	CGCTCAGTTA	TCAAATATTA	ATTTTAAGAA	117060
TTTTTTATAA	AAATAGAACT	TAAACGAATG	GATTTTCAAC	CTTTAGTAAG	TAAAAATTTA	117120
ACTTTTTTTA	AAACTTCATA	CTCTTGTTTA	ATTTTAAAAA	TATTTCTATT	AGGATTTAAC	117180
TCAAGTTCAC	TTTCTACCTT	ATCAATAAAA	TTTATTAATA	TGGCTTTTTT	ATCGCTATTT	117240
AGCACAAACAT	TACTTAAAGA	TTCTTCAGCA	TTAAATTTGC	TTACAACCTT	TTCAACATCA	117300
TTAAAAATTAA	AATTAGAAGG	AAAAGGGTCC	TTAGTTATGC	TTTGAGAGCT	GGGCTTTTCA	117360
TAATTAGCAA	CATCATTACT	TTGGTCTTGA	TCTGATTTAT	CTCTCAAATT	ATCATGCAAA	117420
TTTTTCTCTC	CAGCATTAGA	AAAAGAGCCT	TCGGCAACCG	TAGAATCCAG	ATCCTCTTTT	117480
AAAATATTTT	CAAAATCATC	AAATTCCTTT	GACTCAAAAC	GTTACACAAA	GCTTTTAAGA	117540
ATCGCACAAAT	TATCACCATT	CTCATGCTCA	ATGTTTTTCAT	TCTCATTAAT	TAAATCCAAA	117600
CGTTGTTTAT	TATTATCTAC	AAAGCTCTCC	AATTTTCGAG	AGTTATCGCA	ATTAGCAATA	117660
GAATAGGGAT	CTTCTGCTCC	CACTTCATGT	TCCAAAGAAG	AACTATTATC	CAAATTTTTA	117720
TTAACAGAAT	CTAACAGTTT	ATCTGGCTCT	GTAGTAAAAC	TTTCCAATTT	TTTACTGTGA	117780

TCGTTATTAT	TATTTAACTC	CATATTTCT	ATGGACACAT	TATCACTGTC	AACATTAATA	117840
TCCTCTTTTT	TAAGAATATT	ATTAGAAAA	TTATCAGCCA	CATGTAAATT	GTTAGTCAAA	117900
TTCAAATCTT	TATCTCTATT	AAATTTAACA	TCGTGCTGAA	CTTCTTCATT	TTCTTTTGGG	117960
GTATAATTGA	TACCTTCAAG	CAGCGCATCT	AATTCTTCTT	GACCAATAGA	AATATTAGGC	118020
AAATTATCTT	CTTTTTTTGA	AAATGAATCA	TCCGTCTCGG	ATGATTTTTT	TTCAAAATCC	118080
TTCGAATCAT	AAGAAATAAA	ATCCCTTTGA	ACAAACTTAA	GACTATTATC	AAGCATTTCT	118140
TTTTCAACTC	TCTCAACACG	AAGCTCAACA	CCCTTTAAAC	AATTAATCAG	CTCGCCGTGC	118200
CTTCTTTTTA	AGATGTTATC	GAGTTTTAAC	AGCTTTTCAT	CCAAAAAAGT	TTTAAGATTA	118260
TCTGGGGCTA	TAGAAACAAT	ATCAACAGAC	TCACTTCTTA	AAAATACCTT	TTCAATATCA	118320
AAATTAACCT	CCTTGGGACC	TTCTTTGATA	AAAAAACAC	TTTCCTTCAT	GCCAAACTTG	118380
CTCTCCAAAA	CTACTCAATA	AACTACAAT	CTAAAGCAAT	TTTAACTACT	TGTAAATATA	118440
GTATATTAAG	AATATAATTA	CAAGCTATAT	GACTATTTAT	AAAAAAATTG	CAATGTCTTT	118500
TTACTCAGGA	ATACTAAGCT	ACTTTATAAT	AGCTCCCATA	TTTGGAGAGA	GAGGATTTGT	118560
TAATTATCAA	AAATTGGATA	ACAACCTAAC	ATTAATAAAA	AATCACATCG	AAAAACTAAA	118620
AGAAATTCAA	AAAGAATTAA	AAGCAAGATA	TATTAACCTA	CAAGTATCTA	AATCGGAAAT	118680
TCTAAAAGAA	GCTAAAAAAT	TGGGCTACTA	CCCCAAAAAC	TCAACAGTAA	TAAAAACCAA	118740
CAATAATAAA	GATCAATATA	ACCAAGGGCA	AATATTAACC	TTACAAAAAC	CCCTTTCCAA	118800
GAATCAAAAT	TTTTACCTTA	TATCAATAGC	AATAGGTTTA	ATTTATTATT	TTTTATCAAG	118860
CTGCATTATC	CAAACCAAGA	AAATTACAAA	AATCAATAAA	CTTGCTTCCA	ACAACTCTAA	118920
GGATTAGTCT	TTATTGAAAA	TATTTATTTT	TAAAAATACA	ATATATTTAT	TAATTAATTT	118980
AATTTGTGCA	TCATTTTTTT	GCGTATCGTT	AGTAAATCTT	TTTTCAAATG	AACAACAGTA	119040
TACTCCTTTT	GTTAAAACAA	ATGTCATAAA	AAATTACTTA	CAATACATTG	GAGTATATAA	119100
AAGTATAGAA	AGATATGCCC	TGATACATGA	CTTTAACCCCT	AAATCAAAAT	TAGAAAAAGA	119160
TTGCTTTTTG	AAGCATATAG	CTGGCAATTC	ATATATAATA	TACAAAACAA	AAAATGAAGG	119220
AATGCTGTGG	GGCGATCATC	GATACTCTCT	GCTGAGCAAA	GGAAAGCCAA	CTACTAAAAT	119280
AATTTTTTCAA	AAAATATTTA	ATACTTTAAA	AATCTCAATT	CCAGGCGCCC	TACTCTCTTA	119340
TATTGCGGCA	ATAATCCTTA	TTATAATTTG	GAAAATTTAC	ATAAAAAATA	ATCTAATAAA	119400
TAATATTCTA	GAATATTTAA	TGCTATTGCT	CCACTCCATG	CCAAGAACT	TAACAGTATT	119460
TTTAATACTG	TCTTTAATAT	ATTACCTTAA	TTTAAATCCA	AAAAATTTAA	TAATGGGTGG	119520

ATTTGCATGG	TTTTTTTCAT	TCTTCATATT	TAATTCTGTA	ATTTTAAAC	AATCTCTTGA	119580
CAAACTTTA	TCAGAATTTT	ACATAAAAGC	TGCAAAATCA	AGAGGAATAA	ATAAATTGCA	119640
AATAATCTTA	AAACATGCAT	TAATTCCATC	AATAACACCA	TTACTCACAA	ACATGAGACC	119700
TATTATTACA	ACAGCTTTTT	TTGGAGCATC	AATGATTGAA	TCAATGTTTG	AAATTGATGG	119760
AATTGGGGCC	TTATATTTAA	ATGCTTTGAA	ATTTAACGAT	TATGCTATTT	CTAAAGATTT	119820
GATTTTTATT	GGCGTTTTCA	TTATGCTTAT	TCCAAATATA	ATAACAGATA	TACTAATTTA	119880
CAAAATTAAC	CCATATAAGG	ACACTCTAAA	CTAATGAAAA	CAGATACAAT	AATAAAAAAA	119940
ATTTATATCG	TACTCTTTAA	TATATTTATT	GTGTTGCTAA	TTATTACTCC	GTCATTGGTT	120000
AATGAAAATT	CAAAAATTGC	AATCTATAAA	AAAGATCCAA	ATAAAGTCTA	TTTAAAATCT	120060
ATTAAAAATG	TACCTATGCC	ACCCACAAAA	GACAACCCAT	TAGGAATCGA	CAAAATGGGA	120120
AGAGATATTA	TGGCAAGATT	AATAATTGCA	ACCAGAAACT	CTATTTTACT	TTCACTAAGC	120180
TACGCAACAA	TTTCTGCAAT	AATTGGAATC	TTTATTGGAA	CAATCATTGG	CATGTTTAGT	120240
TTTGAAATTT	GCATGCTGAT	TTCAAAACCA	ATTGAAACAT	TGCAAACATT	ACCTTTTTTT	120300
TACGTTGTGT	CTTTAGTTTT	TTATTACTTT	TTAAACAAA	AACTTACAA	TATGCTTCAA	120360
ACAGCAACAC	TATTAGCATT	GATTCATGGA	TGGATTAGAT	TTGCTTTTAT	TGCAAGAAAC	120420
AATACATTAA	TAATAAAAAA	TTAGATTAT	ATTAAAGCCA	GCGAAGCTAT	GGGAGCAAGC	120480
AAAATTAGAA	TAATATTGTA	TCATATTTTT	CCAGAAGTAT	TCTCATCAAT	ATCATCTATA	120540
ATCCCATTAC	AAATGGGAAG	AAGTCTTACT	ACTTTTGAAG	TAGTAAGTTT	TTTACAAAAA	120600
CAAGATAAAA	ATCTATATCC	CAGTCTTGGA	GAAGTCTCA	ACTATATGCA	AATGGGCAAT	120660
AAATATCTAT	GGATATGGAT	CAATCCCTTA	CTCATATTAA	TAGGCATAAA	CATAATACTA	120720
GCAATTATAA	ATTTTAAGCT	AAGAAAAAAA	ATGAAACATT	TAATATCATC	TTAAATAAAA	120780
AATTAACAAA	CTCTTGAGC	AAATTTTTCT	AAAAACAAT	TATCACAATT	TACATTTCTA	120840
GAAGTACAAA	TTTCTCTTGC	ATGCTTATTA	ATAGCCATAG	AAAATCTATA	CTGCTTACAA	120900
GGCTTTATTC	TTCTTTTTAG	ATCCAATTCA	ATCTTAATAG	GAGAACTTTC	CAAAGAAAGA	120960
GCATGTCTTG	TAATAACTCT	ACTAAAATGA	GTATCTACAA	TAATTGCGGG	TTTATTGTAA	121020
ACAGATCCAA	GAATAACATT	TGCCGTTTTT	CGACCTACTC	CAGGTAGCTT	AATAAGATCA	121080
AAAATATTAT	TTGGAATAAC	ACCATTAAAT	TTTTCTAAAA	TATCAATAGA	GCAATTCACA	121140
ATATTTTTAG	CCTTTCTTGA	ATAAAAACCA	GTCTTATAAA	TTAATTTTTTC	AACATCTCTC	121200
ACATTTGCTC	TTGATAAACT	TTCAAAATTC	TCGTACCTTT	CAAAAAGGTA	TGGAGAAATT	121260
TTATTCACCA	AATTATCTGT	TGTTCTTGCA	CTTAAAATAA	CCATTATTAA	AAGTTCATAA	121320

TTGTTTTTAT	AATTTAAAAA	AGGTTTAAACA	TCAGGATATC	TAAATAAAGT	TTCATCAACA	121380
ATCAAATCAA	GATTAATCAT	AAAAAAATTA	TAAAACATTA	TAAACACAAA	ACAAAAATAA	121440
AAAATATACA	AAGTAAAGGT	ATCTAGACTT	TATTGACAAG	GATTTTTTCAA	AATGATATAC	121500
TCATCATTAG	AATTTTAAAT	GCACCAATAG	CTCAATTGGA	TAGAGCAACA	GACTTCTAAT	121560
CTGTAGGTTT	TAGGTTTCGAG	TCCTAATTGG	TGCGCTTCAT	TCGGGATGTG	GCCTAGTGGC	121620
TAAGGCACCT	GCTTTGGGAG	CAGGGGATCG	TGAGTTCGAA	TCCCACCATC	CCGAAAAAAT	121680
ATTAAAAAAG	CTAAAAACTT	TTGTTTTTAG	CTTTTTTGGT	TTTTTAACGA	TTTATACAAA	121740
TTAAATCTAA	CTGTAAAGTT	ACTTAACTTT	CTTTAAAGTA	TTTACATCTA	AAATAACTAG	121800
ACTTTTAAAC	TCATCTTGCA	AATAAATAAA	ATTTTTTCTC	ACAGAAAAGC	TAGTAAAAGG	121860
CATAATTTTA	TTCTCTGAAA	GAATAAACTC	ATCTAAATTT	TTAGGAGAAA	ATTTGGCCAA	121920
TCTCCAATCA	TTACTACTAT	CTTTATCCCT	AACAGCTACT	AAAATCATTT	TAGAATCAAC	121980
ATAAAGAGAT	GAATTTTTAT	TAATCTCAAA	ATTAGACTCT	GATACCACTT	TTAAATTTTC	122040
AAGTTTATCA	AGTATCTGAA	GCTTAGCTTT	TCCTGAATCC	ATTTTAATAA	CAACCAAATC	122100
TTTTTTCACGT	TCATAAATTC	CATACCGCTG	AATGCCTTGC	TGAGTGCTTT	CTTTAAGCCT	122160
AACACCAGTA	TTTAAATCAA	TAAGTTGAAG	AGTTCCTAAA	TTTGTAATTG	GATCAATAAC	122220
CTCTAAAAAT	ACAGGACTAC	TGGAATCTAT	AGACATAGTA	GTCAAATCTT	CATTCAAAGA	122280
AGTAACTTGG	TCTTTAACCT	GAGGCTTAGT	CTTTTGCAAA	TTAACATCTT	TATTAACGTG	122340
CTCCTCTTTT	GAATCAATGT	CTTTATAAGA	AGATTTATCT	AACGGTGATA	ATTCTCCAAC	122400
ATTGTTATTA	GACTTGAAAA	TCTTATCTAA	TTTCTCAACC	TCAGAAACAG	GTTTAAATTC	122460
TTTTTTTGCTA	TCTAATTTTT	TAACCTCAGG	TAATTTTTGA	TCTTCTGGCA	TCATAAGATT	122520
TTCATCATTA	TTCAAATCGC	CTAAGCTTTT	CTGTGACTTA	CCCTTGGTTA	TTTCTTCTTC	122580
CTTGGCCTTA	CTTTTTTCTT	TGCTAGAAGC	TTTAGAATTT	AATTCTCGAT	CAAGATCCAA	122640
GGCTTTACCA	TCTTTACTTG	CTTTATCATC	TTTACTTTTT	AAAAGCTTTT	CATCACTTTT	122700
TTTGATTTC	ATTTGCTTTT	CAATTTCTCT	TTTCTGATTT	TCATCACCAG	TTTCTTTAAG	122760
CTGCTCCTGC	AAATCTTCCA	GGCTCTCTTT	TATTTGTAGT	TGCTTATCAA	CTTTAGGAGA	122820
ACTTACATCA	CCAGGCTTTG	GTAAATTCTT	TTCTTGTTA	ATTCGTTAA	TATCCTCTTG	122880
AATTTTCTCT	CTAACAGTAT	TTCTTTGAAC	ATCTAAATTA	TCTTCAGCAG	AATCTAATTT	122940
TTGCTGAGCT	TTATCAAGAT	TTATTGCCCT	TTTATCTAGC	TCTTCCTTTT	GTTTCTTTTT	123000
AGCATCAACC	TGACTTTCAA	TCTCTTTTTT	ATGCTCTTCA	TCTGTAGCTT	TTTCAAGCTG	123060

ATCCCTTAAA	TTTTCAATAG	TTTCTGTTAT	ATTGGAATCA	CTTTCATGAA	TATTGTCTAA	123120
TTCAATATCA	ATTTTATCTT	GATCTGCCTT	ATGAGTTTCG	CCTTGAATAT	CTGTAATATC	123180
TCTTGCAAAG	TTAACACCTG	CTTCATTTTC	ACTTAAAAGA	GCTGCCACCA	CCTTATCTGT	123240
AACTAAACTG	TCAATATCAA	TGTCAGACTC	AATATTTCCA	GACAAAATAT	CCTTTTTAAG	123300
AGGAATAAAT	ATTTGTGTCT	TTCCAGCCCA	CTGACTATAA	ACCCTAGAAA	GACCTGCATT	123360
TTCTTTACTT	AAAGACTTTA	AAGCAGCCTC	AATATAAAAC	CCTTTATAAT	AATCCAAATC	123420
TCCTCTATAA	ACAGCATTAT	ATATTGTAAT	AACCTTAGCA	ATTAATTCTG	CACTAGACCT	123480
GTCATAATCG	AAAGACTTTA	TTAAATACCC	TGTAAGAATT	CTTCTTAAAT	TCAATATACT	123540
GTCAAGCTCT	GACTTACTAC	CAATAGAAAA	AACATCAACG	CTTGCTTTTT	TATCTTGATC	123600
ATCAATAAAT	CTATTAATAA	AATATTTACC	ATAATAACTT	GAGTTGCTAT	TGGAATTGGT	123660
CAACGGTCTT	GCTAAAAACT	CCCCAATACC	CACATTTTGT	TCATATGTAT	TTGTAGAATC	123720
ATAAGGGCCT	TTATAATTTA	CAAACCTCAAG	ATCCATATTA	ACAAAGTCCT	TTAATTTTTT	123780
CCTATCAACT	TCTCTTGCAC	TAACAGGAAA	TCCATTCAAG	AAAATAAGAA	AAAAACTAAA	123840
GATTAGTAAC	ATTTTTTTCA	TAAAAGAAAT	TCTCCTATAA	ATTTAATTAT	AATCTACCTT	123900
ACCAACTAAA	TTCACCAATT	TAAACCTAAT	TTTAACACAA	TCGGATTTAT	ATGCAAAACA	123960
GCTAATTCAA	TCTTGGGGAC	TTGAAATATC	TTGAATGCTT	GAAATAATTT	CATTAATGTG	124020
CTTGTTAATA	TTTTTCAGAA	AATTTTGACG	CCTCATAAAC	ATTAATAACT	TTATATACTT	124080
ATGCTTACAA	AGTTTAAGAA	GTTCGGCTGT	TGAATTTAAA	ATTATATTTT	TCAAATTTAA	124140
AATCACAGAA	TAAGCTATTT	CCAAATTACC	CTGATAATTT	AACACTATAT	TTTGATGTGA	124200
ATTGTATATA	ATACAATCTT	GCCCATAATA	ACTTTCAAAT	TTAGTAATAG	TTTTGACTAT	124260
GGTAATTATA	TTATTAATAT	CTCTCTCTCT	AATTGCCAAA	TTAATAAAAC	TCTTAATTGC	124320
AGCTTTATCA	TTAACATATA	CAAAATATCT	ATAAAGCTTG	CCTCTTGAAG	CAATTCTATC	124380
AAACCTCTTT	TCTGACAAAA	GCCACACATT	AAAAGCTTTT	TCATATAAAT	TTAAATATTT	124440
TGCGGGAAAA	TTTCCATGTT	CAGCTGCAAG	AAAATCTAAA	ATCTCTAAAA	ATTTATTATA	124500
AGCAGCATCA	CTATAATTAG	AATTAAGGAT	CTCTTCAAGA	AGTAAATAAT	TTTTATCATA	124560
ATCTACAAAA	CGCTTTTCTT	TTAAATCTAT	TCTGCCTTGA	TTATATTTAT	TACCTCCAAA	124620
ATGGTTCCAA	ACGCTAACAT	CAAGCTCTCT	GTCGTATTCG	TAATAATAAG	TACTAAGAAC	124680
CCAATCATCT	CCCCCTAAGA	CAATAATACC	TGAATTAGCA	CTAAGTCCTG	ACAAGCCCTT	124740
AAGTTTAGCA	TCTGAAAAAG	ATATATCAAA	ATCCTCTTCA	AAAGACAAAA	TTCCATTTGA	124800
TTTGTTTGAA	ATTAAAAGAT	TTCTATTATT	ATAAAGAACA	GCTTTCCTCA	TCTCAAAGTT	124860

CATTTTTTTT TTAAATTTAA GCTTAAAGTT TCTATTCAAA TCAAAAAACA TACCAACATT	124920
TGAAATTGCG ACATATTCAC CATTAACTT TTCAAACAAA AAATTAATAG GAAAATCCAA	124980
CTTAATAGAG CTAATAACTT CCCCAAAATC TCTTCCATAA GCAACAATAT GCCCTGACTT	125040
ATGTCCAACA ACTACCTCTT TTTTGTATT TATCATTAAC AAAAAAGGGA AAGCAACTAA	125100
TCTGAAAAAC CATTTCTTAT TACCCAAAGA ATCAAACAAA AATATTTTCAT CATTTTCACT	125160
TGCAATACAA AAATCCCCAT TATCAAAAAC TACAGGAGAA GTAGCAGGCC TACCACCTAT	125220
GTCAACCTCA AACATTTTTT TACCGCTATT TAAATCAATA GAAACAACCT TTTCATTAGC	125280
AAGAGGAATT AGGATGTTAA CATTTCTTAT TGCAGGAGAG CTCAAAGGTG AAAAATCAAG	125340
CTTATACTTC CAAACGAGTT TTCCTCTTCT GATCTTTTGA ACTTCATTTC TAACTGTAAT	125400
AACATAATAC CCATTATCAA AATCTTTCAA AAGAAAAGGA TATGGCATTTC TATTTAATCT	125460
ATAAGAATAT TTCTTCTCAA ATGACATTGT ATAAGTAGTC AACCATCTAT CTTTTGTTAA	125520
AACTGTAATA GTGTCACGTT TTTTCATCAAT AATTGGATTG CCTGCAACTT TGCCAGTTAA	125580
TGCTTTTTGA AAATATAAAT TAATATCAGA ATAAAGCCTT AAAAAAGAAG CTGAAAACAC	125640
AAATATGAAA AGTAGACCTC TCAAAAATAAA AAACCTTTTG AGTTTCTAAA AACTGCTAC	125700
TAAAGCCTAA AACCAGCATT ATTGCCATAA AGATTATTTTC TCAGATCCCT AATCTTAGCA	125760
TCATCAACAT ACTCAGAAAA AGTCATATAT CGATCAATTA TTCCGTTAGG AGTAACTCT	125820
ATAATCCTAT TAGCAACAGT ATCTATAAAT TGATGATCAT GTGATGTAAA AAGAACAAC	125880
CCTTTAAACT CTTTAAGCCC GGAATTTAAA GATGTAATTG CCTCAAGATC TAAGTGATTT	125940
GTGGGTGGT CCAGTATTAA AACATTAGCT CCGCTAAGCA TAGCCTTAGC AAGCATGCAT	126000
CTTACTTTTT CTCCCCCTGA GAGAACATTT ACCTTTTTTA AAGCTTCATC TTGGCTGAAA	126060
AGCATTCGAC CTAAAAATCC TCTAATATAA GTTTCATCTT GTTCTTTTGA ATACTGACGT	126120
AACCAATCGA CTAAATTTAA ATCTAAATCA AAATATTTTC CATTATCTTT ATTAAAATAC	126180
GAAAAATTAA CGGTAGATCC CCATTCATAA TGACCTTTAT AATTTCTATC TTCATTTGTA	126240
ATAATATCAA ACAAAAAAGT TGCAAACATG GGATTTCCCA AAAAAACAAT CTTTGTCTGA	126300
GGTTCAACAA TAATACTAAA TTTATTTAAA ATTAAATTCC CTTCAAATTC TTTTATTAAA	126360
TTTTTAATTG TAAGAACATT CTTGCCAAGT TCTCTTTCGC TTTTGAAATT AACATAAGGG	126420
AACTTCCTTG AAGAAGGCTT TAAATCTTCA ACCTTTATTT TTTCAATCAA CTTTTCCTT	126480
GATGTTGCTT GCTTAGACTT AGATGCATTA CTAGAAAATC TTTGAATAAA TGTCTTAAGT	126540
TCAGCAATTT TATCTTCAGA TCGCTTTTTA GCATCTTTTA GTTGCTTGTT TAAAATCTGA	126600

CTTGTTTCAT	ACCAAAAAATC	ATAATTTCCA	AGATACACTT	GAATCTTGCC	ATAATCAATG	126660
TCAACAATAT	GAGTACAAAC	TTGATTTAAA	AAATGTCTAT	CGTGAGATAC	AACAATAACT	126720
GTATTTTCAA	AATTAATTAA	AAACTCTTCT	AACCATTTAA	TAGATTGTAG	ATCAAGGTTA	126780
TTAGTAGGCT	CATCAAGAAG	TAATACATCG	GGATCACCAA	AAAGTGCTTG	AGCCAAAAGA	126840
ACCCTAACTT	TTAAAGCCCC	TTCAACATCA	CCCATTAAAT	TATTATGAAT	TGCCTCATCT	126900
ATTCCAAGAC	CTTTAAGAAG	AACCGCTGCA	TCAGATTCAG	CCTCGTATCC	TCCAAGCTCT	126960
GAAAAATTCTG	CTTCAAGCTC	TCCAGCTCTA	ATTCCATCCT	CATCAGTAAA	ATCAAGCTTA	127020
CTATAAATTT	CATCTTTTTT	TTTTTGAACA	GAATAAAGTC	TTTTGTGACC	CATAATAACA	127080
GTATCGATAA	CCTTATATCC	ATCATAAGCA	AATTGATCTT	GTTCAAGAGC	TGCTACTCTT	127140
TGATTTTTTG	GGATAGATAT	TTCACCCTTA	CTAGCTTCAA	TCATTCCCCC	TAATACTTTT	127200
AAAAAAGTGC	TTTTTCCTGC	CCCATTAGCA	CCAATTATTC	CATAGCAATT	TCCAGGAGAA	127260
AATTTAATAT	TTACATCTTT	GAATAAAACT	CTCTCTCCAA	ATGCAACTTC	CAAATTACTT	127320
ACAGTTATCA	AACCATTACC	CTGCCTAAAT	TGATATTCTA	ATAACAAAAT	TATCTTGAAA	127380
ATTAATTTAA	TTTTCAAGCA	CCATATAAAT	ATATTGACTC	AACTCTCAGT	TTTTTCGTAT	127440
ATTTAATATT	ATTATATAAG	GAGATGTTTG	AGATGAAAAA	TATTAAGCCG	TTAGCTGATA	127500
GAGTTTTAAT	AAAAATCAAA	GAAGCTGAGA	GTAAAACAAT	CTCAGGACTT	TACATACCAG	127560
AAAATGCAAA	AGAAAAAACA	AATATTGGGA	CAGTTATAGC	TGTTGGTTCT	AACAAAGAAG	127620
AGATCACTGT	AAAAGTTGGT	GATACTGTGC	TTTATGAAAA	ATACGCAGGA	GCTGCTGTAA	127680
AAATCGAGAA	TAAAGAACAT	TTAATACTAA	AAGCAAAAGA	AATAGTTGCA	ATAATAGAAG	127740
AGTAAAAAGC	TAAGTTTAGC	TACTTAGCTT	TAATTTTTAT	TAAATATTTA	ATAAAAAATTA	127800
CAAATTTATA	CATAAAAACT	TATTATTCTG	ATCAATCAAA	TTAAAAATTT	CAAGCTTACA	127860
AAATTCTGTA	AGCTTGAAAA	AATAAAATTA	AATGAAAAAG	CCAATTTTTA	AAGAAAATAC	127920
CATATATTCA	AGCAAATTCG	ATGACATCTA	TTACAATCCA	AAGCAGGGAA	TTGAAGAGAG	127980
TTTTTATACA	TTTATTAAAG	GTTGCAATTT	AGATTTAGAA	TTAAAAACAA	AAAAAAATAT	128040
TTTAATAGCA	GAGTTGGGAT	TTGGAACAGG	ATTAACTTTT	ATATGTCTTT	TAAAATTCAT	128100
AAAAGAAAAC	AACATAACCT	CAAAAATTAA	TTATTATTCT	ATAGAAAAAT	TTCCACTCGA	128160
AAAAAAAACA	ATAATGCAAA	TTTCAAAGTT	CTTTGCTAAA	GAAACCGCTT	ATTTTAAATT	128220
AATGTTGAAA	AATTATTCTA	AAATTCCAAA	AAAAAATTTA	AAACTAAAAA	TAACAGAAAA	128280
TGTTAATTTA	AAAATTTTAA	TTGGAGACGC	CAAAATAAAA	ATCAAAGAAA	TTCTTGAAAA	128340
TGTAGAATAC	TGGTTTTTAG	ACGGATTTAA	TCCCAAAAAA	AATCCTGAAA	TGTGGAGCAA	128400

TGAAATATTT AATTTAATTT CTGAGAAAAG CAGTCCGAAA TGCAAGCTTT CAACATTTTC	128460
CTCTGCAAGA ATTGTAAAAG ATGGCCTAAA ACTTGCTAAT TTAAATACA TTCACATAGA	128520
AAAAGGATTT GGAAATAAAA GACATATGAT AAAAGCTCAA AAAAATTAAA AATTTATTTT	128580
TAACATAAGT CGTTAAAAAA ATCCCAACAA GTATGATATA CTTCCAAATG GCACAAGGAG	128640
AATTTTAATG ACAAAAAAAT TGTGTGTGAG GGTATTAATC TTTTAAATAT CCAATAATTA	128700
TGCTTTTGCA AAAGACACAA TCAAAGATTT GTTCTTTATA CAAGATATAC TAATAAAAAA	128760
AGAGAAATAT TCCGAGGTTC TAAATAATGC AAGCCTTGAA GGCATTATTG AAATTGAACA	128820
TAACGGACCA TACATTAAAG ATCAGGATTC AGAAGTTAAA CTTATCCTAA AAGAAAACGG	128880
ATATAGAAGA AATTTCAACT TTTTAAATCT TTTAAATACT AGTAATATAA TCAAAAGTCT	128940
AAGCTTATTT GACAGCAGAC CAAAAACAT TAAAGAAAAT GAAATCATAT TATTAGAGAC	129000
AAAAATGATT AAAGAAAATC CCTATAACG ATACAAAGAC GATGATGATT TTGAATTAAA	129060
ACTAAGTGTA ACTCGAAAAA ATAATCAAAT TTATTTAATT CTGATTTC AATTCCTATT	129120
TGATCAAAGA AAAACGTTTC CATCAATTTA CATCAAAGAA GAAGATGTAT CAACAATAAT	129180
AAACAGCTTC ATGAAACTAC AAGATTCAAG CTTTTTATCT CCTCAAGCTT CTTAACAATT	129240
AATAGCACAA AATGTGCTAT TTCTAATAAA AAGCAAGCAT TTTACTGAAA AGCTAACCAT	129300
AGCCAATTC ATTACATAAT AATTTTCAA TCTTTTACA GATTTTAA ATTAATAATA	129360
TAATTATTTA TTTTATTAAT TAAAGAAGAA AATCTACAA ATTTAATTT TTCAGATTCA	129420
ACAATTCCT TGGGAGCATT CATTAAAAA TTTTCATTTT CAAGTTTCTT TGAAACAGAA	129480
ATATTGAGCA TTTTATACTT TTCAAGCTGC TTTTCAAGCC TTATCAACTC TTTGGTTTTA	129540
TCTATCAATG ACTTAACATC TGCATAAAT TCAAAACCAA CTGCAGCTAC ACCAAGCATG	129600
CCATCATAAT TTTCATTGTA AAATATATTT TAAAATTAA TCATTCTTTT TACAATGCTT	129660
TCATTAGCCT TAAAGTATGC CTCATATTTA AAATCAGCAT CAACTTCAA AGCAACATCA	129720
ATTTCAACAC TAGCAGGTAT ATTAAATTCA CTCCTAAGTG TTCTAATAGC TATAATAAAA	129780
GTTTTCAATA CTTTAAAAAT TTCAAATTCT TCTTGAAAAT TATTGGCAAT ATCAAATTTT	129840
GGATATTCAT TTAAAGCTAA AATATCTTCC TTTTCTGCAA ATTCAGAATA AATTTTTTCT	129900
GTAACAAAAG GAATAAACGG ATGCAAAATT AACAATGATT TTTTAAGAAA AAATAGCAAC	129960
TTAGAAATAG CCATATTTTG AATATCAACA TTTTCATTAT TTAAATCAAT TTTGCTAATT	130020
TCAATATACC AATCACAAAA ATCATTCCAA AAAAATCAT AAACAAATTT TGAAGCTTCG	130080
TTATATTTAT AATTTGCAAA AGAAGACTCT ACACCAAGAA TAGTCGAATT TAAGCTTGTA	130140

AGCAGCCATT	TGTCAATGTC	GTTAAATTTT	AAATCATTTA	ATATTTTCT	ATTTTTTAAA	130200
TTTAAAAGAA	TAAATTTGGA	AGCATTAATA	ACTTTGTTTG	CAAATTTAGC	CCCAAACATA	130260
AAATCTTTAG	CGTCAATATT	TAAATCTTGA	CCCTGAACAG	ACAAAAAGGA	TAAAGTAAAC	130320
CGCAAAGAAT	CACTTCCATA	CTCATTAATA	ATATCAAGAG	GGTCTATTCC	ATTGCCTAAA	130380
GACTTTGACA	TTTTTTTACC	TTGTTTGTC	CGCAAAGAG	GTGTTATATA	AACATCTTTG	130440
AAAGGAACTT	GCCCTGTAAA	TTCTAATCCT	GCCATCACCA	TTCTTGCAAC	CCAAAAAAT	130500
ATTATATCGT	AAGCTGTTAT	CAAGGTATTT	GTTGGATAAT	AATTTTTTAA	ATCAACATCA	130560
ACATTGGGCC	ATCCAAGCGA	AGAAAAGGGC	CATAGCCAAG	AAGAAAACCA	AGTATCAAGA	130620
ACATCTGGAT	CTTGAACAAA	CCTCTTCCCC	ATATTCTTTT	CATCTAAAGA	AGGATCAGTA	130680
TCACTAACAA	TAAGTTTACA	TGTATCAACA	TTGTACCAA	CCGGTATTCT	ATGTCCCCAA	130740
ACAAGCTGTC	TTGATATACA	CCAATCTCTA	ATATTTGATA	ACCAATATTT	ATATGTATTT	130800
TCCCACTTTT	TAGGATAAAA	TTTTAATTCT	CCATTCTCTA	AAGCCTTTAA	AGCTTTGTCT	130860
GCTAAAGGCT	TCATTCTCAC	AAACCACTGA	GTAGACAAAT	AAGGTTCAAT	AACCTCACCT	130920
GACCGATAAC	AATGCCCAAC	CTGTTGTTTA	TGCTTCTTAA	CATCTTGCAA	AAAACCTTTT	130980
TCCATTAAAT	CTGTTTCAAT	TTTAAATCTT	GCATCTTTCT	CACTTAATCC	TTGGTATTGC	131040
AAAGGAACAT	TTTTATTAA	TTTTCCATCT	TGAGTTAAAA	TATTGACCTT	AGAAATATTG	131100
TGCCTTTTTG	AAATTTCAAA	ATCATTAGGA	TCGTGTGCAG	GAGTAACTTT	TAAAGCCCCA	131160
GTGCCAAAAG	CGCTGTCAAC	ATAAAAATCT	GCAATAACTT	TTATCTTTTT	AGTTGTCAAA	131220
GGAATTGTAA	CTTCTTTGCC	AACTAAAGAC	TTATATCTCT	CATCATTAGG	ATTAACAGCA	131280
ATAGCAGTAT	CCCCAAACAT	TGTCTCAGGC	CTAGTTGTTG	CAACCTCAAT	AAAAGAAGAG	131340
TTATCAATAA	AATACTTAAC	AAAATAAAGC	TTACCATCAA	CTTCTTTGTA	TTCAATCTCT	131400
TCATCGCTAA	CAACACTCCC	AGATCCAGGA	TCAAGATTAA	CAAGATACTC	ACCCCTATAA	131460
ATCAACCCCT	TAAAATACAA	GTCCTTAAAA	ACCTTGTTAA	CAGCCTTACA	AAGATTCTCA	131520
TCAAGAGTAA	ACCTTTCTCT	TGAGTGATCA	TAAGACGCCC	CAAGTTTGTT	TATCTGATTA	131580
ACAATTATCC	CTCTATGCCT	ATCTTTTAA	TTAAAAATTT	CTTGAACAAG	CTCTTCTCTT	131640
TCAAAATCAT	CTTTGCTTTT	ACCAATCTTT	TTAAGATGTC	TTTCAAAAAC	AGCCTGCGTT	131700
GCTATTCCTG	CATGATCTGT	GCCAAAAAGC	CACAAAGTAT	TGTGTCTTTT	CATTCTTTTA	131760
TACCTTACAA	GAACATCTTG	CAAAACAAAA	TTAAGAGCAT	GCCCCATGTG	CAACACGCCA	131820
GTAACATTAG	GAGGAGGCGC	AACCATACTA	AATTTTTTCA	ATAAAGAATT	ATCTGGCAAA	131880
AAAACATTGT	TTTTAAGCCA	CTTAGTGTA	ATTTATCTTT	CAAATGCCTT	AGGATCATAT	131940

TTTTCAAGAG GTCTACAATT CATCGTTTAA AAATCTCCTA CCATGTCAAT AACTTTTAAA	132000
TTTTCAAAA GCTCTTCATA AGTTTTTGAA TTTATAAGAT TTGAGAAATA CTTACTCTGT	132060
CTTTCCTTCT CAGTAAAATA TATCTTAAAA TATTTTTTAA GTTTATTAAA ATCTTTTTTCA	132120
AGTCCCCAAG TAGCATGAAA ATCCTTTATA TGGAATTTTA ATATATTTAA CCTAAAATTT	132180
AAATTACTAT CTAAAAAGTG TTTTGAAAAG GGC'TTAAATA AATTCAAATT ATCAAAAATT	132240
CCACGACCAA ACATAATTCC ATCAATTAAA TATTTATCAA CATAATATCT AGCTTCCTTG	132300
AGACTCAAAA CATCCCCATT TCCAATAATC AGAGTAGAAG GACTAAGATT ATTTCTGTAAT	132360
TTAACAAGTT CATAAAAAAT ATCAAAATTA ACAGGACCTT TGCTCTGATT AACAGCAAGT	132420
CTTGATAAA CCGTTAACAT ATCAATTTCA AGGCCTAACA AAAACCCAG CCAATCATCA	132480
ACTTCTGGAT ATGAAAATCC ATGCCTGGTC TTAACACTAA GAGGCAAATT AAATCTCGCA	132540
CAAGCTTCTT TGCTTGCAAG AATTATCTCT TTAGCTAAAG ATTTATTATT AATTAAAGCT	132600
GAACAAACTC CTTTTTTAAT TATTTTACTC TTAGGACAAC CCATATTAAT ATCAATTCCC	132660
CAAAACCCCA TGCTCCCTAA TATTTCTATT GCTCTATAAA ATTGCTCAGG AACATTGCCC	132720
CAAATCTGAG CAATTAAAGG CCTATTAAGT TCATTGGGTT TTAAAAAAC ATGTTGAACA	132780
GATTGTTTTG ATCCATTTAA AATTCCTTTT GTAGAAATAA ATTCGGTAAA ATAAATATGA	132840
GGTCTCCTT CTGCAGATCC TATTAAATGA ATTAAATTTT TAAAAACAGT ATCGGTAACA	132900
TCTTCCATTG GAGCTAAAAT CATAATTGGA AGAGGAATAT CAAATAAAAA CTTCATAAAA	132960
TAACTACATA ACAATAAAAT ACAAATTTAA ACAAAGTAAA ACAGTCGTTT AATAAATTTA	133020
AATTTCCAAA AATAACATTG AAATTTTTTA AATAAAGAAA TACCACAAAA GGACCGGCAA	133080
TAAAGGACAT AATCATAAAA TTTTAAAAAG TTAATAAATA ATTTTAATAA AAAAATAATT	133140
TAAAAAATCA ATCCATAATA AGGCTCTCGC CTGGAACCTT GGTTTTTCTT ATTAAAGTAT	133200
CTTTATATCC AGCAGATTTA ATAAGTTCTA TATTTTTTTG AACATCATCG GCATTAGTAG	133260
GAATAAAAC GGTATAAAAC GGCCCATGAG AATTTACTAC AACAAAAAGA CCCGCTTTTT	133320
TTAATATTCG ATAAGCCCTA TCAGCGTAAT CTTTTTTCCT ATAAGATCCA ACTTGATATG	133380
AAAAATCTGT TTCTTTGTCA GCAGAACTG AGTAATCTGC CAATAAATCT TTGGATTTAT	133440
TTTAAACAGA AATATTTTCG TCTGATTGCT TGTTTTTCTT TTCTTCTTA ACCCCAGGAA	133500
TATTAAATGT TTTTTTAAAG TCACTAGATT TTGATACAGA AGGTCTTTTT TCATTCTGAC	133560
TTTCAATCAC TTCAATTTTT ACAGGAGCAA CCCCTATTCC TAAAAAATCA AGCTTCTCAG	133620
CGGCATATTT TGACAAATCG ATTATTCTAT CCTTCCTAAA AGGACCTCTA TCATTAATTC	133680

TTACAACAAC	TGATCTATTA	TTTAAAAGAT	TTGTAACCTT	TACGGTAGTA	TTAAAGGGCA	133740
ATTCTTTGTG	AGCAGCAGTA	AGCGCCATCA	TATCAAATTT	TTCGCCATTA	GCAGTAGTTT	133800
TGCCGTGAAA	AGCTTCGCCA	TACCATGAAG	CAAGACCCAC	TGTGGCAGAA	TTTAAATGAG	133860
AAGCAATAAA	AAAAAATACA	AAGAGAAAAA	CAAAGTTTTT	ATTATCTCTT	AAGATGGCAT	133920
CAATTAAATT	TCTCATAATG	TTTATTATAA	TATAAAAACA	TATTTCAATA	AACAATTAAG	133980
CTTGCAAATT	GCTTATTTAC	ATTTTTTTTT	ATTTAATTAT	AAAAAGAAAA	AAGTCTAAAA	134040
AATGATATCA	ACAGAAATAA	TTAGCAGCAG	CCAAATACAA	AAAGCAGCAA	AACTTATCAA	134100
AATGGGAGAA	CTTGTAGTAT	TCCCAACAGA	AACAGTTTAC	GGAATTGGCG	CAAATGCTTA	134160
CAATGAAGAT	GCTGTAAAAA	TGATTTTTTT	AGTAAAAAAA	AGGCCCATCA	ACAATCCTTT	134220
AATAGTACAT	GTTGATACGG	TAAAAAAAAT	AAAAGAATTA	TCAGAATATA	TTCCCAAAAG	134280
TGCCCTCATG	CTAATCAAAA	AATTTAGTCC	AGGCCCTTTA	ACTTATGTTC	TTAAAAAATC	134340
AATAAAAATA	TCTAGATTTG	TAAGTGGAAG	CCTAGACACA	GTGGCAATAA	GAATTCCTGC	134400
AAATAAAACA	GCTTTAAGCC	TAATAAAAGC	ATCTAAAGTC	CCCATAGTAG	CACCGTCTGC	134460
AAACATATCA	AAAAGACCAA	GCTCAACAAA	TTTCGAAATG	GCCTTAAAAG	AATTAAATGG	134520
ACTTGTAAGA	GGAATAATAA	AACCGGAAGA	GAACAAAGAC	TTTAATATTG	GAATCGAATC	134580
AACTGTGGTT	GGGTTTGACC	TAAAAGATAA	CGTACTGATA	TTAAGACCAG	GCGCAATAAC	134640
AAAAAAAATG	ATAGAAAATG	AAC TTCAAGG	AAAATATACA	GTAAATTACG	CAGAAACAAA	134700
AATGGAAC TA	GAAAAATCAC	CTGGAAACAT	AATTGAACAT	TATAAGCCAA	AAATTCCCGT	134760
TTATTTATTT	AAAAGTCAAG	ATAACATAAG	AAGATACTTA	AACAAAGATA	CGAAAAATACT	134820
TATCACAAAA	GCTACTCTAA	AATCCTATTT	ATTCAATTTT	TTTTGGAATA	AAAAAAATAT	134880
TACAGTATTT	AACACTCTTG	AAGAATATGC	ACAAAACCTT	TACAAAGAGT	TGGTAAATTC	134940
TGAAAACAAC	TACAAACAAA	TACTTAGCGA	ATTCTTAAAA	GACGAAGAAC	TTGGACATTC	135000
AATAACAAT	AGAATCAAAA	AAGCTAGTTC	AAATAGATTC	ATTAACAAAA	AATGACGCTA	135060
AATTGTTATT	TAAAATAATT	CAAAAAGCAT	AAATATTCAT	TAATAAAAATA	ATGCTAAAGC	135120
TAAAAGCAAA	AGTCTAAAAAC	ACGCCACACC	TCTCCTCCCA	ACCCGAGCAA	AACCAGCAAA	135180
TACAACCAAG	AAGACTTAAA	CTTAAATATT	ACAAGTAAAT	TTTCGCATAA	TCACATAAGA	135240
AAAATTTCAA	TCCTTTGATT	AATTGAAATA	ATCATGGATC	AACATAGTAT	ACTCAAGTGG	135300
TATTTTATCT	TCATCAAAAG	CAATACCAAG	CGCAAAAACC	TTTCCGCTGG	GAGTCTGAAT	135360
AACGCTTAAG	CTTTTTGATT	TACCTTCAAT	AAAAATTTCT	CCATCTATAA	ATTCAAAACT	135420
AAAAATCAAA	TCAATTGCAT	CTTCCTCGAC	ATCCCCATAA	TCAAAAGAAG	AAATTACTAA	135480

AGCACCCCCA TAAGATAAAT CTTTTATTAA GCATTTATGT TTTGCTCCAT TAACTTGAT 135540
AAAAGCTTTA TCAGAATCAA TTTTAGCTT TCTAATAGAA TCTTTATCGA TAATAATCCT 135600
CTCATGAATT CTCTGATTTT GCCCAAGCTT TAAATCAAGA AGCTTTCCAA CTTTAATAGC 135660
AATCTCTTCT GGTGCAGGAG ATAAAAATTC TAATGTAAAT AAATTGTATT CTTTATTCAA 135720
AGAAGAATAA GCAGAAGCAC TCAATAGTTT TACAGACAAA AAAGGGAAAA AAGCTGCACT 135780
ACTCTTAGAA TCTGAATTTT TCTTAAGTTG AATAGAGCCT AAATTTTTAT TTTTAGCCAA 135840
AGCGGGCAAT ACTGTATCTT CTGAAAAAT AAGCTTAAGA GAATCCATAG AAATAGAATA 135900
AATTACTCCA AAAGCGGTAT AAGAGCCTAT TCTCATCTCA ATAGTATTGC GAAGATTTAA 135960
AAAACATTTT ATCTCTGTGC TCATTTTAAT CTCTTTACCC CTATACTTAG CCCATAATC 136020
TCTTATTTTT CTAGATAAAA GCATAAACCT CTCCTTTCTC CTTTTTTTGA ATATAAAAAAT 136080
ACTAAACAAA GCTTCAAATT GTTTTAAACA GTTTTACACA AATAAAAAAG TTTAAACAA 136140
TTAAGCTATA AACACGCTTA GCCAAAAATC AATAAATCTA CCCTTAAAT CAAAAACATA 136200
CCATCATCCA CCTCTCACAG CATCTTTCAA TTAACAAAAC TTACAAAATG CTGTTTACAT 136260
AGTGTAATTA TATAACAATA ATTTTACACT ATAACAATCA ACCCATAACA TTATTAATTC 136320
TTATGCACTT ATAGTATACT TTAGTAAAAA GTATGAAATT GAATAGCCCT AATTGAAAA 136380
AAATAAATAC GCATAAGCTG CTTATATATT TAACATATTT CGCAGTTAGC TTTTCTATTA 136440
TCACACTCTC ATTAGCAGTA TCTAAGACTA TAAACATACA AAAAGATAAA AATTTCGGAT 136500
ATGTAAATCC AGCAGTTCCT TCAAGACTTT TAGATATTAA TGGAAAACAA ATAACCTCAAT 136560
TTATATCTGA TGAGAACAGA GAATTAATGC CTTTGAGAAA AATGCCTGAC AATCTAATTA 136620
ATACGCTTTT GATACGGGAA GATATTGGTT TTTTTTCTCA TCGAGGTTTT TCCTTGATAG 136680
GAATATTTAG AGCCGCATTT AATATTGTTC TTGGCAGATA TTTTTCAGGC GGCAGCACAT 136740
TAACCCAAAC ACTTGCAAAG CTTCTCTACA CAAATCAAGC AAGAAGATCT ATTTTGAGAA 136800
AATTACATGA AATATGGTGG GCAATTCAAC TTGAAAAAAA ACTCTCAAAA TACGAAATAC 136860
TAGAGAAGTA CCTTAATAAA GTTTATTTTG GAAACGGAAA CTATGGAATA GTTGCAGCAT 136920
CAAAATTCTT TTTTGGCAAA AGTGTAATAA AAATCAATAC AGCAGAATCA GTAATGATGA 136980
TAATCCAGCT TCCAAATGCA AAAC'TTATT CACCTCTTTA CAATCCAGAA TTTTCAAAAA 137040
AAATACAACG TGCAGTTTTA AACCAAGTTG TATCAAATGG AATAGTCAAG GCTGAAATTG 137100
CTGAAAAAGA ATTTAATGAA TACTGGCAAA ATTATGATTG GACTAGAATG GCTGACACAT 137160
CTGCAATTTT AAACAAAAAA GACCAAGCTC CTTATTTCTC TGAATATATA AGGCAAAAAA 137220

TACTAAAATA	TTTACCAGAT	GGCGCAAACA	TATATAAAGA	TGGGTACTCA	ATATATTCAA	137280
CCCTTGATCT	TGAAGCACAA	AAATATGCAG	ATAAAGTTAC	AAACGACATG	ATTAATAAAG	137340
CAAGAACAAT	GCACAATTTA	AATAGATCAT	CTGAAACAAT	AATCATTAAT	TCAGAAATTG	137400
TCCCTGTAGT	AGATGCGATA	TCAGATTTAT	TGGGAATTAA	AAATTTAAGA	ATAAATGGAA	137460
GACAATATAA	AAACTGAGA	AAAAGAAAAT	TTTACGAAGA	CAATATTGAT	CTAATTGCAA	137520
GTTTTGGAGC	TATACTTGGA	ATTGATAAAA	TAGATAAGGC	GACAAAAGAA	TATATTATCA	137580
AAAATAAATT	AACACCGAAA	CTTATTGCAC	AGCCTGAAGG	AGCAATGATA	GCAATAGATA	137640
CAACAAGTGG	AGCAATAAGA	GCCATGGTTG	GGGGAAGTGG	ACACACTAAA	GACAAATGAAT	137700
TTAATCGAGC	CACACAAGCA	AAAGTTCAGC	CTGGAAGTGC	ATTCAAAGCA	TTATATTTTG	137760
CAGCCGCAAT	TGATCTAAAA	AAAATAACAG	CTGCGACAAT	GTTTTTCAGAC	TCTCCAGTAG	137820
CATTTCTAAA	TAAAAATGGA	GAAGTTTATG	CTCCGGGAAA	TTATGGCGGC	AAATGGAGAG	137880
GCAACGTTTT	AACGCGCCAA	GCATTAGCTT	TGTCCTTAAA	TATTCCGGCA	TTAAGAATAT	137940
TAGACCGGCT	AGGCTTTGAC	TCTGCAATTA	GCTACTCCTC	AAACTACTA	GGAATAACAG	138000
ATCCAAAAGA	AATAGAAAAA	ACGTTTCCAA	AAGTTTATCC	ACTAGCGCTA	GGTGTAATAT	138060
CAGTTTCTCC	AATCCAAATG	GCAAGAGCCT	TTGCAATTTT	AGGAAATAGT	GGTAGCGAAA	138120
TCGAACCTTA	TGGGATAAGA	TACATTGAAG	ACAGAGCTGG	AAGAATAATA	ACAAATGAAG	138180
AAGCAAGCAT	ATTGGCTAAA	ATAAAAACA	AAGAACACCA	AACTCAAATA	GTATCTCCTC	138240
AAACCGCTTA	CATAATCACA	GATATGATGA	AATCAACAAT	TCAATACGGA	ACCCTAGCAA	138300
ATCAAAGATA	TACAAATCTC	AAAAATTTTA	AATCAGACAT	TGCTGGAAAA	TCGGGAACAA	138360
CACAAAATTG	GGCAGACGGA	TGGGCAATAG	GATACTCTCC	TTATATAACA	ACAGCATTTT	138420
GGGTGGGATT	TGACAAAAAA	GGATATTCAC	TGGGAATATC	TGGAACAGGA	ACAGGATTGG	138480
CAGGGCCTAG	TTGGGGAGAA	TTTATGGCAG	AATATCACAA	AAACTTACCC	AAAAAAGTTT	138540
TTGTAAAACC	TGCAGGAATA	ATTAGCATCC	CCGTACAAGC	AGAAACGGGT	CTACTACCGG	138600
AAGAAATTGC	TGATGAAAAA	ATAATAAATG	AACTATTTAT	TTCCGGCACC	CAGCCAGTTG	138660
AAAAATCAAA	ATATTATGAA	AATAACAAG	AATTTAAAAA	TACAATAGAA	TTTAACATAT	138720
ATGGAATTGA	TGAGATTAAT	AATAACGATG	AAATAAATTT	TGACACTCCT	GAATTTGAAT	138780
ATCTTGATAA	TAATCTTGAA	AGCTTTAATA	ACAATAGTAA	TAATGATAAT	AATCTTGAAA	138840
GCTTTAACAA	TAATAACAAT	GATCTTGAAA	GCATTAATGA	TAATGAAGAA	AATAAAAAATG	138900
AAGATGAAAT	AGAAATGAAC	ATTGAAGAAC	CCTTAAATGA	AATAGAAAAT	AAAAATCCAC	138960
AACAAGATCT	AGTTAATAAC	AATAATAACC	AGGAAATGCT	TATTGAAAAAC	ACCAAAGAAA	139020

TTAAAGACGA AGTCATTGTT AATGAAACAA ACATAGAAAC ACAAAGCACA AAAGAATTAA	139080
ATTCAAACAA CAATGAAAAT GAAAAAATTA ACAACAAAGA CGTCAACGGA GAAGATATCC	139140
AATTGGATTA AAACAATATG TTAATAGATA TCGATCAAAT AAAAATAAAA AAAAGAATTA	139200
GAAAAAATAT AGGAGACATT GAAACTCTTA AAAACAGTAT TATAAAACAT GGATTAATTT	139260
ATCCAATAAT AATAGATAAA AATAAAAACT TGATAGCAGG ACTTAGAAGA TATCAGGCCT	139320
TAAAAGAAAT AGGCTATAAA GAAATTGAAG TAAAGGTAAT CTCAATTGAA AACAAAAAAA	139380
CTTTACTTGA AATTGAACTT GATGAGAATA ATGTTAGAAA ATCATTACACA AGAAGCGAGG	139440
CAAACGAAGG AGAAGCTTAC TTAAAAATTT ATTCTGAAAAG CAATATAATA ATAAGATTCC	139500
TTAAATTTAT TATCTTAAAA ATTAAAAACA TGTGTAAAAT AAGAAATAGA AAAATTTAAA	139560
TCATAATAAA GAGGTGTGTT TATGTTAAAT TACAAAAATC TTAATGAACT TGAAAATTTT	139620
AAAATCCTTG AAGGTATTGC TCCAGAAGTG CTCAAACGG CATTAACCTGG AAAAAGGATA	139680
AAAGAATACG ACATTACAAT AGAAGGAGAT AGTGTACATT ATAACATATGC TTCAAACAA	139740
ATTAATGAAA CCCACCTTAA AATTTTTCOA AATTTAAGCG ATGAAGCAA TTTAATAGAA	139800
AAATATAAAG AAGTGCTTGA TGGGGAAAAG ATCAATATTA GTGAAAATAG AAAAGTCCTG	139860
CATCACCTTA CAAGAGGGCA AATTGGTAAG GACGTAATAG AAGACAATAA AGAAAATATG	139920
AGAGAGTTTT TCCAATCAGA ACTTGAAAAA ATATATAATT TTGCAAAGCA AATTCATTCT	139980
GGGAACATTA AAAGTTCAA TGGCAAAAAG TTTAAAAATG TAGTTCAAAT AGGAATTGGT	140040
GGATCTAGCC TGGGGCCAAA AGCTCTTTAC AGCTCAATAA AAAATTATGC AAAAAACAC	140100
AATCTAGCCC TAATGAATGG TTATTTTATT TCAAACATTG ATCCAGACGA ATCAGAAGAA	140160
GTATTAAGCA GCATTAATGT TGATGAAACG CTTTTTATTA TTGTCTCAA AAGTGGAAT	140220
ACATTAGAAA CTAAAGCTAA TATGCAATTC TTAATAAACA AATTAAAATT AAATGGCATA	140280
AAAGAATATA AAAAACAAAT GGTCATTATA AACTAAAAG ATAGCATGTT GGCAATAGAA	140340
GAAAAGGAT ATCTTGAATA TTTCTTCATG CATGACTCAA TAGGTGGAAG ATTTTCTCCA	140400
ACATCAGCAG TTGGACTTAC ACTACTTACT CTTTGCTTCA CAGAAAAAGT TGCAAAAGAA	140460
ATTCTAAAAG GAGCCAATGA GGCTGACAAA AAATCATTA AAAAAACGT AAAAGACAAT	140520
GCATCTCTCT TGGCAGCACT AATTAGCATA TATGAAAGAA ATGTTCTAAA TTACAGTAGC	140580
AACTGCATCA TTGCTTATTC TAAAGCAATG GAAAATTTTT ATCTTCATTT ACAACAATT	140640
GAAATGGAGA GTAATGGAAA AAGTGTAAC AGATTTAATG AAACAATAAA CTACAAAAC	140700
GTAAGAATAA TTTGGGGAGG CATTGGAACA GATGTTCAAC ACTCATCTT TCAAATGCTT	140760

CACCAAGGAA CGGATATAGT TCCAATGGAT TTCATAGGTT TTAATGAAAC ACAACTTAAA	140820
GAAGATGTAA TATCTGATAA CAGCTCAAGC AATGATAAAT TAAAAGCAAA TTTAATAGCC	140880
CAAATAATAG CATTTTCAAA AGGTAAAGAA AATAGCAATA AAAATAAAAA TTTCCAAGGC	140940
GAGAGACCTT CTGCACTAAT ATATTCAAAA GAATTAACAC CTTATGCAAT AGGAGCAATA	141000
CTCTCCCATT ATGAAAATAA AGTAATGTTT GAGGGATTTT TATTAAATAT AAATCATTC	141060
GACCAAGAAG GAGTTCAGCT AGGAAAAATT ATTGCAAATC AAATTTTAAA AAATGACAAT	141120
TTTAAAGATG AAGTAATAGA ATCTTATTCT AAAAAAATTC TAAAAAATT TTAACAAG	141180
ATTAATTAAT TTTTGAATAT ACCCCCTTAA GTTTAAAAA GAATGCACTA AGCTTATATA	141240
AGAGGTAATA ATGGATAAAA TAAGTATATT ATATACATTA ATCAATATTA TAATAATGCT	141300
TATTCTAATA AGCATAGTTT ATCTTTGTAA AAGAAAAAT GTTCTTTTA CAAAAGAGT	141360
GTTTATAGCG TTAGCAATCG GAATAGTATT TGGAATGACC ATTCAATATT TTTATGGAAC	141420
AAATTCAGAA ATAACAAACG AAATATAAA TTGGATAAGT ATTTTGGGCG ATGGATACGT	141480
AAGGCTCCTT AAAATGATTA TAATCCCCTT AATAATAACA TCAATAATCT CTGCAATAAT	141540
AAAATAACC AATAGTAAAG ATGTTGGGAA AATGAGCCTA CTTGTAATAT TAACACTAGT	141600
ATTTACAGCA GGTATTGCTG CCATAATTGG CATTTTCACT GCTTTAGCAT TGGGATTAAC	141660
AGCCGAAGGA CTACAAGCGG GAACCATCGA AATTTTACAA AGTGAAAAAT TGCAAAAAGG	141720
CCTTGAAATA TTAAATCAAA CAACAATCAC AAAAAAATC ACAGATCTTA TTCCACAAAA	141780
TATATTTGAA GATTTTGCAG GGCTTAGAAA AAATCAACC ATCGGGGTCG TGATATTTTC	141840
AGCTATCATA GGAATAGCCG CCCTTAAAAC ATCTATCAAA AAGCCAGAAT CAATAGAATT	141900
TTTTAAAAA ATAATATTAA CACTCCAAGA CATAATATTA GGTGTAGTAA CTTTGATTTT	141960
AAAATAACG CCTTATGCTA TATTAGCTTT AATGACAAAA ATTACAGCAA CCAGCGAAT	142020
CAAAAGCATA ATAAAGCTTG GAGAATTTGT AATTGCTTCC TACATTGCCA TAGGTCTTAC	142080
ATTTCTTATG CATATGACAT TAATTGCAAT AAATAAATTA AACCCAATTA CTTTATAAA	142140
AAAAATATTC CCAGCACTAT CATTTGCATT CATATCTAGG TCGAGTGCTG CAACCATACC	142200
CATTAATATA GAAATTCAAA CTAAAAATCT GGGAGTAAGC GAAGGAATAG CAAATTTATC	142260
AAGCTCCTTT GGAACATCAA TTGGGCAAAA TGGTTGTGCA GCACTACACC CCGCTATGCT	142320
TGCAATAATG ATAGCACCAA CTCAGGGAAT AAACCCACA GATATTTTAT TTATACTCAC	142380
ACTTATTGGA TTAATAATAA TAACTTCATT TGGAGCTGCT GGCGCTGGTG GAGGCGCAAC	142440
AACAGCCTCA CTAATGGTGC TCTCAGCAAT GAACTTTCCA GTGGGATTGG TAGGACTTGT	142500
AATATCTGTT GAGCCTATAA TTGACATGGG AAGAACAGCT GTTAATGTAG GCGGCTCAAT	142560

GCTTGCAGGC GTTATATCTG CTAAACAGCT CAAACAATTC AACCATAATA TATACAACCA 142620
AAAAGAGCTT GTAAACAAAT AAATAGGAAA ACAATGATGA AAATAATAAT TATTGGGGGC 142680
ACATCAGCAG GAACTAGTGC CGCAGCTAAA GCAAACCGCT TAAACAAAAA GCTAGACATT 142740
ACTATCTATG AAAAAACAAA TATTGTATCT TTTGGAACCT GTGGCCTGCC TTTACTTTGTG 142800
GGGGGATTCT TTGACAACCC CAATACAATG ATCTCAAGAA CACAAGAAGA ATTCGAAAAA 142860
ACTGGAATCT CTGTTAAAC TAACCACGAA GTTATCAAAG TAGATGCAA AAACAATACA 142920
ATTGTAATAA AAAATCAAAA AACAGGAACC ATTTTAAACA ATACTTACGA TCAACTTATG 142980
ATAGCAACTG GTGCAAAACC TATTATTCCA CCAATCAATA ATATCAATCT AGAAAAATTTT 143040
CATACTCTGA AAAATTTAGA AGACGGTCAA AAAATAAAAA AATTAATGGA TAGAGAAGAG 143100
ATTAAAAATA TAGTGATAAT TGGTGGTGGA TACATTGGAA TTGAAATGGT AGAAGCAGCA 143160
AAAAATAAAA GAAAAATGT AAGATTAATT CAACTAGATA AGCACATACT CATAGATTCC 143220
TTTGACGAAG AAATAGTCAC AATAATGGAA GAAGAACTAA CAAAAAGGG GGTTAATCTT 143280
CATACAAATG AGTTTGTAAG AAGTTTAATA GGAGAAAAAA AGGCAGAAGG AGTAGTAACA 143340
AACAAAAATA CTTATCAAGC TGACGCTGTT ATACTTGCTA CCGGAATAAA ACCTGACACT 143400
GAATTTTTAG AAAACCAGCT TAAAACTACT AAAAATGGAG CAATAATTGT AAATGAGTAT 143460
GGCGAAACTA GCATAAAAAA TATTTTTTCT GCAGGAGATT GTGCAACTAT TTATAATATA 143520
GTAAGTAAAA AAAATGAATA CATACCCTTG GCAACAACAG CCAACAACT TGGAAGAATA 143580
GTTGGTGAAA ATTTAGCTGG GAATCATACA GCATTTAAAG GCACATTGGG CTCAGCTTCA 143640
ATTAAAATAC TATCTTTAGA AGCTGCAAGA ACAGGACTTA CAGAAAAAGA TGCAAAAAAG 143700
CTCCAAATAA AATATAAAAC GATTTTGTGA AAGGACAAAA ATCATACAAA TTATTATCCA 143760
GGCCAAGAAG ATCTTTATAT TAAATTAATT TATGAGGAAA ATACCAAAAT AATCCTTGGG 143820
GCACAAGCAA TAGGAAAAAA TGGAGCCGTA ATAAGAATTC ATGCTTTATC AATTGCAATC 143880
TATTCAAAAC TTACAACAAA AGAGCTAGGG ATGATGGATT TCTCATATTC CCCACCCTTC 143940
TCAAGAACTT GGGATATATT AAATATTGCT GGCAATGCTG CCAATAGAA AGAATTAAAT 144000
TAATTTAATT CTTTCATGCTA ATTGGTTGCC CCGTACTTGA AAGAACATCT CTCCAAAAAG 144060
AACCATTTGG ATTAACCTTA TTTCTGTCAA TTACTGCCAT CTTAATAGGT ATATGAACAA 144120
ATTTTGTACT CCATAAACTA ATCAACATTT TTGTCTTACC AGCCATTGCA GCATGCACAG 144180
CATTCGACCC AAGCCTAGCA CAATAAAGCG AATCACTGGC ATTAGCAGGT GAACTTCTAA 144240
TAATATAGCT GGGATCAATG TATTTAAGAG TAAATTGTAT ATTTTTTGCT TTAAAAATAT 144300

CTGTAATTTT ATCTTTAATA TAAAGCCCAA TATCCTCATA AAGCAAATTC CCAGAATCGT	144360
CTTTCTTCTT AGGAAAATGA TCAAAATATT TTTGGCCTGC TCCTTCTGCT ATCAATATTA	144420
CTGCATGGGG AATCTCTTCT AAGCTTTCTT TCTCTAAAAG TCGTCTTTCA AGATGAACAA	144480
GAAATCCATT AGGACCTTCT ATGTCAAAAT CAAGTTCTGG GATTAAACAA AAATTAACAT	144540
CATTAGAAGA AAGTGCGGTA TGAGCAGCAA TAAAGCCAGA ATCCCGTCCC ATAACTTTAA	144600
CAAGTCCAAT GCCATTATAA GCACTATTAG CTTCAAAATG AGCACCAGCA ACAGCTGCAA	144660
CAGCTTGTTT TACAGCAGTC TCAAATCCAA AAGATTTTTG AACAAACATA AAATCATTGT	144720
CTACGGTTTT AGGAATGCCC ACAACTGCTA TTTTAAATT TCTTTTTTCT ATCTCCTCAG	144780
CAATAAGAAG AGACCCCTTT TGAGTACCAT CCCCGCCAAT GTTAAAAATC ATATTAATGT	144840
TCATTCTCTC TAAAGTATCA ACTATTTCCA CAGGCTTAAT ACCACCCCTT GAAGAACCA	144900
GAATAGTACC TCCAAATTTA TTAATATCAT CAACAACATC TGGATTAAGA TTAATAAAAG	144960
GTGAATTTGA CTCAGGAAGA AGCCCTTGAT ATCCAAATTT TACTCCATAA ATATTGCGAA	145020
CCCCATATAT TTTCCATAAA GTTCGCACAA TAGAGCGAAT AACATCGTTA AAACCAGGAC	145080
AAAGCCCACC ACAAGTAGTA ATAGCAGCTT TAACATGCCT GGGCACAAAA TAAATTTTTT	145140
CTCTAGGCCC AGCTTTTTCT AAAAGAACAT CTTCATACCT ATCTCCCTTA TCCTCATTC	145200
TATATACACT AAACCTGATT TTATTTTTTT CATTAACAAA ATGGGAAGAA CCCTCACTAG	145260
CATAAAAATC AATCAAAGGA TTGTTTTGCT TGCATTCTCC CAAGCTATCT ATTTTAAAA	145320
CTAAATTTTC ATTTTAAATT CTATACACCA AATACTCCTT TATAGAATTA TAACCTAATT	145380
ATTTTCTAAT AAATCGACTT TGATCTTTAA TCATATCGTA TATGTCATCG TAAATATAAG	145440
GAGACCCTTC AATAGGAGAT TTAATTAAAT TACCAGCTAT GAATTCAAAA TATTTATTCA	145500
ACTTTGAATT TTTCTCAAAA TCAATAAATG GAACTCTATT ATTAATAGCC TCTCTGAAAC	145560
TTTTTGCAAA AGGCACAAAA CCTATAAACT CTATTGGTAT ATTAATATTA TTCTTAACAA	145620
CATTAATCAA ATTTTCACAC ATAGCAATCT CTTCACTAGT TTCTATTCTA TTTAGCACCA	145680
CTCTAGGATA AAAATTATTC ATCATCCTCT TAACTTTCAA AGAGGAACTC AAAGAAATAA	145740
GTTCAATCCC AACAACCAAA TCTTTAAATC CAAGGTTTGT CCCCTCAATC TTATCTTTAA	145800
AAAAATTACC AATATAATCC CGTTCGGGGC TTTTTTGCGG AAATCCTAAA TATAAAAGAC	145860
GATAAAGAGC ATTCTTTAAA AAAGAATAAG CATTAAGTAT GGAAGGGGTT TCTGGTATTG	145920
TAACAATTAC ACCGCTGTAA GATGCCAAAT AAAAATCTAT TGTATTATAA GAAGTTCCAG	145980
ATCCCAAATy TAAAAAATA AAATCAGCAA TAAGATCTTT TTGAATGGAT TCTATAATCT	146040
TTTTCTTAAT AGAAAAAGGA AGATTAGCTG TTCCCGTATA AAGAGCATCA CCTGGAATAA	146100

GATAAAGCTT ATCATAAGAT GTTTTACATA CTAAATCTGA AAAACTTTTA CTCTTTTAT	146160
TAATAAAAGA ACCAATGCCC ACACCCTTAT TTTTAACCCC CAAACACGTA TGTAGATTAG	146220
AGCCACCAAG ATCAAGGTCA ACAAGTATTA CAGTTTACC CAACTAGAA AGCTTATAAC	146280
CAACATTTGC AACAAAAGAT GTTTTCCAA CACCGCCTTT GCCACTTGCC ACAGGAATAA	146340
TTTtagTCAT TCTTAAATCC TAATTATCCT TACGATCTTT TTGAAAAATT TTCATAAAAT	146400
TGAAAATCCC TAAAAATCTA GATTTTTTCT CAGCATCTTT ATTTAAATTT TCATCCTCTT	146460
TAGAGCCTGA AATTAAATCT TTAATTAAAT CTTTATTATT TGTAATAATTT TCAATGCTAT	146520
CTGGTTTACC ACAAATTACA ATTTTATCAT CTTTTAAAAA AAAATAATCG CCATCAACAA	146580
ATTCATACCT AGAATTACTT AAATTTCTAA CAGCAATAAC TGTAATCCCA CATTCTCTTC	146640
TAAGATCGGC TTCAAAAAGA GTTTTACCA CATATTCTTT GGGAATAACA GTTTCAGCAA	146700
CAATAATATC ATACCCAATA ATATTATAAG TTGAAAGATT TGGAGATACT AATAATGGAG	146760
TTAATCTTCT TGCAGCATCT TACTTGGA ATATAATTTT TGTTGCCCCA AGAGTTTTTA	146820
AGATTTTCAGC ATCATCTCTA TTTTCTGTCT TAACGCATAT TTCTTTCAAA CCTAAAAGAT	146880
TACAATAGTG AGTAACAAGA GCACTTTTGC CAAGATCATC ATCAAAATCA ATAACAACAG	146940
CGTCTGTATC TACTGGAATT ATTCTTTTCA AAGCATTTTT AGTGAATTGC TCAACAACAA	147000
AGCTTTCTGT AGATATCACA TCATATTCTT CAATAAGCTC TTTAGATGTA TCTATAATAA	147060
TAATTTGACA ATCAAGCCTG CTTAAATCTT CAAGTAAGTG AATGCCTAAA TACTAAGTC	147120
CAATAATAAC AAATGTTTTT ATATGCTTCA ACCAACCAAA ATATCTTGCC TTGGCCTTGT	147180
AAATCTTCA AAACGCGACT TTCTTGAAAC AAAACAGCC ATTGAAAAA GCCCTATTCG	147240
TCCTGCAAAC ATAGTAAAAA TTATAATGAC TTTCCCCCA AATGACAAAT CCTGAGTTAC	147300
TCCAAGTAA AGACCAACCG TTCCAAAAGC AGAAAATACT TCATAACCTA AATCAATAAC	147360
CTTCCAATTG CCAGATCCTC CCTCAAAAAA AAGAAGCATG AAAAAAGAAA AACTTAAAAT	147420
AAAAATAGCT CTTGCAAAAA ATAAAAGTGC AAATCTTATA CTATCTATTG AAACCTTGTA	147480
AGAACCAATA ATATATCCAT TGCCGTTTTG ATTTTAAACA ACAGCCAATA CAATTAAAAA	147540
AAATGTTGTA ATCTTAATCC CTCCTGCAGT TGATCCGGGT GCACCACCAA TAAACATGAA	147600
TGGTAGAGAA ATTATTTGAG TTCTTCGCT TATTAAAGAA TTATCAAGAT AATTAAAACC	147660
AGCTGTTCTG GTACTAATCG AATAAAAAAT TGAATTAAAT ATTAAAGTGC TCATTGAATA	147720
ACCAGCTTTT AATTTATGCA TCTCTGTAAA AAAAAATAAA ATTGCACCAA TTATAATTAA	147780
AAAGAAGCTT AAAGAAAAA CTATCTTGGC ATGAAGCGAT AGTTTTTTTT TGTTTTTAAT	147840

AGTGTATT	TTT ACATCTCTAT	AGACCATAAA	CCCAAGCCCA	CCACAAATTA	TTAAAATAGA	147900
GACCACAAC	T ATAGCTTCAG	GAACATCTCG	CCATGCATAA	ATACTCTCAG	AATGCATGGA	147960
AAAACCTGCA	TTGCAAAAAG	CAGAAATTGT	CGTAAACAAA	GCCTCTAAGA	ATGAAATATT	148020
CACTCCCCTA	AGTTTAAAC	AAATAAGTAT	TAATATTAAA	CCTATCATTT	CAATTGAAAA	148080
AGTTATAAAC	AATATGCTTT	TTAAAATTCT	AATAGGATTA	TATTCTATAT	TTGAAAGGGA	148140
ATACTGCTTT	ATTATTCTTG	CATCTGTAA	ATTCATTTTC	TTTTTAGGTA	TAAGCAAATA	148200
AAAAGTAGTA	ATACTTATAA	ATCCAAGTCC	CCCAAGCTGG	ATTAGCAACA	TTATCAAAAT	148260
AAATCCAAAA	G TAGAAAAGC	CTTCCATTTT	AACCGTTGTA	AGGCCCGTAA	TACTTACAGC	148320
AGAAACAGCA	GTAAAAAGAG	CATCAATGTA	TGCTAATTTG	CCATCACCTT	CCCAGGAAAT	148380
AGGCAACATC	AACAAAAGAG	AGCCTATAAA	CATAATTAAA	ACAAAATAAC	TAAAAAGTAA	148440
AAACCTGTCG	CTAAATTCAA	ATTTCAACAT	ATCATACAAA	AAGTTGTTTA	AATTATTAAA	148500
AATTTATCTT	ATATAGCATA	ATATTTTAAC	ATTGAAATAT	TATCATAATT	ACATTATTTT	148560
TAATATATGT	TTGAAATAGA	ATCAAAAGCA	TTTATTCCTA	CAAAAGAGTT	AAAAAGAATT	148620
ATCAAGCTAG	CAAATAAAAA	ATTTAAGTTT	ATTAAAGAAG	AAATAAAAAC	TGACATyTAT	148680
TACTCAAACC	AAAAAAAAAT	TATAAGAATA	AGAAAATTAA	ATACTCTAGA	AAAAATTGTC	148740
ACATTCAAAA	AAAAAATATT	AGACAACAAC	AATACTGTAG	AAATTAATAA	AGAGATAGAA	148800
TTCAAAATAG	ATAGTATTAA	TAATTTTTTA	ACCCTTATAA	AAGAGCTTAA	ATTTAAAAAG	148860
CTATACAAA	AGATAAAAA	AAGTTTAATT	TATCAAATA	ACAATTTAAA	TGTAGAGATA	148920
AACGAAATAA	AAAATCTTGG	GTFTTTTTTTA	GAAATAGAAA	AAATAATTAA	CAATCAAAAT	148980
GATATAGACT	TGGCAAAAAA	AGAAATTGAC	AACATAATCA	ACCAATTTGG	ATTAAAAGAA	149040
AACATTGAAA	CTAGACCTTA	CTCTGAATTA	CTTTCATTGG	CAAATCAAAG	TAAAAAATAA	149100
TTCATTGGAA	TTAGAGCTTA	AAGTAGAGAT	TACAAGCCCT	TGATTGCCAT	AAATTCCAAT	149160
CTGAGGGCTT	TTAACATTAC	TCTTAAAATT	CTCAAGCTTA	TTTAAAAAAT	ACCAATTTTTT	149220
ATTCTTAAAA	TAAATTAATC	TCACATTATT	ATTGTCCTCA	AAAGCTAAAA	ACAAATTATT	149280
TTTATAAAGC	CCAATGTCAG	CACTTAAACC	TTCCATTTCA	ACATTAGGAC	TTATATTAAT	149340
CCATCTACTA	CTTTTCAAAG	GACAAATGTT	TACAATAGGT	CTATTTTCAG	AAACAAAAC	149400
CATAATTATT	TGATTAAAAT	TAGAATCAAA	AAAGCCTTTA	ATAAAATTGG	CCATATAAAC	149460
AGAAGGAATA	TTTGCATTTA	CCCAAGCATT	TTCATTGTTT	ACAATAAATT	CAGATTTAAT	149520
CTCATTATTT	GACTTATAAT	TATAAAAAAT	GCCCCAAAAA	GGTTCAGATA	TTAAACCAAT	149580
GTTTGATGAA	TTAACATTAG	AATCACCTTT	ACTTAAATAA	GCATGTATTA	CATCGGTCCA	149640

AATACTTCCG	TAACCCATAT	TCGAGATTAA	ATTAATTTTA	TATTCACCCC	TAATTTCCCT	149700
TAAATATGCT	AAATACAACC	TATCTTTTAA	ATCAATGCTA	ATATTTAATA	AAGATCCAAA	149760
ATTTTCTATG	TGACCAGGAC	TAATATCAAT	CCATTTTCTA	CTATTAAATT	TTTAACTAT	149820
AAGCTCGCTG	GCAAAATCAG	CCCCTGATTT	CGTAACAAAA	GCAATATATA	AATTCCTTT	149880
AGAATTAATT	GAAAAATCAA	AATTAECTAT	ATTAGTAATA	TTTCTATTAA	CAGATGAATC	149940
AAGATTAAAC	CAACCAACAT	CCTCAATAAA	TTCAGCAACT	TTAATATCAT	CGCTATTTTC	150000
TAGCTGATAA	GCAATATAAA	TATTGCTTTT	ATAAATCCTT	AATACATATT	TTTAAAGCTT	150060
GGCAGTTAAA	TTTAAACAG	GCAAATCTTT	TAAAGTAAAA	AATAAACTTT	CTTTTCAAT	150120
CTTAGATGTT	TTAGCTTTCA	GGGAATCGCT	ACTTAAAATT	GAAAAATCTA	AATCTGTAAG	150180
CGAAACTTTT	ATGTTTTTCAT	TTTTAGTACC	AACATATATT	ATTGCATAAA	GAGAATTTTT	150240
ATCTAATCTT	ATTTTAAAT	CTCTTCTTTT	TACTTTATCG	GTTATATATT	TTTTATTAGA	150300
AATGTCATAA	ATTTTAAAAA	CAAAATCGGA	ATTTGAACTC	TTATCTAGGG	TTAAAATATA	150360
ATCGGAAGAT	TTGCTAACTT	TTAAGTAAAC	ACTTCCTTTC	CCATTTTGC	TTAAAATACT	150420
TAAAGGACTA	ATTTCTGTTA	ATATTTGATT	TGCTTGAGCT	TGAACAAAAG	AAAATTTTGT	150480
AAATAAAAAT	AGCAAAATGA	ATGTCTTATT	TATTTTCATA	TTTTTTTACA	TTCAAAAATA	150540
TTAACACATA	TTCTAAAAAT	GATAAAATTG	CAAAAAAAGC	AGCACAAACA	TATGTCATTT	150600
GAACAATAAA	TAAAAATTTA	AATTTAAAAG	TTAAAATGTA	ACTAATAAAA	TTTTGAACAG	150660
ACTCTGTAAA	GTTGAGTTGA	TTTAAAGTAT	AAAATAAAAG	GCTTGCAAAA	GTGCAACAG	150720
CATAAGAAG	TGACTTTAAT	TTCCCCAAAA	AATTTGCTTG	TTGAACTACA	TTAACTGAA	150780
TAATTAAATT	TCTAACAAAC	CCAATAGAAA	TTTCACGATA	AATAAATATT	ACAAAAAAT	150840
AATAGGGGGT	TATACCTTTG	TAAAAGAAAA	AAACAAAATA	TGTTAAATGC	TGCAAAACAT	150900
CCGCATAAGG	ATCTAAAATT	TTACCTACAT	TGCTAACAAG	ACCATATTTT	CTTGCAAGAT	150960
AACCATCAAT	AAAATCAGTA	AATTCATTAA	AAATAATTAA	AAACCAAATA	ATTCCAAAAA	151020
ACAAATACGA	AAAAAATACA	TTTTCCAAAA	AAAATAAAAT	TAATATGATA	AAGGAAAGTG	151080
CAATTCTAAC	TAATGTTATT	TTATTAGGGG	TAATGACCTT	GATTAAATTA	TTCAATTTAT	151140
CAAATCTCCT	TATCTCTTAT	TTTAAATAAA	ATAAATTTAA	GAGCTTCATC	AAGTTTCATT	151200
CCATTTATTT	GCTCATTTGT	TCTTGTTCTA	ATAGATATTC	TCTCTTCTGT	TGCTTCTCTC	151260
TCACCAATTA	TAAACATATA	AGGTATTTTT	TTAGCCTGAT	ATTCTCTAAT	TTTAGCATTC	151320
ATTCTTGAGG	AACTATTATC	AAGCTTTATT	CTAATCCCCT	CATTTTTTAA	TTTATTAAAA	151380

ACCTTAATAG	CATAATCTTC	GACAATATTG	TTAACAGGAA	TGATTACTAC	TTGAACAGGA	151440
GATAACCATA	AAGGAAAAGC	ACCACCATAG	TGCTCTACAA	GAATTCCAAA	AAATCTTTCA	151500
ATAGATCCCA	ACAAAGCTCT	ATGAATCATA	AATGGTCTTT	TTTCTTTACC	ATCCTCAGCG	151560
GTATAAGTCA	TATTAAATCT	CTCAGGGAGA	TTAAAATCAA	ATTGAATTGT	ACTCATCTGC	151620
CACTCTCTCT	CAAGCGAATC	AACATCTTCA	AGATCAATTT	TAGGCCCATTA	AAAAGCACCT	151680
CCACCCTTAT	CAATTTTCATA	AGGAACCTCA	AAATCGCTTA	AAGTCTCTTC	AAGAACTTTT	151740
AAAGACATTT	CCCAATCAGA	ATCATTGCCA	ACAGATTTGT	CAGGCTTTGT	AGAAAGATAT	151800
GCCTTTGGGT	TGCTAAAGCC	AAATTTACTC	CACATATAAA	TAGCAAACCT	AAGAACTTCT	151860
TTAATCTCAT	CTAAAACCTG	AGAATGGGTG	CATATAATAT	GAGCATCATC	CTGAGTAAAC	151920
CCTCTGGCTC	TCATCATACC	ATGCAAAGCA	CCTATCTTTT	CATAACGATA	CACAGTGCCA	151980
AGTTCGGCCC	ATCTAAATGG	CAAATCTCTA	TAAGAATGCT	TACCTGTATT	GTAAATTGCA	152040
ATATGAAAAG	GACAATTCAT	GGGTTTAAGA	TAATAATCAC	TTTTATCCAT	TTCTATTTTT	152100
TCAAACATGC	TATCCTTATA	AAAGTCTAAA	TGACCAGAAG	TTTGCCAAAG	CCAAGATTTG	152160
CCAATATGAG	GAGTAAAAAG	AATATCATAC	CCATTTTTTG	AGTGCTCTTC	TCTCCAAAAA	152220
TCTTCTATTA	AAGCTCTTAT	TTTGGCACCA	TTGGGATGAA	AAAAACAAG	TCCTGGTCCA	152280
ATCTCTTCAT	GTATAGAAAA	TAAATCAAGC	TCTTTTCCAA	GCTTTCTATG	ATCTCTTTTT	152340
TTTATTTTCT	CTCTCAAATT	AAGATAAGAT	CTCAGTTCTT	TTTCATTATT	CCATAAAGTT	152400
CCATAAATTC	TGGTAAGCAT	TGGGTTTTTT	TCACTGCCCC	GCCAATAAGC	CCCAGCAATA	152460
CTAGTAAGCT	TAAATGCCTT	TGGATCAATT	TTATTCATAT	TCTCAACATG	AGGACCTCTA	152520
CAAAGATCAA	CAAAATTGTG	ACTCTTGTA	ATAGAACTT	CATTTTGTA	ATCAAAATTT	152580
TTAATCAAAT	CAATCTTATA	AGGTTTCATCT	TTAAAAATTT	CAAGAGCCTG	TTCTACGCTT	152640
ATTATCTCTT	TTTCAAAAGA	ACTTCCGGTC	TTTAAAAATTT	CTCTCATTTCT	ATTTTCTATG	152700
TCTAAAAGAG	AATCTTCTGT	AATCTGCTTT	TTAAATTCAA	AATCATAATA	AAAACCATCT	152760
TTAATAGGAG	GACCTATTGC	AATCTTGCTA	TTTGGAATA	AATCAAGAAC	AGCTTCTGCC	152820
ATAACATGAG	CTATTGAGTG	TCTTTTTTTG	TAAAGAATAT	CTTCTTTATC	TAAATCTTTG	152880
CTCACAACAA	TACCTTTTGC	CTTTCGCTTT	TTATTAAAAA	ATTAAAAATC	ACACTCATCA	152940
CTTTTACGTA	AAAATACGCA	CCTCAAATAT	TTATAATTAC	TAAATTAAAA	TATACAAAAA	153000
AATTTTCTAA	AAAAATAGAG	ATAAGAAAAC	AAAAACCTGA	AAATAAATTT	TCAATCCATA	153060
GCAACTATTG	ATTCAATATT	AAAATAAAAA	GACATTGCTA	AAAAAAATGT	AATAGTAGAA	153120
GAACCTCCAT	AAGAGAGAAA	AGGAAAGGGA	ATCCCGGTAA	TAGGAAGAAC	TCCTAAAGAC	153180

ATTCCAACAT	TAAAAGAAGT	ATGAAAAAAT	AAAAGTCCCA	AAATTCCAGA	TATTACTAAG	153240
GCCATATATC	TATCTTGACT	TTTATTTCATT	ATTATCAAAA	ATTTAAAAAA	AAGGAAAAAA	153300
AATAATATTA	AAATAGTGCT	AACACCCAAA	AACCCAAACT	CTTCGGCAAG	AATAGAAAAA	153360
ATAAAATCTG	TGCTTTGAGA	TGGCACATAA	TTAGCGTGGG	TATAAGGTCC	CTTTAAAAAT	153420
CCTTTGCCCCA	AAAGACCGCC	AGAACCAATT	GCTATTTTAA	CCTGATTTAA	ATTCCAACCA	153480
GCACCCTTAG	CATCAATAGC	CGGATCTAAG	AATACCAAAA	ACCGTTTAAT	CTGATAAGTC	153540
TTCATTAACT	TTGAAAGAAC	CTTTGAAAAC	ACTATTGAAA	CTAATAAAAT	AGAACTTGCA	153600
AAAAATACAT	AAAAATAAAT	TATTTTAATA	CTCAAACCAT	ATTTAGAAAT	GAAAAATCCT	153660
AAAACAGAAA	TCAAAAGAAT	TAAAAGCAGC	ACTCCCATTA	TTACTCTAAA	ATAAAAAGGA	153720
TTTGAGAAAA	TAAGATAAAA	TACATTACCC	ATATTCACCT	TATATTCATA	CCAAACCGGT	153780
AAAATTGCAA	AAACAAAAGA	AAAAAACCTT	ATCAACGCAA	ATGCTAAAC	ATAGTGCAAA	153840
TCTATTCCTG	CAAAAAAGA	AATAAATATA	AAAATGGTTA	AATATACTAT	TGCTGTACCA	153900
AAATCAGGTT	GCAATAATAT	AAGAATTACC	GATGGAAAAA	TTAATAAAAA	TGCAGTAATA	153960
AAGGTAAAAA	ATTCATTATA	ACCCTTTTTT	TCAGTGTAAG	ATTTTGAAAG	GGTTAAAATA	154020
ATAACAACCTT	TACCAAATTC	AGAAGGCTGT	CCTCCAAGTT	TCCATATGCC	AATCCAAGAT	154080
CTTGCTCCAT	TTACTGTCAT	TCCAAAAAAT	GCAGTAAAAA	TTAAAGCCAA	TATTAATAAA	154140
AAATATAAAG	GATATACCAT	GCTATAAACA	AATTTTAAAT	CATATTTGCC	CACTATAAAA	154200
ATTAGAAAAA	ATCCAATAAT	TACCCAAAAG	GTTTGTTTTA	TATATTCATT	CTTGGTAA	154260
GATCCACTAA	TATTATAATC	GCTAGAATAA	ATCAACAATA	TACCAACAAA	AGAACTATA	154320
AGTAAGCTTA	TCAAAGCCAA	ATAATCATAA	TTTTTTCTAA	AAACCATTAA	TCTACCTAAT	154380
ATACCACGGC	CTATAACCTT	TAAGAATATC	TTCATAACTT	TGATTTGCAA	AAATGCCTTG	154440
CATTATTAAA	TCTGTAGATT	TTGCAGGCCA	CCAATCCACA	TTACTTTTTG	CCTCAACCAA	154500
ACTAAAAACA	ATAATTTGAT	TATCAGCTGA	ACCGTTATAA	GGGCAAGTC	CAATAAAAGA	154560
ACTATTTTCA	AAACCATCTA	TTCCAGTTTG	ACCAGTACCT	GTTTTTCCTC	CAACCTCAAC	154620
AGCTTTGGTA	AGAACTGCAT	ATCTTGCTGT	ACCATAAGTT	ATAACACTTC	TCATATATTT	154680
TTTCAGAAGT	TTAAATGTGT	TTTTACTAAT	AAGATTTGTC	TTTCTTAATA	TTTCTGGTTT	154740
ATTTTCAAGA	ACAACCTTAT	TAGTACCACC	TTTTAAAATT	TTATTTACAA	TTCTAGGTTT	154800
ATATACAACA	CCTTCATTTG	CAATCATAGC	AACCATATTA	ACAATCTGCA	TAGGAGTAGC	154860
ATTTAAAAAT	CCTTGACCTA	TTGAAAAATT	TACAGTATCT	CCTCCTACCC	AAGGCTGATT	154920

AAAAGTTTTT	TCTTTCCACT	CAGGACTAGG	AAGAAGGCCA	GCTACTTCAT	TTGGCAAATC	154980
AATTCCTGTT	TTTTCTCCAA	ACCCAAATTC	TTTTGCATAT	TTTCTAATTC	TATCAACTCC	155040
AAGATACTTA	AGCCCAAGTG	TATAAAAATA	AACATTAGAA	GAATGTGCAA	TCGCCTCTTC	155100
TAAATTAACA	TACCCATGAC	CTCCGGGCTT	CCAGCAATGA	AAAATTCTAT	TTCCAACTTT	155160
AAAATATCCA	GGACAATAAA	TTTTACGATC	TTTGTCTATA	ACTCTTTCTT	CAAGAATGGC	155220
AGCAGCAACA	ACTAATTAA	AAATAGACGC	AGGCGGGTAA	ACAGATTGAA	TTGCTTTATT	155280
TAAAAAAGAG	TAATCTTCCT	TATTATCTTT	ATTGTAAACA	TCTTTCATAG	AATAATAAGG	155340
ATAATTGTGA	AGAGCAAGAA	CAGCACCTGT	TGATGGTTTT	AATACTACAA	CAGAACCATA	155400
CCTTTTGCCT	AAAGCATTCT	TAGCAAGATC	TTGAATATCT	TTATTGATAT	TAAGCACAAC	155460
ATCATTACCG	GGCACCATAT	TTTTTATAAT	AGAACCATCG	TCTATTCTTC	TCTCCTTAGA	155520
ATCTACCTTG	TATTTTATTA	ATCCCTCTTG	CCCTCTAATG	TAATTATCAT	AACTTGTTTC	155580
AACGCCCAAC	TTTCCAATCG	TAGAAGTATT	ATCATACCCA	CTAACATTGT	AAAACGTCCT	155640
AAGTTCTCTT	TGATTTATTT	GCCCAACATA	ACCGATTGAA	TGAGAATATG	AATCGTCAAC	155700
TAAATAGTTA	CGCTTAAAAG	AATAGGTCCA	CAAAAGAGCA	GGATAATAAA	ACTTTTTTTC	155760
AGAAATTTTG	AAAAGCATCT	TTGGGGTAAG	TTCAATTATT	TCAACATCTT	TAAGATATCC	155820
ACCAGGCTCT	TGAAGTTTAG	ACAAAATAAT	TGATTTATCA	ATATCTAGAG	TGCTTGATAA	155880
AAAATCTATC	ATCTCAATTC	TAGTAGCAGC	AGGCATATTG	TAATACTGTT	GTAAGCTTAT	155940
CTTTAAGATA	AACATAGTTA	AATTATTTGC	CAAAACATTG	GAATTAGAAT	CCAAAATTTTC	156000
ACCTCTTGAG	GCATTGATTT	TTTCCAATCT	TGATAAAAAA	ACATTGGCTT	CTCTGTCATA	156060
AAACAAATGC	TTACCAATTT	GCATTTGGAA	TAAAATCGCC	AAATAAAGCA	CCATAATTAC	156120
TATTAAAAAA	AATATGCCGA	ACTTGTATCT	AAAATTTGTT	ATAACACCCA	CTAATAATCC	156180
TCTTTAAAAG	AATAAAAATT	TCTAGTAAAA	TAATTTTGAA	TTGGATATAA	AAAGTTAATA	156240
GACATTATAT	TTACAAAAAG	ATCAAGGTTG	AAAATTGAAT	AATTAAAAGA	TTTTAAGTCT	156300
ACAAAATCAT	AAAACACAAT	AGCTAAAAAC	CATAATATAA	TTTTTGAAAG	AATAAAAAAT	156360
ATTGTCATGC	TAAGCATATT	TTTGGGCATG	AATAATTTTA	TTTTATTGTT	AAAATAAAAT	156420
ATTATCGTAT	ACCCAAAAAC	AAAAAATCCA	AGTGGTAATC	CTGTAAAATA	ATCCATAAGA	156480
AGACCATATA	AAATGCTAGA	TAATAATCCC	ACATTAAAAA	TAAAATTCAA	AGAATTAAAA	156540
ACTAGAAAAA	TTAAAAAAT	ATCTATTGAA	AAATAAAAAAT	AAGTTGCAAA	ATAGTGTTGA	156600
AAAATTTTGC	CTAAAAATGC	GCTGGAAATA	AAATATGTAA	AAAATGTTGC	CATTATTAC	156660
CAATCTCTTT	GTTGTTTTTA	ACAAGAAAAA	CATACTCAAG	CTTATCTAAA	ACTATAGCTG	156720

GCTCTACTTC TATTTTAAAA AGAGAATTAT AATCAAGAAT ATGAAAATTT GTAATCTTTC 156780
CAATATAAAT ACCAACTGGA TATTCACATA ATCCAGCAGT AACAATAGAA TCCCCTATTT 156840
TTAAATCTTT TTCAGCAAGT CTATTAACGT AATTCATTTT AAGTTTTTTT CCATAACCAT 156900
TGCCTTCTAT AAGGCCTATA AACCTACTAC TTTGAATCCT TGCGGACACA AAATTTTCAT 156960
AATTAGTTAA AGGCAAAATT TTAGCAGTAT TAGAATAAAC CTTTACAACT TTGCCTACAA 157020
GGCCACTAAA TCCATCCTGA TATGCAACTG CTATCATATC TTTTCTATC CCATCATTTGA 157080
ATCCTTTATT AATAGCCATT AAAGTCGATA TGTTTGAATA GTTTAGATAT ATAATCTCTG 157140
CCGAAATAAA ATCGCTAGAG CTTGACGAAT AAAAATTTAA TTGCTCTTTA AGACGAACAT 157200
TCTCTTGCCT TAGTGACTGT ATATTCTGAG TGACTATTTT AAGCTGTTGT ATCCTTTTTT 157260
TATAAAATTC TATCTTGTCC TTGTAATTTT TGTATTCATT TACAGTTTTA AAAACATTGG 157320
AAATAAACT AAAAACCCCA TGCATTCTGC TTTGAATATA AGAATTAAGA GTAAAAACA 157380
AAAAATTATC TGATCTTCTC TTTTGAATGC TGCTTGAATC ATGAATCATA AAAACAAGAG 157440
AACTATCAA TACCAAAAGT ACTTTGATAA AATCTTGAA TTTGACAAGA AAATTCATAA 157500
CTTATTCATT GATAAACTG TAAATATTTT TACTAATATC TATTCTATTG GCATAATCAT 157560
AAAATAACCC GGCACCAACA GCTACCGAGA GAAGCGGATT GTCTGCAACA TAAACAGGAA 157620
CTCCAGTCTC TTTTGAAAGA AGTCTATTTA AACCCTTAAG AAGAGCCCCT CCCCCTGTCA 157680
AAATAATGCC ACGCTCAACA ATGTCTGTAG CAAGCTCTGG GGGAGTTGCA CCAAGAGTGC 157740
GCTTAACTTC ATCCACAACA ACATTTATAG GTTCTTGCAA AGACTCTCTT ACTTCCATAG 157800
AATCAACAAG TTGCTTTCTA GGAAGACCAG TTACAGCATC TGTACCCTTA ATGTCTATTT 157860
TTTCTACCCCT TAAATTTTGA ATATCGGGAT ATACATTTCC TATCTTAATT TTCAATTTTT 157920
CTGCTGTCTG TTGACCAATT ATAATATTAT GAGAATTTCT CATATACTTT ATTATGCTCT 157980
CATCAAATTC GTCACCACCA GTCCTAATTG CTCTACTTAC AACCATGCCG CCAAGAGAAA 158040
TAACAGATAT TTCTGTAGTT CCACCCCAA TATCACACAC CATATGACCT GTAGGTTCAA 158100
AAATAGGAAT ATCAGATCCA ATAGCAGCTG CAAGAGATTC TTCTATTACT TTAATTCTC 158160
TTGCACCGGC ATTCATTGCG CTCTCTTTTA CAGCTCTTCG CTCAACCTCT GTAATACAAG 158220
TTGGAACACC TATTACCATT CTCGGCTTAA AAAATAATTT TTTACGAGAA AAAATTTGAT 158280
TAATAAAATA TTTGATCATC TTCTCTGTAT TCTCAATGTC AGCAATAACT CCATCTCTAA 158340
GTGGGCGTAC GGCTTTAATA TTTTCTGGAG TTTTCCAAAG CATTTTTTTA GCATTTCTAC 158400
CAACCGCAAC AACTTTATTA CCTTTGGTTA TATCTATTGC AACAACAGAA GGCTCGCTCA 158460

TAACCACGCC	ATAATCTTTA	ATATAAACCA	ATGTATTACA	TGTTCCAAGA	TCAATGCCAA	158520
TATCTATCAA	AAAAGACTTA	AACAAATTCA	AAACAACCTC	CCTAAAAGTC	TTCCAAAGTA	158580
ATTCCAAGCC	TCTCTCTTGC	TGCTTCTAAA	TAAGGATTAA	GATTGAGAGC	TTCTCTCCAG	158640
TATTTTCTAG	CTTTAGGATA	ATCTTTATCT	TTCTTTCTAT	ATATATCTCC	TATTTTAACA	158700
TAAACGCTAG	AATTTGAACT	ATTAATTTCT	AGAACTTTAT	TATAGTAATT	AAAAGCACTG	158760
TCATAATCGC	CTTTATCTAA	TAGAATGTCT	CCATAAAGCA	AATATACCTT	TTGAATTAAA	158820
TTTTCATCCG	TTTTCTCACC	CTTTGATAAT	TTCTTTTCT	CTTCTTCTAT	TATTTTTTTT	158880
ATATACTCAA	TGCTTTTGTT	TATATCATTC	AACTTATAAT	TAACATAAGC	CAAACCTCAA	158940
AGCACTAAAT	CAGATTTATT	TTCATTAAAA	GCTTTTTC	AAACTTCAA	ACTAGATTTG	159000
TAATCTCTTA	AAAGCTGATA	CGAATATCCC	AAATATTCAA	AAATATCTTC	TCTAATGTTC	159060
ATGAAATCAA	AATTATCGGC	ATTTAAGGCC	TTCTTTAAAA	ATTTTACAGC	AAGCTCGCTA	159120
TAAAACTCTC	CTTTATGAGA	ATATGCCTTT	CCCAATATGT	AATACAAAGG	GCTTATGGAG	159180
ACTCCATCAT	TTATAGAAAT	TAAAAATCTT	AGTCTTTCTA	TGGATTTATC	TAAAACTCT	159240
CCTTTTAAAT	ACCCTTCATT	TACTATTAAA	GAATAATAAA	AATATGAAAA	TCCTAAAAGT	159300
AAATTCAAAT	TAAAATCAAA	TCTATGATTT	TTAATGTCAT	TCTCAGCATA	ATCTATTATT	159360
TCTTTATATT	CTTTTTTATC	CCAGAGTAAA	AGCAAATCAA	CTTCTGTTGG	ACCTGCCTTT	159420
AAATAAGAAC	TAGAAAAAGA	TTTAAAATAT	GATAAAATGT	AATAAATTAA	AAAAATGAAA	159480
ATGAAAATCA	TAAATGAGTA	AAAAATATAT	CTTAAATATC	TTATTTCCAT	TTAAAACTCT	159540
CTTTTAGGTC	AATGAAATTA	AGCTGACACC	CATAAGCCGA	GTTCTGTACT	ATGCCATCAT	159600
CTCTCTTATT	TTTTTATCGC	TAAAAAAATC	GTGCGATCTA	CCCGTAAGCA	TGTCCTCAAG	159660
AACAAAGGGT	GCTTACATAC	TTGATCTTGC	TCCTAATGAG	GTTTATCTTG	CCTGTATTTA	159720
TTGCTAAATA	AGCGGTGAGC	TCTTACCTCA	CCTTTTCACC	CTTACCTTTT	ACGGCGGTAA	159780
TTTTCTGCGA	CACTTTCTTA	GGTTTAAAC	CCCTAGGCAT	TACCTAGCAT	TATGTTCTTA	159840
TTGGAGCTCG	GACTTTCCTC	TTAAGCTTTA	ATTATAAAAC	TAAGCGATGG	CTGACTGCCA	159900
GCTTAAATAA	AAAGTATCAA	ATTAATAAAT	TTTATTCAAC	AAGATCTGCT	AACTACCAG	159960
GAATTATTTT	ATCGCTTATC	TGAACCTTAT	CCTGATAATA	AAGTATTCTG	CTGCAATAAG	160020
GACAAAATTT	AATATCGTTG	GGCTCACGTC	TTACTTTATT	TGCAAATTCA	ATAGGAAGTA	160080
TCATATGACA	ACCTTTGCAA	ACATTGTTAA	CCAAAGGCAC	AACTCCATTT	GATTTATTTT	160140
TTATTATTCT	TTGAAATTTA	AATAAAAAAT	CTTCATTTCAT	TTAGAAGCA	CAATTTAAC	160200
CTTCACTCTC	TATTTCTAAA	AGTTTCTTTT	CAATTTCTAA	AAGCTCCAGC	TCAAACTAC	160260

TGCTTTCAGC TCTAAACAT TCCTCTTCTT TGATGTGCTT CTCGTTGACA TCTAATATTT 160320
CCTTTTCTAT TTTAGTTTTA AGCCCATTA CATGTGTCAT CTTTTTCTA ATTGTAACCT 160380
CATCGTCAAT AATAACCTGA AGTTCTTTTT CAAGAGCCTC ATATTCTCTT TGCGTTTTAA 160440
TGCTATCAAT TTTTCTTCA GCCTTGCTCT TTCTTGAATT AATATCTTGA ATATCTAACT 160500
TTAAAGCAGA GTCTTCTTTT TGATACTCCT TAACTTTTG TTGCAAATCA ACAAGAACTT 160560
TCGACAATTC TTCAATCTGA TTTTTTTTCG CCTCCAAATA CTGGGAATA CTTTTTCGCC 160620
TTTCTTCAAG CTCAAACCTA GATTATATA TAACTTCAAG TTTTTTTAAT GTATCAATAT 160680
TGTTTTCCAT CAATCCTCCT GTTCAATTTA AATCTTCAAG ATAATCTTTT AATTTTTTGAG 160740
TTTTTTTGGG ATTTTGAAGC CGCCTTAATG CTTTAGATTC AATTGCTTA ATTCTTTCTC 160800
TTGTAACATT AAAATGAAGT CCAACCTCTT CAAGAGTTAA AGAATAGCCA TCTTCAAGTC 160860
CAAATCTCAT TTTTACAACT TCTTGTTCTC TTTAGGAAG AGTTCCAAGA ATTGCTCTTA 160920
TTTGATCTTG CAAAACCTACA AAAGATGTGT GATTGTCAGG ATTTTTTATT GCCTTATCCT 160980
CAATAAAATC GCTAAGAACA GAATCTTCCT CTTCTCCAAT TGGTGTTCAT AGAGAAACAG 161040
GTTCTCTTGA AACACTCTTT ACAGTTTTAA CCTTTTTAAG TTCCCATCCA AGCCTGTCTG 161100
AAAGCTCTTC ATCTGTGGGA TCTTGCCTA AAACCTGAAT TAAATATCTA GTTCTCTAT 161160
TAAGCCTATT TATTTGCTCA ATCATGTGCA CAGGAACCTT AATTGTGCGA GCTTGATCAG 161220
AAATAGATCT TGTTATGGCT TGTCTAATCC ACCAAGTAGC ATAGGTTGAA AACTTAAAC 161280
CTCTCTTATA TTCGAACCTT TCAACAGCCT TAATCAATCC AATATTGCCT TCTTGAACAA 161340
GATCAAAAAA ATGAAGACCT CTATTTGCAT ATTTTTTAGC AATGCTTACA ACAAGCCTTA 161400
AATTAGCCTT AATCAACTGA TCTTTAGCAT GCTGCATCAT TTGCTTCCCT TTAGCAATCT 161460
CTTCTGACAT GCTTATTATT TTATCAGTTG GATATTCATA ATACATCTCA ATTCTCTCAA 161520
GTTCTTTTTG GGCAAGCTGA GCCTCTGTAA TCTGCTCTTT AATAGCATCT TCTTTAAGCT 161580
TGAGAGATTT TTCTATCTCT ATTTTTTTTT CAGCAATAGT CAAATCTCTT CCAAGCACCC 161640
TCAAATCTCT TATTTTTTCA ATTTTCAGCC TGCTTAGAAT TATCTTTGT TGTCTTTGTA 161700
AATCTTTTAT TTTGTTAGCA GAGTCAATAT AATCATCTGA GAAAATCCTT AATTCCTCTT 161760
GATACAAAGG AATGTCTCTC AAAAGCTCTT TTAGGGCCAA TCTTTCCTTT TTAAATTCT 161820
TTTCAAAAAT ATCCCCCCA AGATCATACA CCCTATGCTT ATTATCTACA TAACTTATTA 161880
AACGATCTTG AATTGGCTTT AAAGGAATTT TGTA AAAAGA GGCAATTCTT TTTTTTTTAT 161940
TATAATAATC CGGACTACTC TCTTTATCCT TATCTTTTTC TCTTTTAAAA AACTCTTCTC 162000

TTTCCATTCT	TGAGTAAATA	GTATTCACAA	GATTATAATA	ATTTTCTATA	ACAAGTCCCT	162060
CATTCTTAAG	AATATTCTCA	ATTATACTCT	CTCCAGAATC	CATTTGCTTT	GCAAGTTCAA	162120
CTTCTTGATT	TCCCGTTAAT	AAAACTCTT	TTCCTATTTT	CTTTAAATAA	AGCTTGATTG	162180
GATCTTCTGA	GTGACTATCT	TTTAAAACAT	TGCCTTTAAT	ATACCCTGAA	CCTAAATCAT	162240
CCTTAACAGA	AATATCTTCT	TCATCACAA	CATCCAGCTT	AACATCAATG	TCAATATCTT	162300
CCTCATCACT	TTGAAAACCA	TCATCTAAAA	TCATAAAATT	TCTATCAGAT	TCAATCTCAA	162360
CCTCTTCCTC	TTCATCATTT	CCATCTTCAC	TGACAACCAG	ATCTAATTCC	GAAATTTTAT	162420
TAACCAACCT	TATTCCCCTA	TCCTCAAGTA	CCGAACAAAT	ACAATCAAGA	ATCTCTGGTT	162480
CTAATATATC	ATCGGGAAGC	AAATTTGATA	ATTCATAAAA	ACTAAGAGAT	TTTCTATCTC	162540
CCAAATGAGT	AATAATACCC	TCTATCAGCT	TCGAATATTT	CTTTTCCAAA	TCCGACAAAA	162600
CCTAACTCCC	TGGAACATCA	TCTATGTAGA	TTTTTTAAAT	TTTTCTCTGC	ATATTTAAAA	162660
ACATTAAGTC	ATTTATTTGA	ATCTTAGCAT	TTACCAAAGA	GTCCCCATCA	TATCTTTTTT	162720
TGCAAAGCAA	AACACGAGAA	TCTAATTTTC	TTCTCTTGAT	TGCAAGTAAA	ATATGAATGA	162780
GCATCTCATC	ATCCACTTCA	AATTCAGAAT	TTAAAATTTT	TTCAAAAAAA	ATTCATAAC	162840
TTTATAGGTA	TCCTTTAAAT	TTTTTTTTTAA	ATCCATTAAT	GAAAAATCTT	TATTATTTTC	162900
AAATAAATTT	TCAAAGCACA	TAAAACTTT	TCTGGCATCG	ACATTAATTA	AATCACTATC	162960
AATAATATTG	CGCCTTACTA	TGCTAAAATA	ACTAAAATTT	TTCAACAAAG	CTACTATTAG	163020
ATACCTCTCA	TAAGAATCAT	CATTATGAGC	ATACAAATTT	CTTTTATTAT	TGTCAACTAC	163080
AAATCTTTCT	TTTATTCTGT	AATAATCTTT	CAATAAAGTT	GTCACACCAA	TACCAAGTTT	163140
ATTGCTTAGC	TTGTCTAAAA	AAATTTTTTTT	CTGAGTATCT	ACTTTTGATA	AATTTATCAA	163200
ATTTAAAAAT	AAATTAATCA	TGGCATTTAA	ATCTACAGTT	TTATTTAAAT	TATATTTATT	163260
AGAATAAACA	TCCAAAAGAT	ATTCAAAAGC	ATCACATCTA	TTATTTAAAA	TTTTTTGCAA	163320
GGAGTCTACA	CCCTCACTTT	TAAGAACATC	TGCAGGATCA	GTACCAAAAT	CCATTCGAAC	163380
AACATAACA	TTGATATTAA	ACGGCAAACA	AATTTGATAA	GCTTTTAAAG	TTGCAGAAAG	163440
TCCAGCATCA	TCCCCATCAA	AAGAAAATAT	TATCTCATCA	GCATATCTTT	GAATTAAAGC	163500
TAAATGCTCT	TTTGAAAAAG	CAGTGCCAAG	AGTAGATACG	GCTCTCTTAA	TCCCAGATGT	163560
AAAAAAAGCA	AGAACATCTA	TATACCCTTC	TACCAATATA	ACTGATTTTG	TAGATTTAAT	163620
CTCCTCAAAA	CCCTCATAAA	ATCCATAAAG	AAGCTCCCTT	TTTTTAAAAA	CTTCAGTTTC	163680
ACCTAAATTA	ATATACTTAG	AACCTTTCCC	ATCTAAATCT	CGACCTCCAA	AACCAACAAC	163740
GTTTCCTTTA	AAGTCTTTAA	TTGGAAAAAT	TAATCTTTGA	AATAAAATAG	AAACTTTGGG	163800

ATTGGTTTTC GAGAACAAAC CACTTTTTCT AAGTACTTCA GAAGAGTATC CTTTGTAAAC 163860
TAAAAAATCA TGAAGCTCTA AACCATTTTT AAAGTTAAAT GGCAAATAAC CAAGTTCAAA 163920
TAAATCAACA ATTCCTTAG ATATTGCTCT ACTCTTTAAA ACATAATCTA AAGCTTTTTT 163980
GTTTTTACTT AAAAAAATT TAATGGTATT AATTAACCGA GAATTCAAAG AGTAAATTTT 164040
TGAAACCATG TCTTTATTTT CATTTTTATT TTCACTTCCT CGACTTATTT TTAAATCATC 164100
ATAATGAATA CCGGATTTTT CGCATAAAAT CTTAAGAGCA TCATTGTAAT TGATTTTTTC 164160
CATATCCATT AAAAATCCAA TAACATCTCC ACCCTTTTTG CATCCAAAAC AATAAAAATA 164220
TCCTTGCAAA GGATTTACAA AAAAAGAGGG AGTCTTCTCA GCATGAAAAG GACAAAGACC 164280
TTTGTAAGCA GATCCCGATT TAACAAGCTT AATATATTGC TCCACAATAG CTACAATATC 164340
AAATTTGCTT TTCATTGAAG CTACAGTTT TAAATACTTC ATACTTCTTA ATCCTTAGTA 164400
ATAAAATTTT TAATATAATC TTTTGCCCTT AAAAGATGTG AAGAATATTC TGATGAAAAT 164460
TGATGTGTGC CCAACTTAGA GTCTTTTACA ACAAAAAATA AATATTGCGT ATTTTTTGGG 164520
AAAAAAGCTG CTTGCAGCGA AATAATACCA GCATTTGAAA TTGGAGTAGG AGGATATCCT 164580
TTATTAATAT ATGTATTATA AGGAGAATCT ATCTCTAAAT CTGAAAAATA AATTCTCTTA 164640
GGATGGCTTC GTCCTAGCTC CTCTGTAATA ACATATTCAA TAGTAGCACA GGATTGTAAT 164700
GCCATACCAG ATTTTATTCT ATTATAAAAA ACCGAAGACA TTATTGGGGC TTCACTTTTA 164760
ACCCTATATT CACGTTCAAC AATAGATGCT ATTATTACCC TATTGTAAAG CTCCTTACTT 164820
GAATAATCGC TAAGAACAAC GCCTATAGAC TTAAGCTTAT TCAAAAAATT ATCAACAAAC 164880
ATGCGAACTA CATTCCTTAT TTCTATACCC TTATAAAATT TATAAGTATC TGGAAATAAA 164940
AATCCTTCAA GAGAGTCATA ATCAAGCCCA AGCTCATAAA TAAATGATTT TTTGTTGATT 165000
AAAAAAAAGAA AATCTTGAAC ATCATCAATA ACAGAAAATT CCTTAAGCTT TAAAGCAATT 165060
CTTCTGCTAG TATACCCTTC GGGTATTGTA ACATCAATAT TTACGTTAGA AGATCCCTTT 165120
AAAAACTCTT TATATATTTT AAATGTAGAA AGATCGCCAT TTATTAAATA TTTCCCTCTT 165180
TTAAATTGTT TATCACTACC TAAAATATAT GAAATAAAAA CAAGAAGCAG CTCGGATTTA 165240
ATTAATTTTT GTTTTTTCAA TTCTTTAGCT ATTTTTTTAA CTCCCCAACC TTTTCAATA 165300
TTAAATTCAT AACTAAGCC ATTTGCCAAA GAAGATAAAT TTAAAAAATA TATAAAAATT 165360
GACAAAATAG ATCCCAAAAA GAAAAAAGA ATAAACACTT TCCAATTTT AATAAGCACA 165420
AGAATCTCCT AGCTAAACAA AAGTCTTTGC TAATTACACT TTAGCTATCA ATTAAATTTT 165480
TTAATTGATA GCTAACATCA TATTTTATAA CCAATAATAA CTTTCTAAA TAGACAAAAA 165540

TAAAAGCACC AAAATGAAAC GACATAACAC ATTTAAAAGA TCACAATAAA AATTATAAAA	165600
AGGCAAACGC TTATAATTTC ACTAAATTGG GGAGGGTGGG ATTCGAACCC ACGTAGGCAA	165660
AGCCAACAGA TTTACAGTCT GCCCCGGTTA ACCACTTCGG TACCGCCCCA TAAAAGCCGA	165720
CTGTCCGATT CGAACCGACG ACTGCGGTTT ACAAGACCCG CTGCTCTGGC CAGCTGAGCT	165780
AAGTCGGCAA ACAAAAACTA ATAGTTAGTT TATAAAAAATA AAATTCATTA GTCAATAGAA	165840
TAATGATAAA TAATTAATAT AATCTTCCTA TTAATCTATT TATTACCAGA AAGAAAAATT	165900
TTAAAAACAA GAGCAATAAA AAAAATTATA AACTAAAAA TTAAAATTAA ATAATACTTA	165960
ATTTTTTTTAT TTTTCAAAAA ATAAAAAAAT ATCAGTCTAG TAGATTCAAG TCCAAAAGAA	166020
ACAGAGCTTA AAATAATAGC AAGATCAAGA TAAAATTTCT GAAAATTGTA AACAAAAATA	166080
TTGTAAGAAC CAGCCAAAAA CACGAACAAA CTTAACAAAG AATTTAAAAA CAATACAATA	166140
ACCAAAATTC TAATAAAATT TGAAAAACGT CTTAGATTTT TTAAGTTAAA AGCTTTTCATG	166200
AAATTTATAA ATTCTTTATT ATAAAAAGTG CTTGATTTAT GATTTCCAA AGATTGCCAA	166260
TAACATCGGC TAATGTAATT GTTTTATTTT CAGTTACCAT TGATTTGTAA GAAACCGTTA	166320
AAGATTTTCG AATAAAAACA TTATGATTTT CCAACAAAGA CAAGCACCTC TTTTAAAGCT	166380
CAATAAAATA ATCCACAAAT CTACTTGAAA CCTTATCAAT AGAAACGGAT TCAGTTAAGC	166440
ACCACTTCAA AATCCTTTCC TTATAAGAGT TATCAATTTT ACCGTCTCTT TTATACCTTT	166500
CAAACTCTTC ATTTTATAA TCAATCTCAA AGTAAATATT ATAAATTTCT TTTTCAAAG	166560
CAGTAATATT ATTTTCAATG TCAACATATA TATTTCTCAA ATCATGATTA TTGATTAATA	166620
CGACATTATT TATAGTTCTT AAACTTCCA TCATTCTAAC ATCATATATG TTTTAAAAA	166680
AATCATTAAG AAAATATAAC TTTTAAAAAC TATAACGCCC AAGATTTAAT TCATTAAAAA	166740
TCTCGCCTTT TAAATTTAAA ATTAACTAG GATCTCTAAC AAGATTTTTT ATTTCTTTGA	166800
TAACAAGAAC TTTTAAAGAG CTATCACGCT TTTTAATAGC CTGACCCATA ACATTTAAAA	166860
ATAAAATGTT CTCATAAAAA TTTTTCACAT CAAAAAAGG TACATATTTT TTAGGAGATG	166920
CAACAGGATT TTTGCAATAT ACTCTAAAAA TATCTAAATA AGGCAAAGTC CTCGACAAGC	166980
CAACAATCTT AGATACAATA GATAAACAT TTTTAAATAC ATATTCTACC CGAGATATAT	167040
GATCTTCTCT TGAAATTATC TCTGAATTAC TAATATCATC AGATATTGAA AAATAATTCTG	167100
ATATAATGCT TTTAACAATA TCCTCATCTA TCTCAATATC TTTTAATGTA TACAAAATGT	167160
CAAAAAAGA ATTCAAATAC TTAATAACAC TTGAAAAGCT GGTTCCAAAT CCAACCTCAA	167220
AGTCAACAAT GCTAATATTC TCAGCACTAT CTAAAAGATC TACATTAAAA AATGAAAAAA	167280
AAGATTTGTA AGGGAAAAAC GCCAACTAT TAAAAACATA ATAAAACTCA AACATATCCG	167340

AGACGATTTT GTAAGTACTA GATGGAATAG AATTAATATA TTCATTTATC TTGACCTTAA 167400
GAGATTCTTC TAAATCGTTT TGGGTTTTTT CTTTTTTTAA AAAAAGCTCA TATTCACCTT 167460
CATCTAAAAA ATCTTCCAAA TTGTTCTTAG AGTTAAGAAC TTTGCTTTGA ATAATTCTA 167520
AAATAGTTTG CTCAACAACA ATACCACCTT TTTCTAATTT CCTAAAAAAT TCTTTCAATT 167580
CCATTGAATA TCGGCAAACA CTAAAAACA TTTCCACAAA ACCAACATGC AAACATTCTC 167640
TCTTAAAATC TATTACTGGA TTTTACACA TTTTATTAAT TTGATTTTCC AGGTTTTTTA 167700
TAACATAAGC TTTATATATA TCTTCTTGC TTTTATCTTT CTGAAAAAA TTTAAAATAG 167760
TTAACCACAT TCTAATAAGA AATGATTCTT CCATTAAGCG CCCCAGAAAGA AATTTTTCAA 167820
GCTGAGAATC AACATAAGGC TCATTACTAC TATTGGGCAA AACAAAATCG GAAGAATTCA 167880
AACCTAAGCT TTTTCTTATA TCATTCATCA ACCTATCTTT AGTCTCTTTT GAAAGTTGAC 167940
CTATAGAGTT GTATACGCTA TTGTTATTAC CACTCATAAA ACCCCAATAA AACCATTTAA 168000
AAAATAAAGT ACTACTTACA ACATACTTCA AATAAATTAA AATTGTAAAT CAATTTTAGA 168060
AAAAAATTAT TTACACTATA ATATAATTTT ATATGAATCT AGGGAAAAAC AATCCAAATA 168120
TAATTAATAA TGGTAAAATA TTTAAAAAAA ATAACTACGA ATTTTATTTA GTTGGAGGCG 168180
CTTTAAGAGA CTTACTGCTT AATAAACAGC CTTACGATTT TGATTTTGCA ACAAATGCAA 168240
CTCCTGAAGA AATAATAACA TTATTTCCAA ATAACATCAA AACAGGAATA AAACATGGCA 168300
CAATTGGTAT TATTTTAAAT AAAAAAATCT TTGAAATCAC CACATACAGA ATAGAAAAAG 168360
AATATGAAA CAACAGAGCC CCCAAACAAG TAGAATATAC TAAAAATTTA CTTAAAGATC 168420
TTGAAAGAAG AGATTTTACA ATTAATGCAA TTGCAATGGA TATTTTCAAC TTCAACATAA 168480
TAGATTGCTA TAATGGGAAA AAAGACCTTA ATAAGAAAAT AATAAGATGC ATAGGAAATC 168540
CAAACAAAAG ACTTGAAGAA GACGCCCTTA GAATACTTAG AGCAGCAAGA TTTTCATCCA 168600
CACTTAATTT TAACATTGAA AAAAATACTT TAATTTCAAT GAAATATAAA AAAGAAAATA 168660
TTTTAATGAT TTCAAAGAA AGAATAAAAA ATGAATTTCA CAAATTGTGA GAAGGCATAA 168720
ATATACAAAA AGGAATTTAT TATCTTAAAA AAGTTGATTT TTTTAAAAAT TTTTTTAATC 168780
TAGAAATAAA AACAAAAGTA ATCAAAAAA TTGCTCTACT TGATAAAAAAC AAATTTTATC 168840
TAAAGGCAAT CACAATATTG ACAATTAAAA AACCTATAAA AGAACTAAAA GAAAAATTAA 168900
CTTACTTAA ATTCTCAAAT AAAGAAATTA AGCTGATTTT ATTTTATAGA GGCATAATCG 168960
ATAATAACAA TATTTTAAAT GTCAAAAAAT TAAGTGATAT TAGATATTTG CTTAGCAAAA 169020
GCACAAGAGA ACATTATAAA GAAATAATTG ATATATACAA AGCACTCAA GAAAAAATA 169080

AAAGATATTT ATTTATAATA AAAACATAA AAAGAAAAAA ATTGCTAAAA AATCCTCTCT 169140
CTTTAAAAGA TTTAAAAATA AACGGAAAAG ATATTCAAAA TCTAGAACAA ATAGAAAACA 169200
AAAATATAGG TAAAATTTTA AATATGCTAC TAAGATGTGT AATTGAAAAT CCCAAGCTTA 169260
ATACTAAAAA TTATCTTATA AAAAAAATCA AAACCTTAAA GGTTAATGTT TTCCATAGCT 169320
TTTAAAGCTA CTTCAGCCGC TCTCATTTCG GCTTCTTTTT TAGATTGCGC CTTTCCATTT 169380
GATATAAAAT TTTCTCCAAC ATAAAGTTC ACACAAAAAA CTTTATCATG GTCTGGACCT 169440
ATTCCTTGT CTAGCTTATA ACTTGGCGAG ATTTTATATT TCTTTGAAC ATATCCTTGC 169500
AACAACTCT TATAATCTTT AAAATCCCC CTATTAAACA TCAATCTTAT ATACATATCA 169560
AAAAGTCCAA CCACAAATTC TGTTGCTCTT GAAAACCCAC TATCAAGATA AATAGCGCCT 169620
ACAAAAGCTT CAATAGCATC TGCAAGAATG CCTTTTTTAT TTCGACCATC ATTACTCTCC 169680
TCCCCTCTAC CTAGCAAAT ATAAGAACCA AGATTAATCT CTCTAGCAAT ATTAGATAGG 169740
GAATCTTCAC TAACAATATA AGATCTGGCC TTACTGAGCT CTCCTTCACT TTTATTTGGA 169800
TAAGTTTTAT AAAGATGATC TGTAATAATC AAATTAAGCA CAGAATCTCC CAAAAATTCT 169860
AATCTCTCAT TATTACTAGA TTTTGTATCC AACTCATTAG AATACGACGA ATGACACAAT 169920
GCTGTATTCA ATAAATCAAA ATTACTAAAG TCAATGCTCA AATTTTCCAA AAATTTACTC 169980
AATTGAGATT TTCTTTCATT ACACAAACAA AAATCAGAAG ATTTTTTTTT CATCAACCCT 170040
TTCTCTTTTT AATAAAATTA ACAACATCGC CTACCGTCTC AAATTCATTG GCTTCATTCT 170100
CTGGAATCTT ATCATCAAAG GCCTCTTCAA GCAAATACAA AAGCTCATAA ATATCTAGAC 170160
TATCTGCATT AAGATCTTCA ACAAATCTAG AGTCTGTGGT AATTTCATCT TCTTTTTTAT 170220
CAAGTTGCTC AGATATAATA GACCTAACCT TGCTAAAAAT TTCATCATTA TCCATGAATA 170280
CACCTTCCTT ACTACAAGCT ACAAACCTAT TTCTAGATAT TGGTTATTCC TATAATATCC 170340
ACATTTTAAA CAAATCCTAT GTCTCAGCC AAGATTACCA CAATTAGAAC ATTCTTGAAA 170400
TTGTGGAATT TTTTTTCTCA TATTTATACT CCGCCTTGTT CTACTTCTAG ATTTTGAAGG 170460
CTTAAATTTT GGAACAGCCA TTACTTTCTC CTAACACTT TTAAACTACA TTAAATTATC 170520
TTAATAATAT ATATATTAAC CAAGTCATTT GTCAATAAAC TTAGATTTTA ATCTATTA 170580
CACCAATTCT GGAACAAAAT TAGAAAGATC AACATCCTTT TTCAACATCA ATTCCTTTAC 170640
AAAATCCGAC CTTACATATA AATGTTCTGC ACTACTTGGT AAAAATATAG TATCAATTTT 170700
AAAATTTAAC TTATTATTAA CAAGATATCT TTCAAACCT ATATCAAAAT CATTAAAAGC 170760
CCTAATTCCT CTAACAATAA ATTTAATAGA ATTAATTAAT GCATAATCAA CAATAAACCC 170820
GCTATACCTA TCTACAAGCA CATTTGAAAA ATTTAAAGAC GAAATAACAT CTTTTGTAAG 170880

GCTAAACCTC TCAATATCAC TTAGGAAATA TTTTGTGAT TTATTTTGTAG CTACTAAAAC 170940
AATAACTTTG TCAAAAATAG CCAACGATCT TTTAATTAAA TCAATATGAC CCCAAGTAAT 171000
TGGATCAAAA GATCCTGGAA AAACCTGCCAC CCTCATATCA AGAAAGCCTA AACCCCTAT 171060
TAATATCTTT GAGAATTTTT TTACGCCATA GTGGTTGTTC TTCTAAATTT TCAAATTCAA 171120
TTTCTTTAAT AATTTTGAAA TATAAATATT CTCCTCTAGA AGATGTATCC ACAATAAAAA 171180
ATTTACCAGC ACCTTTATAA ACTACTTTTT CATTACTTGA AAGATTATTT TCAGATGTTA 171240
ATTTATTGAT AACACAATCA AAATGAACAG GTTTATCTTC ATTTTCAACC TTTAAAGACA 171300
TGCTATAAAC AATATCATTT ATTTTTTTTT CACAAATAGC ACAAGCAACA TCAAGATTTA 171360
TTCTTGTTTT AAATTTTATA CTTTTTCTTC TAAATTTACC TTTAAAAACA TTTTGTTTTAT 171420
CTGTATTCAA GACAGTCGAT TTATTATTAA AACTGTTTAG CGGGGCAACA TTTTGACTTT 171480
TGCTCTCAGA ATTTAATCTT TTATTCTTAA AACCATAAAA ACGCTTATTG TGTTTCTGAA 171540
AATTACTACT CTTGAACTTA CTTTGAGTAT ATTTCAAAAAT TAACTCTCCT TAACTATAAA 171600
AAATAAATAT TTAATCTTCA AAAAAATAAA AACAAATATT TAAGAACAAA ATCACTCACA 171660
TAGCCTGAAA GTTTTTTCAA AAATCAAAAC TTTAAATCTT CAGCTTTTAA AAGACAAAAG 171720
CACAATTAAA CCCTCATTGA AATTTAATAA GAATGGTTAA TTAATGCTCT CAATTATAAT 171780
AAATACACAA CCAAGCTTGC CAAAATTATT TCCCAAAACA GCAAAACTC TACTAAATCT 171840
TGAATAAAAA TTTACAAAAC AAAAGATCAA TCAAAAACA TTTTAAACCT CAATCTAATT 171900
TGATTCATCT TATGACCTAA TTTGCTAAAA TATTTAAAT AATTAAAAAC TAATGCTTAA 171960
CTTTTTTAAT AGTAAGGCGC TCCTTTATCT TCATAGCAGC CTTACCGATT CTATTCCTCA 172020
TATAATAAAG CTTTGCCCTT CTAACCTTTC CCCTTCTTAA AACTTCAACC TTTTCTATAA 172080
TAGGAGAATA TACTGGGAAA ATTTTTTCAA CACCTATTCC TGAAGAAATT TTTCTAATCA 172140
AAAATGTTTT GCCAATTCCC TTGTTTTGGA AAGAAATAAC AATCCCTTCA AAACCTCTGCA 172200
ACCTTTCATT ACTACCCTCA ATAATTTTGT AAACAACCCT CACAGTATCT CCCACATTAA 172260
AAACAAAAGC CTCATTTTTT TTATTCTGAG CTTCAATTTT TCTTATCAA TCCATTATCT 172320
TCTCCTATTA TCTCTAAATA TTTAAGGTAT AAATCATATC TATTTTCTT AGTTTTTCT 172380
CTAGCTTTAA CAAGCCTCCA ATTCTTTATA TTTGCATGAT GTCCCGAAAG AAGAACTTCT 172440
GGGACCTTTA TCCCCTTAAA ATCATAGGGC CTGGTATAAT GAGGATATTC AAGCAATCCA 172500
TTTTTTACAC CAAATGATTC TTCTAATAAA GAATTGGGAT TTATTACTCC ATCTAGCAAC 172560
CTATATACAC TATCTATTAA AACAAAGAGCT GCAATCTCTC CTGAAGATAA AACATAATCT 172620

CCAATAGAAA TCTCAAAATC AACATACAAA TCTATAATAC GTTGATCAAT TCCTTCATAT	172680
CTTCCACAAA TTATAACAAT TTCTTCTCTT TTTGACAAGG AATACGCCAA CTCTTGGCTA	172740
TACTTTATCC CAGAAGGACT TAAAAATATT GTCGTTTTCT TGGCAGACTC TACATGCTCA	172800
AGAGCAAAAG AAATCGGTTC GGCCTTCAAT ACCATCCCAG CACCGCCTCC ATAAGGCAAA	172860
TCATCACATC TTTTATGCTT ATCTTTTGAA AAATCTCTAA CATCAACAAG CTCAAAACTT	172920
ACTATCCCT TATTAATAGC TTTTTTCATT ATTGAATTTT CAAAAATGG CTTAATTATT	172980
GCTGGAAAAA GGGATAAAAC CGTAAATTC ATTTTAAAAG ATCTAGAACC TTAAGCTCAA	173040
TTGTTTTTTC TTGAGTATTT ATATCTCCAA TATATATACT TAAAAAGGA ATAAAGAAAA	173100
ATTTAATACC CACTCTGACC TCAAGAAATA CACTATTTAA ATATTCAAAG AAAGCTACAA	173160
CTTCTCCTAG TTTTTTATTA TTATTAACAA TGGCATAGCC AATAAGCTTT CCTAAATAAT	173220
ATTCGCCTTC TTTTAAACTC GATGCAAGCG AATCATCAAC CCACAATTCA AAACCAATCA	173280
GCGGCCTAAC TGCCTCTGGA GTATCAATCT CTTCAAACTT CAAAAATAAG GAATTACCCT	173340
TTATATTAAC ATCTACAACT TTAACCTCAA CACTGGAACCT ATTGCTTTTT TTTAAAAGAA	173400
CTTTATTGTT TTTTAGATTA ATAAAATCAC AAAAATTATT GGATATGCTT TTAACCCTAG	173460
CATACCCATT AACTCCATAA GACGATAATA TAACGCCTTT AATAAACATA GATTAATCTA	173520
AAATTTCCAA TTGCACTCGC CTATTGGTTT TGGCAGCACA AGCTCCAAGC AAAGTTCTAA	173580
TAGCCCGCGC AATACGACCC CGTCTTCCGA TTATCTTGCC CACATCACTT TGAGAAACCC	173640
TTAATTCCAA AATAGTTGAT TTTTCCCCTT CAATTACATT TAACTTTACT TCATCTTCTT	173700
TATCTACAAG AGACTTTACT ATAAACTCTA TAAGTTCAAT CTCATTCCCA TACTCTTTCA	173760
TTTAAACCTC CTGACTTTTC GCATTCAAGT TGTTTTTATT TAAAAGCATT TTCACTGTAT	173820
CACTTAAAAT TGCTCCCTTG CTTATCCAAT CTTTCATTCT ATCTTCCTTA ATTTTTATTT	173880
GGTTTTGCTT TTCAACAGGA TGATAATAAC CAAGTTCTTC AATTGCTCTA CCATCTCTAG	173940
GAGACGTAGA ATTCATAACT ACAACCCTAT AATAAGGTCT TTTTTTAGCT CCCATTCTTT	174000
TCAATCTTAT CTTAACGCTC AAATTTATTC CTCCTTATTT TCCCAAAGG GATGCAATCT	174060
TATTTTGAAA ATCTTTATTT TTCATTTTTT TCATAATCAA AGTTGCTTGA CTAAACTTTT	174120
TTATGAGCTT ATTAACATCA AAAACAGTTG TTCCACTTCC CATGGCTATT CTTTTTTTTT	174180
TTGAGGGATT ATTCAAAATC ACTGGATTTA TTCTTTCTTT TTTAGTCATA GAAAGAATAA	174240
TAGCTTCTTC TTTATTAAAA CTTTCTTCAT TTAAATTATT GCTATTCAGC ATTGATTTTG	174300
AAACACCTGG TAAAAAACTT ACAAATTAG AAAACCCTCC TACTTGCTA ATGCGCCTAA	174360
ATTGACTCAG ATAATCTTCA AAATTAAAAC TGGCTTTATT AATTTTTTCT TCAAGCTTAA	174420

TAGCCTCTTC TTTGTCAACA ACACTTTGAA CCTTCTCTAC AAGACTAACA ACATCCCCCA 174480
TGCCAAGAAT TCTAGAAGCA ATTCTTTCTG GGTAAGGA ATCAAGATCT TCGATTTTCT 174540
CTCCAACACC AATAAATTTA ATGGGAACTG CACAAATACT TTTAAAAGAT AATACAGCTC 174600
CCCCCCTAGT ATCTGAATCA AACTTAGAAA ATATTGCACC GGTAAGTCCA ACATTCTCAT 174660
TAAATTCCCTT AGCAATATTT ACAGCAACTT GCCCATCAT AGAGTCTACT ACTAAAATGG 174720
TTTCTGCGGG TCGCAAAATC CCCTTTATTT TTTTATCTC TTCAACCAAC AAAGATTCAA 174780
TTTCAAGTCG TCCTCTAGTA TCAACTATTA CAGAATCAAA AAAATTAGAT TCAGCAAAT 174840
TCATAGACGC TTTAACAATT TTAATAGGAT CTTTTTCCCC TTCAATTGAA AATACTGGAA 174900
CACCTACTTG ACCACCCAAT ATTTTAACT GTTCTACGGC CGCCGCTCTA AAAGTATCAG 174960
CAGCTACAAG AAGTACTTTT CTATTTTCCT TTTTAAGCTT TAAAGAAAGC TTGGCGCATG 175020
TCGTGGTCTT GCCAGAACCT TGAAGTCCCA ACATAAGAAT ATAAGATTGC TTATTGGCAG 175080
GATGTAACT AAGCTCATAA TTTTGCCTC CAAAAATTT AACAAGATTA TCATTGACAA 175140
TTTTAATAAA CTGAGATTTA GGATCAATGC CCCTTAAAC TTTTACTCCC TTGGATTCTT 175200
CAATTATAGA ATTTAAAAA CGCCTTATAA CTCTTAAGTT AACATCAGCA TCAACTAAAG 175260
AATTTTTAAT AATCTCAATA GCCTCTGCAA TGTTTTTATC ATTTATCGTA GATTTTCCAG 175320
AAAGATAGTT TATAAAATTT CTAAATTTG ACCCCAACT TTCAAGCATT AAAACAACC 175380
CTTATTCTCA AAAATAATCT TGTCAAATAT AAGATACAA AAAAGGCAAT ATTAATCAAT 175440
ATCTCCTCCA GTCAAATAAA ATTTATTAAA AATAACACTG GAAGCGGGCC CAACAACAGA 175500
AACTTCAGTA TCTAATGAAC TAAGCTTTAA TACTATATTC TCTTTATTGA GCTTTTAAAT 175560
CTCTCTTTT AACAAATCAA AAAAAGCTTT TAATTTAAAA CTTTGACCAT AGAGTACTAA 175620
ATAATTAAAA TCAAGCATTC TTTGAATATT AATAATAATT ATTGCCAAT ATTTAACAGT 175680
ATCTTGATA ATTTTATTTA TAAAATCATA TTTTTCATAA AGAGAAAAA TGTCATATAT 175740
TGTAACCTTT TTCAATCTGC CCTCATACTT TTCATAAAGC TCAGGAATCT CACCATTCAT 175800
AAATTCTTTG GAAATCAATC TCTGCAAAGC AAAATTAGAT ATTAGCATAT TGACACAACC 175860
CTTATTACCA CAAGTTGGAC AATTTTTTTC TCCCTCATAA TCAATTATCA TGTGACTAAC 175920
CATACCTGAT TTATTATTAA AACCAGGGTA AACATTGCCG CCTGACCAA TCGAAAGTTC 175980
AGCAGTATCT GTGTAGTCAA AAAACATAAT ATTATCTATA TTTTACCCA TAAATTCAGC 176040
AAGAGATAAA TTTTAAACAT AACTTTCAAG ATAACTGTT AGTGAAAAGT ATTCCTCAAG 176100
TATTCTCTTA ACAGGAACAT CTTTTTCAAT CCACGATCCA TAGCTATCAT TAACAATGCC 176160

CAATTCTTTA TCCTTTATTA ACCCTGTAAT ACTAAAGCCT AAGCCAATAA ACTTATCTCT	176220
TGAGAAATTA TGTTTCCAAA TAATTTCTAT CATATGATCT TTTATTTTTT CTAAAAATATC	176280
ATAAGCGCTA ACTGGGGGCT CAAAAGAATG AGTCTCGCTT ATTAAACCT CGCATTTAAG	176340
ATTGGCAATA CCTATTTGAA AATAATTGCT AGAAATAATA ACTCCCATTTG AATACGCATA	176400
ATCTTTATTA ATATCGAGAA GTATTTCTTT TCGTCCATGT TTTTAAACAT CAGACACCCCT	176460
AGAGCCAAC TCAATCAAAA GATTTTCTTT TATCATTTGA TTAGTCAAAA TAGTAACTGC	176520
AGCATTTGTC AAGCTTAACT TACGAGCCAG GTCTGTTCTT GAATATTGCA TATTTTTCAA	176580
ACTAAGAAGA ATTTTCTTTC TATTTCCGCC TCTAATTGAA ACCATATTTT CACCCTGCAT	176640
AATACACCTC CTTTATTTTT AAAATAAAAA AAATATTATA AAATATCATA TCAAAAAAAC	176700
CAATACAATA TTTTATCTAT TCTTAAAAGA CAAACATGCC TTTATAAGGC TAAAAAACAT	176760
TTTACATCAT AATATCACAT TCATAAAATA TCAAAAACCTT AAAGCTTAAC AAAAAAGGGA	176820
ATAAAATCAT TTTTACATAA AAACATCA CAATAAAATTA TTGGATTTAA AAATAATAAA	176880
TACAAGAAAA GCCATTTTGC CTTAAAAACC ACTAACTTTA ACTTAATTTT TCCTTAAAT	176940
AAGAAAATTC CATAGTAAAA CTGCCCCTTC CTTTAGTAGA ACTTCTCAA ATAGAAGCAT	177000
ACCCAAAAAG TTTCTCAAAC GCCGCCTCTG ATTTTATCAA GTCATACTCT CCAATATTGC	177060
TAACTGAATG AATAACACCC CCCATAACAT TTAATGTAGA AATAATTCG CCTGTATGCT	177120
CAATGGGTGT TCTAATTTCT AATAACATTA TTGGCTCAAG TCTAATAGGA TCTGATTTTT	177180
GAAAAATACT ATGAAAAGCA AATCCTGAAA TTGACTCAA AGCACTCTCG CTAATCTTAT	177240
TGGCCCCACA AACAATAGAA AAAATACTAA CATTAATATC AATAATGGGA TATCCAAAAA	177300
TTCCACTTAC AAATGCAGAT GTAATTCCCC TCAATATTGC AGACTTAATT ACAGGTTCAA	177360
TGCCACATTC AAAATCAATT TTATTTCCCG CACCCCGCGA CAAAGGTTTA ATGATCATTC	177420
CAATTTTAAA ATCAATATTT TTGCCAGCAA AAATATTGTT AACTCAAAA ACTTCTTTTA	177480
CAATTTTGCC AGCACTTTCT CTGTAACCTA CTTGAGGCTT TCCTGTATAA ACATTAAGAT	177540
TAAATTCATC TTTAATCTT GTTAAAATAA TCTCAAGATG TAATTCACCC ATTCCAGATA	177600
TAATTAATTG CCCTGTTTCT TTAATCTCAG AATAACTAAA GGATAGGATCT TCTTTAGATA	177660
TTATTTCAA AATTTCCCTA AGCCTAACCT CATCTGATGA TCTTTCAGGC TCAACAGACA	177720
TTAAAACAAC CGGCTCTGGA AACATAACAG CCTCAAGTAA AACATTATTA TTCTCTTCAA	177780
CAAGAGTATC TCCTGTAACA GAAAACCTTA ATCCCAAAAC AGCACCAATA TCGCCTGTTT	177840
TTACAAAATC TATTTGTTCA TTTTATTTG AAAAACTCT AAAAATTTT GTAAACTTTT	177900
CACGCTTACC ATTTGAAGCA TTGATAATTT TTTTATTAGG ATTAATCTCG CCAGAATAAA	177960

CTCTAACAAA ATAAAGATGA GAAGCAATCA CGCTTGAATA TTGAACCTTA AAAACAAGGG 178020
CTGACAATTT TTTATTTTCA TTAGGATCAA CTAAAATTTT TTTATTTGTG TCTAAAGAAA 178080
AAGCGCTAAA ACTTTTTTCA AAAGGACTTG GCAAGTAATC TACAATCGAA TCAATCAAAG 178140
GTTCTATTCC AATATTTTTT AAAC TAGTTC CCATTAAAAC AGGAATAATA AATCTAGAAA 178200
TAGTGCCTCT TCTAATCTCT CTTTAAATAA TATCTAAACC AATCTCTTTG TCTTCAAGAA 178260
ATAATTGAGT AATTTCTTCA CTAAATTGGC TAAGAATGTC TATTAATTTT TTTTAAAAA 178320
GAATCACTTT TTCAATAAAT TCTTCTCTAA TTTGACTATA AGTTAATTTT GGAATTCCAT 178380
TTTCCATTGA AAAATGAAGC TCTTTATTTA AAATAATATC AACTACTCCT TCAAAATTGC 178440
TTTCATTTCC AATTGGAATT TGCAAAACCA AAGGAATAGT TTTAAATTTA TTTTCAATAT 178500
CTCCCAACAAC TTTAAAAAAA TCAGCACCTA TTCTATCCAT CTTATTAACA TAAGCAAGTC 178560
GTGGGATTTC GTATTTTTCT GCCTGTTTCC ATACAGTTTC TGTTTGGGCC TGAATTCCAT 178620
CAACAGCGCT AAAAATAACA ATACCCCCAT CAAGAACTCG AAGAGATCTT TCAACTTCTG 178680
CTGTAAAATC CACATGCCCCA GGAGTATCAA TAATGTTTAT TTGGCAATCC TTCCAATGAC 178740
AAGTAATGGC AGCTGAACTA ATAGTAATTC CTCTTTCTTG CTCTTGAGGC ATCCAGTCAG 178800
TAATAGTGTT TCCTGAATCT ACATCCCCCA TTTTATGACT TTTGCCAGTA TAATAAATAA 178860
TTCTTTCTGT GGTAGTAGTT TTTCCAGCGT CAATATGAGC CATAATTCCA ATATTTCTAA 178920
TACTCATAAA TCCCCAACAA CTACCACAGC CTCAATGCAG ATAAATTCAT TAGCACAGGT 178980
TAAACCTTTT AATAAAATTG CTATTTTGCA TCACACTCGC AACATTTGCT TTCATTCTCA 179040
TCGTGACAAA AACAATCGCA ATTTTCAAGC AATGCCTTAT GCATCCATAA ATGTTTCTCA 179100
AGATCACTCA TGATATCATC CATAATATTA GCAGTACCAT AATCACCAGC AGTATCAATT 179160
AATTTTCTCA TTCCAAAAAT ATTCTTCAAA ATCTCAGTAA GACTGCAAAC AATGCTTTCC 179220
ATTGAGGGCA AAAAATTAGA AGTTGATTCA ATATCAAGCT CCTTAATAAA GGATTTTTTC 179280
ATAAACTCAG AATATCTAAA TTCAGAATCA TATCCAAGCA TTCTTGAGCG TTCTGCAACA 179340
ATATCAATAA TTTTTTCAAT ATATTCATAA AGTTTTTGAG TTTTTTTGTG AATAACAAAG 179400
AAATTGGTAT CTTTTATATT CCAATGAATA CCTCTTAAAT TAGAATAAAA AATATGCAAA 179460
CTTGCTAACA ATTCTTGTA TTTTAATTGT ATTGCGTCTA AATCATCCTT TTTTATATAG 179520
CTTAAATACT TTTCCATAAC TATCTCCTTT ATATAATTAT TATAATACAT AATGAGATAT 179580
AATTATGGTT TTAATACCAT AATAAATAA AAGGATATTT AATGAAAAA TTGATTATAA 179640
TTTTTACACT GTTTTTATCT CAAGCATGCA ATTTAAGTAC AATGCATAAA ATAGATACAA 179700

AAGAAGATAT GAAAATTCTA TATTCAGAAA TTGCTGAATT GAGAAAAAAA TTAAATCTAA	179760
ACCATCTAGA AATAGATGAT ACCCTTGAAA AAGTTGCAAA AGAATATGCC ATTAACTGG	179820
GAGAAAATAG AACAATAACT CACACCCTTT TTGGCACAAC CCCAATGCAA AGAATACATA	179880
AATACGATCA ATCCTTTAAT TTAACAAGAG AAATACTGGC ATCAGGAATT GAACTTAACA	179940
GAGTAGTTAA TGCATGGCTT AATAGTCCAA GCCACAAAGA AGCTCTTATT AATACAGATA	180000
CCGATAAAAT AGGTGGCTAT AGATTAAAA CGACTGACAA TATAGATATA TTTGTAGTTC	180060
TTTTTTGAAA AAGAAAATAT AAGAATTGAC ACCATTAAAG CTTATACTGT ATACTACTTA	180120
TTAGTAATAA AAGGGCTCAT AGCTCAGTTG GTCAGAGCGC CTGCCTTACA AGCAGGATGT	180180
CGGGAGTTCTG AATCTCTCTG GGCCCCAAAA TAATCTAAGT CTCAATTACC TTTAGCTTTA	180240
AAAGCAAATC TATTTTAGAA TCTTTAAGCA TGTTATTTAA TTCTTTTTGC ACTATATTAG	180300
CTTTTATTAG GCTTTCAAAA AGAAAAATAA ATGCTCCTCC TTTACCAGCG CCACTTAACT	180360
TACCAGAAAG AGCGCCCAAT TTGATTCCCT CACTTATCAG CCAATCAAGA GTATCATTAG	180420
ACAACCCCAA ACGCTTTAAA CAACATTGTG CAATATTCAT TTCATTAGCT AAAGAATACA	180480
CATCCTTATT CTGAAAAGAA GCATAAGAAT TGCTTACGGC AAGGCCAAGC TTTTCAATAA	180540
AAACAAATAA ATAAGCATTT GATAATAGAT CTTTTTTCAA ATTAACAACT ATTTCTTTAG	180600
TTGTAAATC TCTTTTTATT GCTCCTATTA GAAAATAAAA ACCAGAATCT TTTATTTTCT	180660
TTGAATGTAA AACATTTTCT TTTTCTCTA AATAAAAAGT TCCATTAAGA TCGATTAGTC	180720
TAATATCCAT TCCAGAAGAT TTGCCATGAA AAATGTTTTT AATTGATTT GCCAACAAAA	180780
TTTTATTACA ATCCTTATAT TCAAAATGAC TTGTAATATA TTCTGCAAAG CATAAACTAA	180840
GACTAGCAGA AGAACCAAGA CCAACTCCAA TAGGAATTTT AGAAATTATA TCAAACTCAA	180900
TAGGATTAAC TTTGCTATAA TTTGAAACAA TAAACTTAT AAGGCTATTT AATCTTGATC	180960
TGGGTTTTCC TAAATATTTT CAATTTTTAG ATACACTATA AATCAGATCC ATATAAATTG	181020
GAACTGTAGC GCCAATAACT GGGAACCCAT AAACAGCGCT ATGTTGCGCT AAGAACAATA	181080
TTTTAGCAGG CTTTCTTATT CTTAGCATTT ATCGCTTTCA AACTTAATGC CTTCAATCTC	181140
TAAAACAATT GAAATAATTT TTGACAAATT AAAAGCTTCA ATATTGGGCC TGTAAACTAA	181200
AAAAGTTTCG TTTCCGGCTC CCAAAGCTTT AATCAAATCA CATTGACCTA AAAGGTGATC	181260
AAAAC TTGAA GGCAAAGCTG CCGAAACTCC TATTGCCTCT CCAATTGCCA ATCCCAATTC	181320
TTTAGCCCTT CTAAACTAG AAATTAATGC GGATTGGAAT TTGCTAGCAT TTAAAACAAG	181380
CTTTTTCATC TCCAAATTGC ATTTCAATAT AAAATCTAAA ATAGAATTTT TATGTTTTATT	181440
GTATTCACAA ATAGACGTAG TAGTTTTAAT TGCTTGCAAA CCCTGCATCA AATAAAAATC	181500

ATTAACTCT	ACAGCACCCA	GCTGCCTGCA	TTTAGGATTA	AAGCCGCCTT	CAAACCTCAAT	181560
AACACCCCCA	AAAATACTAG	TAGCAATATC	ATATCCACTG	CCTATTCCTC	CTTGAGAATA	181620
CCTGTAAGCT	TCCAAACAAT	ATTTAAAAAT	TTCACCTTTC	TCAACAACAT	TGGTAGCATT	181680
GTGAATTAAA	AAAAGCCCAC	ACACTATGCC	AATAGCAACG	ACAGCACTTG	AACCAAATCC	181740
CTTTTtagTt	CCATCATTAA	AGAAAAAATT	ACTTGTATCA	ATATATACAT	CATACGCAAA	181800
ATTCTCTAGA	TTAAAAAAAC	AATTTTGA CT	CAAGTAAGCA	AACATTTTAA	AAACAAAATC	181860
GCTTCTATTT	TCTATTAAAG	AAAAATCGTC	TATTTTTTTC	TTTTTACTAA	AAAAGCGCCA	181920
AGAATCGCTC	TTTTTAAAG	AAAAAATGC	TCTCTGTGTTG	ATGGCAATTG	CCAACCCCAA	181980
TCCCTTTTCC	TCTAAATAG	TATACTCCCC	CATTAAAAAGT	AAATTTCCGG	GTACAGAAAA	182040
ACTAATCAAA	TCCATTCTAA	GTCACACCCA	ACCTTTGAAA	CAATAAAATC	AATGCCAGTA	182100
AAATTTTGCT	TAAGTCCTTT	TAAAATAGTA	TTTAAATTTT	CCTCCAAACA	AAGAACTTTT	182160
ACTTGGGGGC	CTGCATCCAT	CGTCTCAAAT	ACAAAAATCC	CCTCATTTCT	CAAATCAGCA	182220
GCATACCTAA	TTAAATCTAT	TGTACTATTT	TTAAAATAAA	AAATAGAAGA	TGCAAACATT	182280
AAGGCAAACA	TATCTGATA	ACTTTTTTACA	ATAGTTGCTC	CAAAATGTAT	AAAATCCTTT	182340
TTTTAAAAAA	AAATATAAAG	CGTCTTTAAA	AATCTTTTTTA	CTAGAGGCAA	TCCAAGCATC	182400
ATAATAAAAT	TTATGCCGTT	TGCAAATATT	CATTGCGGCT	CTTGAAGACA	ATTCTTTTTTC	182460
ATTACTATCA	ATTATGGCAA	ATATTATTCTG	CAAATCATTA	AAATAAGATT	GATCTCTTAA	182520
TTGAAAAGAT	TCTTTTGAAC	CCTCTTTTAA	AATAGTAAAC	CCCCCGTAAA	TAGCCCTTGC	182580
CGCAGAAGCC	GATCCTACTC	TTGCAAGATT	AGATGCGCTA	TTACAAGAAT	ATTTATTAAA	182640
ATATTTCAAA	ATACAAGCAG	CAATAGAAGC	AAAACCTGAA	CTTGAACCTG	CAAGGCCTGC	182700
TGCTGTGCGG	AAATTGTTTT	TACTTTTAAT	TTTAAATCTA	ACATTTGGTT	CATTAAGAAT	182760
TTTTCTTGCA	TAATCAAAAA	ACACCTTTTC	TCTATTTTTT	AATATAACTG	GCTTTGAATT	182820
TAAAAATTATT	TCATCTCGAT	TTGAAAGTTC	AAGCTCACTT	ATTGAATAAA	ACTTGTC AAC	182880
ACTAACAGCA	AGACTGGAAG	TAGCTGGAAT	GTTTAAAAAA	ACATCCTTTT	TCCCCCAATA	182940
TTTAATTAAA	GCTAAGCTTG	CATGAACCTT	ACACTTTATT	TTCATTCTCT	AACCTTATTT	183000
TCTTCAAAAT	TTTAAAAGCA	AAATCAAAAG	AATAAATATT	CATTCTTTCC	ATTTCCAATA	183060
ATAATTTGTC	TTTTTCAAAA	TCAGAAATAT	TATATTTTGT	CTTTAAAAGA	TGGAGTATTT	183120
TATTAACATG	CAATCTCATA	TGACCCTTTT	GAATCCCATT	AAATGCAAGA	GCCCTTAATG	183180
CTGCAAAATT	ACTAGCAAGT	CCAACACAAG	AGAGAATACC	AATAAATTCG	CTCTTACTAT	183240

TTACATTCAT AATTTTAAAA CTTAAAATTG AAGCTTCATT AAAAGATATA ACCCCACCTT	183300
TAGTTCCAAC TTGCAAAGGA ATTTCAATTT CTCCAATAAG AGCATTGTCA GTAGTATAAA	183360
ATTTACTAAG GGGAAAATAT TTGCCGCTTT TTGAAGCAAA TTTATGAACA GAGGCCTCAA	183420
GAGCTCTTGT GTCATTAAAA GTTGCAAGAC ACACCCCTGT AATTCCATTC ATAATACCTT	183480
TATTATTAGT AACAGCTCGC TCCTCTTCGT AAAAACCTAT ACTAGAAATA AGTTCAATTT	183540
TTTLAGCCAA ATTCCAAGAA TCCTCTTTAC CCGGTAGCAA ATGCTTAAAA TCTAAAACAA	183600
AACGGGCTTT GGCTGTAAAT TCACTAATAT CATTGCTTAA AACTTTTAAA ACACACTCAT	183660
ATCCGAATTC TAAAAAATA AATTCTGCTA CACGCTCTGC AATTGAGTTT AGCAAATTAG	183720
CACCCATAGC ATCACAAGTA TCCACATAAA TATTTAATTT TTGAATACCT AATTCTTTAA	183780
TGTGCCTAGT TGACAACCTT CTAAATCCAC CCCCCTTTG ATTCATATTG GTTAAAAGAG	183840
GTTCAATCCA AGTCTTAATT TTATCACCAA GGTCAACAAA AATTTTACTT AAATCTTTTT	183900
CCGATTTTAT ATAAATTTGC GAAATTCCCA ACACTTCACC CAAAGAATAC CTTAAATCAG	183960
CATTTTCAAG AATCTTTGCC GCAAAATTTA GGGCAGCAAC AACAGAAGAT TCTTCTGTTG	184020
CAATTGGCAA AGAATAGTAT TTGCCATTTA TTTTCAAATT TTTTACAATT CCAATAGGAA	184080
AAGATAAATA TCCAATATAA TTTTCTATCA TATTAAAAAG AAAATCTTCA TTGGCATTAT	184140
TATAAAAAAA ATCTTTTATAA GATAATTCCA AAAAATTTT TATCTCTTGC CTTTTTCTA	184200
AAACGCTTTT ATGTCTAAAA TTTTACTAA GTTCCATAAA ACTGCTTAAA GACTCCAAGT	184260
TCATCAAGCA AATAACTACT TAAAAAATAC TTATTATTTT TAAACTCTAA TAACTTTTGT	184320
CTTCCACTTA AAAACATAGA CATTTTAAA ATATGTTTAT AATCAGAAAA AAGACCAAAT	184380
ACAGCATCTT CTCCTGAATC ATAAAAAGCC CTAAGAACAA CTGCTGCAAC ACCTATAAGC	184440
CTGGCTCCAA GGGCAATGCC TTTAGCAATA TCCATGCCCC TCTCATATCC ACCAGATGCA	184500
AAAATATTAG CCTTTAGAGA ATCATCAATA CTAAGTAAAG TAAAAACCGA AGGTATACCC	184560
CAATCAGAAA AACAAGATGC AATGTTTAGA TTATTACTCT TCATGCCTTC TACTAAAATC	184620
CAATTAGTTC CACCACTCCC TGCAAGATCA ACATAAGAAG CACCAAGGCT GAACAATTCC	184680
TTAACGTCTT TTGGCGAAAT TCCAAAACCT GTCTCTTTAA CAATCAATGG AACACTTAAA	184740
AAGTCTGACA ATTTGGCTAT TGAATCTCTT ATTCCTTTAA AATTTCTATC TCCATCAACC	184800
TTCATCAATT CTGTCTCTGC ATTAAGATGA ACAATAATTG CATCAACTTC TAATCTTTTA	184860
ATCATTTTCA CTATTTTAGA AATACCAAAT TCAACAATCT GAACAGCACC AACATTGGCA	184920
AACAAAGGAA TATTATGAGC ATACCTTTTA AGAGTAAAGT CTCTTATGTA CTCGGGATAC	184980
TTAAACAAAA GCTTAAAAGA ACCTAGCCCT ATAGGAATTT TTAAATAATT TGCAATTCTA	185040

ACTAAAGATT TATTAAAGTC ATTCCCCTCT TTACTGCCCC CTGTCATGGA AGAAATAAAA 185100
ACAGGCATAC TAATATTGTA TCCAAATATC TCTTCTTTTA TGTTTATCTC GGAAAAATTA 185160
AAATCACTAA GAGCATTGTG TTTTAGCTTA ATAACTTTA AGAAATTACA GCCACCTTTA 185220
ACATCGTTTT TATTTAAACA AATCTCAATA TGCCTTTTTT TATTTTCTAA TATATTAGGC 185280
TCGATACCCA TAAACTCGGT ATCCATCATT CCTTAGTTCT TTAAATAAA ATCCTCTGGA 185340
TTCACCAGGA ATTATTTTAT TTTGAAAAA ATCTTTATAT TCTTCAAAT TTGCATTATT 185400
TCTATTTTTT ATAAGACCTT CAAGATCCCA TAATTTAATA ACATCAAAAG CACTCTTTTC 185460
GATGGTAAGT TCATAAATAA TCATAATATT GCCAGATCCA TAAGAGCAAA ACAATATCTT 185520
TTCCCCTGTA ATATCTTTCT TGGAAAATAC TCTTTTTTAA TAAATGCTA AAGATAGAAA 185580
AATTGAACCT GTATACAAAT TTCCCACTTC CATAGCAGCT TCAACTCCAT CGTAAAAATC 185640
TATTGATTCT AAATAAGCAT TTCTAACAGA TTCGTCATCG CTATAATATT TTTTCAAAT 185700
ATAATGCATT GAATCTATTG GCATTTTAGC AAAAGGAACA TGCAAAACAA ACCTATAATT 185760
AGAAAATAAA TCTTTCATAC TAAGTTGCTT TTTGAAAGCA AAATCTCTTA AAGCATTTTC 185820
GTTTGCATTA TTGTAACATT CAACTGAATA CTGACCTCGC ACCTTAGCCT CAACACTTCC 185880
AAAAGGCCTA AAAAAATCGT CAACATCATC AGTATAAACT CCAAATTCAG ATAAATTGAT 185940
CGAAAGTAGC TTTGGATTTT TTTCAATCAA AATTGCAGTT GCGCCGGCTC CTTGGGTAAT 186000
CTCAGCCGTA GTAAGATTGC TATAATGTGC AATATCTGAA GAAAAAATA TGCCGTATTC 186060
AGAATTATTG GAATGGCTTA AAACACTTGC CACAGTGTGC AAAGACATAG CAGCACCAGC 186120
ACACGCATGT TGAACCTGGA AAGTTAGAAA ATTATTTCCC AGACAAATAC CAGATTGCTT 186180
TAAGGCTCCA AAAACATAAG AAGAAATGGC CTTTGAATGA TCAACGCCTG TTTCAGTTCC 186240
ACCCAAAAGT ATTCTAATTT TGCTTAAATC AAGATTATTG TTGTCAAAAA TAAGCTTAAC 186300
AGCCGAACCT GCCATGGTTA CACTATCCTC ATTAGGACTG GTAAACCTAA AACCTTTTTG 186360
CAAGGTTGCA TCTATTGCTC TATTGATTTT TTTAAAAAA ACTTCATTAG AAAAATATAA 186420
AGGATTTTCC AAAAGAACAG AAAAATCTAA ATAATTTAAA GGTAACAAAA TTCTAATATC 186480
ACTAATACCT ATTCTCATAT ACTCCTCAAT GAATTAATGG CCTTAAGTAT TATATTATAA 186540
TTTACAAAAA TTAGCAAAAT CTTATATAAT AAAACCTAAA AATGGAAGTT TATGAAAATA 186600
GCCGTGCTTT TATCTGGAGG AGTCGACAGT TCTGTTGCC TTTATAGAAT TATAAACAAA 186660
GGATATTCAA ATATAAAATG CTACTATTTA AAAATCTGGG TTGAAGATGA ACTGTCTTAT 186720
ATTGGAAACT GCCCTTGGCA AGAAGATTTA AATTATGTTG AAGCTATATG CAACAAATTT 186780

AATGTACCGT	ATGAAATAAT	AAACTTTCAA	AAAGAATATT	ATAACAAAGT	AGTAAGCTAT	186840
ACTATTGAAG	AACTTAAAAA	TGGCAATACC	CCAAGTCCAG	ATATTTTTTTG	CAATCAAAGG	186900
ATAAAGTTTG	GAGCATTTTT	TGAGAAAATC	AATAGCCAAT	ATGATTTGGT	TGTAACGGGA	186960
CATTACGCTA	AAATACAAAT	AAAAGAAAGT	AAATTTTTAT	TAAACAGGC	AAAAGATAAA	187020
ATTAAAGACC	AAAGCTACTT	TTTATCTCAT	CTCTCTCAAA	AACAAATGTC	AAAACATATAC	187080
TTTCCCTTAG	GCACATTACT	TAAAAGCGAA	GTAAGACAAA	TAGCTAAAAA	CATAAATTTA	187140
CCCAACAAAG	ATAGAAAAGA	TAGTCAGGGT	ATTTGCTTTT	TAGGAAAAAT	TAAATATAAC	187200
GAATTTATCA	AATACCATCT	TGGAGAGAAA	AAGGGAAATA	TAATTGAAAA	AGAAACGGGA	187260
AAAAATAATAG	GAATTCACAA	CGGATATTGG	TTTTTTTACAG	TTGGACAAAG	AAGAGGAATA	187320
AAACTTAGCA	ACGGGCCATG	GTTCGTCATA	GAAAAAGATC	TGGAAAAAAA	TATTATATAC	187380
ATATCCCATA	ACGAGAATTA	TTTAAAACAA	GCAAAACGCA	AATTTTTTAGT	TCACGAAATA	187440
CATTGGATAA	ACGACACACC	TACGAACTTT	GAAAATTTCA	AAATTAAAAAT	AAGACATGGC	187500
GAAAAGAAAT	ACTCATGCAA	ATTAAAACTT	ATTACAAATA	ACTTAATGGA	AATTTCTTTA	187560
AACAAAAAAG	ATCAAGGAAT	CTCCCCAGGA	CAATTTGCAA	TTTTTTTATAA	AAACACAGAA	187620
TGCCTGGGGG	GTGCTAAAAAT	TTTTAAAATC	ATAGAATAAT	AATCCGCCCA	AAAAGTTAGA	187680
GAAGATTTTT	CAATCTTCTA	CTTACTTTTC	GATCTTAAAA	TAATCAACAG	ATTCTTTTAA	187740
ATCTTTTACA	CTCTCTAACA	TCTTTTCAGA	CATTGCAGAA	AGCTCTTCAC	TGCTTGAGGC	187800
TGTAGTTTGG	ACTAACTGAC	TAACCTGCTC	TATTGCATTT	TTAAATTGCT	CTATTTGAAC	187860
ACTTTGCTTA	TAACTTTTCAT	TAGAAATATT	TTTACAAGT	CTGGCTGTTT	GTTCCATACC	187920
AGGAACATT	TGTTCAAAAT	TTTCCCCAGC	ACGACTTGCA	ACAGTTAAAC	TTCTGTTTGC	187980
AATATCAATA	ATCTCTCTTG	CTGATTCTTT	GCTTTGATCT	GCAAGCTTTC	TAACCTCAGC	188040
AGCTACCACT	TCAAATCCCT	TGCCCTTTTC	TCCCACTCGT	GCAGCTTCAA	TCGAGGCATT	188100
TAAAGCAAGC	AAATTGGTTT	GCCTTGTTAT	CTCATCAATA	ATTCCAATTT	TTTCAGTAAT	188160
TACAGTCATT	GCCTCAATAG	CCTTAACAAC	AGATTTATGC	CCCTCTTTAG	TCCTTTCATT	188220
AGTATTAACA	GCAATTTTTT	CAGTAGTAGC	TGCATTTTCA	GTATTCTCAG	AAACACCTTG	188280
TGAAATTTGC	TCAATATTTG	CTGTCATTTG	CTCTAAAGTA	GAAGCCTGCT	CAACAGCGCC	188340
AGAACTTAAA	TTCTGGCTTG	CATTTGCTAT	TTGAATTGCA	TTTTCATAAA	GATAATCTAG	188400
ATTTTCAATA	ACTCCTTTTG	CAACTGAAGA	AAAATTGGTT	CTCAACTGCT	CAAGCCCTTC	188460
GTACAAACTG	TAAAGCTCTA	CAGTATCCCA	TTTGCCAAAA	TTAATATCAG	CAGTAAATTT	188520
ACCAGAAGCA	AGTCTCTCAG	AATATTCCAG	TATCTTATTC	AAAGAAGAGC	TTAACTTTTT	188580

CACAAGATAA AGAGTTGCAA TAGCAAGCAT AAGTAATGTA AATACAAAAC TAATTGCTAA	188640
GATTATAGTT GTAGCTCGTG ACATGTAATA AAAATCGTCC TCTGAAGTTC TCATTAAAAG	188700
AATAAATTTA TTATTAGACA AGTTTAATAA CACCTTTTGA CTAATTCCCA CATATTTCTT	188760
ATTGCTTTTA GGATCATAAT AATAACAGT TGAAATTTCT TTATTCTTTT GCAACAAATC	188820
TTCAGATGTT TTCTTAATAA TATTGGAATA AGAAGCACTA ATATCAGTCA AAATATCACC	188880
TGGCAATACT ACATGATGAA CCAACAATCT ACCCGTAGTA TCATAAGCTA GCGCACGACC	188940
GCTAGAGAGT ATTCCAAAAT TAATCCCTCT AAAAGACCTA TATATATAAT CCATTGAATA	189000
AAGAAACATA AAATAACCAA AAATGTTATC TGTTCAAAA TCTCTTAATG GCATACCTAT	189060
TAATATGTAA GGAATCTGAC CTTTTTTATT TTTTATCTTG GAAATATCTT TAAGTAAAGA	189120
CTCCTCAATA GACCCGGGAT CTGCCAACAT GACAAAGGAA TTGTAAACAA TACTATTAGA	189180
CTCCTTAAGT TTTGTAAAAT ATTCTCTATC CCCAATAGAT TTGCCAAAAT CACTATTATC	189240
CTTAACCGCC GTAGTAAACA CTATTTTACC TTCTTTGTCT GTAACCATCA TATTACTACC	189300
GGTTTGAATA AGAATTTTCAG ATTGATCTGA AATAAAGCTC AACCTTTTGG ATTTAATTTT	189360
ACTAGCCTCA TTAAATTTTT CAGCAGAGTT GAAATACATG GAACTAACCC TAACTTTCTC	189420
TTCCATTGAA GAGATGTAAA GATTAAAAGA ACTTTTAATG CTTTCAATAA GATTTATCAT	189480
AAGATTAAAC TGTTGATCCA CCAATTTACT ATTAATAAGC ATTCAAAAG CAAAAACAA	189540
AATTGATATA AAGAATGCTA TCAGAATAAG AACAAGTAGC AACATCCTAG CTTTAAGCTT	189600
CATACTAACC ACCTCTTTTA CAAAAATAA ATTCTAAAAC TCTGAAAAAT CATCATCAA	189660
ATTTAAATCC TTATCAGCAA TATCGATAGC TTTTTTAGGA TCAACTCGCT TATTAATAGT	189720
TCTTACAGAA GATTCGCTCT CAATATCTAA AGAATAATTA TTATGCCAC TGGCATTGTA	189780
AGTAGAAATT CCATTGCTTT TCAAATTTTG ATTTTCATCT TTTAAAGAAT TTTCAGGACA	189840
ATCTATTAAC CTGAAATCAT AATCATCATT TTCTGGATTT TCAATTTTAG AATCTTTAAT	189900
TTTGAAAAAT AATACAGATT TTCTAAGTTC CTTAGACTTT TCTAACATTT TATCGGACAT	189960
ACTAGAAAGC TGCTCACTGC TTGAAGCTGA AGATTGAACA ACTTCTCCAA CCTGATCTAA	190020
AGCCATTTTA AATTGAGCAA TCTGATCGCT TTGCTTAGAG CTACCTTCTG AAATCTTCTT	190080
AACAAGATTA GCCGTTTCTT CAATTTCTGG TAGCATTTCT TTAAAGATCA CTCCCGCTTC	190140
AGTTGCTACC TTAGAGTTAT CTTCAACTAA CTCTCCAATC TCAAGAGCAG AAATTTTACT	190200
CAAATCAGCC AACTTTCTAA TCTCACTGGC CACAACAGCA AATCCCTTTC CCTCATCTCC	190260
TGCTCTTGCA GCTTCAATAG CCGCATTCOA AGCAAGTAAA TTGGTTTTTC TAGCTATCTC	190320

TTCAATAACA CTAAC TTTCT CCACAATGTC TTGCATAGCA ATAACAGATT CTTCAACGGC	190380
CCTACCACCT ATCTGAGAA TTTTCATTCGT CTTTAAAGCT ATTTGTTCTG TTTCATAAGA	190440
ATTATTGGCG CTCATGTTGA CACCTGAGGC TATTTGCTCA ACATTAGCTG ACATTTCTTC	190500
AAGAGCAGAT GCCTGTTGCA ATGCACTAGA GCTTAAATTT TGACTTGAAC TGGCAACTTC	190560
TAACTTGCC TTATTTACAT AGCTAATATT TCTCAAAACA CTAGAAATTG CTACAGAAAT	190620
AGCTTTTTTC ATTTTAACAA CCTGAAGACT TAACATGCCA AGTTCATCAA GAGTATTTTC	190680
ATCATCATCA AGAGCATAAT CTTTATCTAA ATTGCCCTTA ACCATATCTT GAACTAGAAC	190740
TCTAATTGCG TTAAACGAA AACTAATAAT CCTGTCTATT CTAATTGAAA GAACAATACT	190800
TAATGCTATA ATGCCTAAGA CTGAATATAA AATATACTGA AATCTTAGAC TAGATATTAC	190860
TCCGTAAATA TCCTTATAAG GAAGCCTAGC AATAAGTACT CCACTCTTTT CTCCAATTT	190920
ACTACTTATG GGCAACATTG CATAATAACA ATCTTCTCCC ATTTCCGACA AAAGTATTCT	190980
ATCAATAGTG TAAACCGACA CTTCACTGGC AATGTTTGAT GGAAAAGGGG GCTTAGAGAA	191040
AACATCTTTA AGAACATTCA AAAATTTAGA ACTAACCTG CTGGTTTCAT TATATCTTC	191100
AAAAGGATTA ACTGCTATAT TGTTGGGATC CACATAAATA AAATTGCCTC TTTTATAAAA	191160
ACCGAATCTA AATCTATCAA AACTATCTGC CACAATATCA TTAAGCAAAT ATCCGGCCAA	191220
ATACCCACAA ACAAGTTTAT CTTCTGGGGA ATATACAGGT ACAATTATTG CAAAAGCCTT	191280
TTTTTCGCTT TGTTTAGACC TAATAGCAAC TTCTGCGGAT ATTCCTTCAG AAAGATTGGA	191340
ATACCAACCT ATAAATTTTA ATTGGTTTTG CCTATAATCC TCAACAGCTT TTTTAAAATA	191400
ATTGGTATTA GCCTCAGAAT GACCAAATC CATATTATTC TCATGTCTTG TGCTAACAAT	191460
TACTCTCCCT TCAAAATCAA AAAAAGCGAA TTCTTCAAAA AGGGTATCAT TTTTAAGATT	191520
GGCCATAAAA TTGTATAAGT ATTGTCGATA TTTTTTGCTC ACCTTTACAG AGTCAATAAC	191580
AAATTTTGGA TTTTTTCTTA AATCTATCAA TTCCGACTCA GAGAAATCTT TTCCTCTATT	191640
CTCAGACATT GCAAATCTG ATATGGTTTC AAGTGCCAAA TTAGAAGCTG CACCATTGAT	191700
TATGACATGC AGGGTGCTA AAAAAGATTG CAAAGAAAAA GCTGCTCTTC TTA CTGCGC	191760
CCTTGTAAGC TGCTTATAAT AATCTTCTAA ATAACCGCAT AAAACAAAAT TAAAAATCGT	191820
GGAAAAAGT AGCAGTATAA AAATTAAAA CAATAATAA AATCCAACAA ACCTGTATTT	191880
AAGCTTCAAT AACATAATA ACTACCTCAC AAATCACCTA CTTATTTAAT CAAATAAACT	191940
CAAGACCAA GGGTATCAA AAAAAATTTA CAGCAAAAAA TCAAAAACTC TCAAAAAAT	192000
AAAAGAATTT TCACAACATG AAAAACAAAT TATAAACTAT TATTATTAAC TGCTAATGCT	192060
TTTTATAGGT TATTCCTAAG AACTTAGGCG CATAATTTTT TTTTGAAAAA AAGATAAGAC	192120

TTAGAATAAT AATTAAATAT GGGGTAATCA CTAACATTTT GGGAGGCATT ATTAAAGAAA 192180
AAAAGGGTAA TTGAGCCAAA ACAATTGCCA AAGTTTTTAC AAATGAAAAC AAAAACTGC 192240
CTATTAAAAC TCCCAAAGGC GTCCATTTTC CAAAAATCAA CATTACAATA GCAATAAAAC 192300
CTTGTCACC TGTAACCCCT TGCACATAAC TTGATGCAAC CACCGTTGTA AGAACAGCAC 192360
CTGAAACCCC TGCTAAAAA CCACTCAAAA GAACGCAAAA AAATCTAATT TTATTTACAC 192420
TAACTCCAAC AGACTCTAAT ACCTCTGGAT TTTCACTACT TGCATTAATT CTAAGCCCAA 192480
TTTtagTGTA TTTGAAAACA ATATGAAAACA AAACCACACT TAGGATTGCA ATGTATACAG 192540
AATATCTTTT GCCAAAAATT TGAAAAATAA AAGATGTTTT GTTTAAAATT CCATCAAAAA 192600
GTATCGGCAA CTTTATTTCT ATAGGCGGAG TTGAAATAGA AGAAAAATC AAAGTGCTTA 192660
TAAAAACAGC AATAGCGGGT CCTAAAAAAT TAAGTGCCAT TCCGGTTATA ATTTGATCTG 192720
ATTTTAAAAA AATTGTAAAA ACAGCGTGCA AAATAGCAAG AACAAGCCCT GCTAGCCCAC 192780
CAGCAAAAAT TGAAAACAAT GGATCATTTG TAAAATATGC AACTGTAGCT CCTGAAAATG 192840
CTCCTATTGT CATTATTCCT TCAAGTCCAA TATTAATAAT TCCACTTTTC TCGCTTATAA 192900
GACCCCCAAG ACCAGCTAAA ATTAAGGTTT GAGAATTTAT TAAAGTTTCA CTAATCAAGA 192960
ATATTATTAT ATTTGACACG CTTAACACCT TTTAAACAA TTTTATTTAA AAAATAGCTA 193020
GCAGAAATTA CAAGAACAAT TATCCCATC ATCAAAGATA CAATTGAAGA TGGAAGGCCC 193080
ATTAACTTT GAACCTACT GCTTCCATA AGCAATATAG AAAAAAGAAT GCTAGAAAAT 193140
ATTATGCCAA TTGGCGAATT GTTCCCATA AGAGAAGCAG CTATCCCATT AAAACCAATT 193200
CCTTGCATAT AAGAAAGCTT AAATATAGCT TTATTAACAC CCATAAGTTG AATAGCACCA 193260
GCAAGACCTG CAACAGCTGC TGAGAGAAAC ATTGAAAAA TTAGCACAGC TTTTACATTA 193320
ATACCCATAC ATCTTGAAGC TTCAATATTA CTCCTGTGG CATTTATTTT AAATCCAATA 193380
ATAGTTTTAT TAAGTAAAA CCATATTAAA ATAGCAAAAA TTATACCTAA AATTATTCCA 193440
AAATGAAGAG GTGCTTTTAA AAGCTCATTA ACAAAGGAT GAGAAGATCT ATAAGCAAGA 193500
CCTTCTGGTG AGAGCTTCCA AGAAGCTAAA AAATCAATAT ATGCGCTTTC TTTAATGGGT 193560
TTTGAAAAAT CACTATTATC TCTTTTAATA AAATAAAAT CTAAATTAT ATTATTTAAA 193620
TGAAATAATA TCCAATTAAA CATTATTCCT GAAATCACTT CGCTAATATT GAATTTGGCT 193680
TTTAAATATC CGATTAAAAT TCCTAAACTG CCTGAAGCTA AAAAAGTAAT AATAAAAATA 193740
GTAATTACAT GTAAAATTGG AGGCAATCA AGTAAACTG ATGCTATTAA AGCAACAATA 193800
GATCCTAGTA TAACTGGCC TTCAACCCCA ATATTAAAAA GACCCGCTTT TAAAGAAATA 193860

CCAATAGAAA	GACCTGTAAA	AATCAAAGGA	GCTGAATAAC	TTAAAACATA	ACCTAAATGT	193920
TTGGGAGAAG	AAAAAATAAT	TTCTAATATT	ATAAAATACA	TTCTAAAAGG	AGAATGACCA	193980
AGCCCCATCA	CCACTAGCCC	AACAATTAAA	AATCCAACAA	ATAGAGCAAA	TACACTAACA	194040
AATGCTGAAG	AATTTAAAAA	TTTCAAAATA	AATTTACTAA	ATACGTTTTT	ACTAATTGTC	194100
ATTTAGCTTA	AGCCTATCAT	CATTTTACCA	ATAACATCAA	TATCAAAATT	ATCCTCTAAA	194160
ATGCCCCACTA	TTCTTCCACC	ATGCATTACA	GCTATCCTGT	CACAAACATT	AACAAGCTCA	194220
TCAAGTTCAA	GAGAAACCAA	TAAAACAGAT	CTACCCGCAT	CTCTTTGCTC	TATTATTCTT	194280
TTGTAAATAT	TCTCAACAGC	TCCAACATCA	AGGCCTCTTG	TAGGCTGAAT	AGCCAAAAGA	194340
ATATCTGGCT	CTAAACTAAT	CTCACGAGCA	ACAATAACTT	TTTGTTGATT	ACCTCCGGAT	194400
AAATGCTTTA	CCTTGCTTAA	AATATCTCTT	GGTCTAATAT	CAAAATGACT	TACAAGTTGA	194460
TTGCTCAATT	TTCTTAAAT	ATTAAGATCA	AACCCACAA	ATTGTTTTTT	AACTTATTG	194520
AATTGTCTTT	TAATAAAATT	GAAAAAATTG	AATTTTAAAT	CAAAATTACT	CTTCAAATGA	194580
ATTGTTTTTA	ATCTCAAATA	ATCAGGATTA	TCAAAGCTCT	TAAGTCCAAT	ATTTTGCATA	194640
ACATTGAATT	CTAAAATAAG	GCCGTGTTTT	TGCCTGTCCG	AAGAATATTG	CCAATTTTTT	194700
TATCTATTCT	TTGTTTAATA	GTAAACCTT	TTAAAGATTC	CAAATTCCCC	GAAGAATTTT	194760
TTTTCAAAT	ATCGCCCTTA	AATATGCTTT	TCAAACCCAA	AATTGCATCA	ACTAAATCCT	194820
CCTGACCACT	CCCCTCAATA	CCTGATATTC	CAAGAATTTT	TCCATTTCTC	AGATCAAGAT	194880
TAACGTCTTT	AACTTTTAAA	ACTCCTCTCT	CATCTTTAAC	ACTTAAATTC	TTTATTTCAA	194940
GAATATTAAA	ATGATTTTCA	AATTTAATTT	TAGATGAGCG	AAGTGCAACT	TCTTTTCCTA	195000
TCATTAATTT	TGTAAGATCT	TTGTCATCAA	TATCAGCAAT	ATTAACAGTT	TTTACAACCT	195060
TCCAAGACG	CATAATTGTA	CATTTCTTTG	CAATAGATCT	AATTTCTTTT	ATTTTATGGG	195120
TAATAAGTAT	TACAGTATGA	CCCTCTTGGG	CGAGTACCTT	TAAAATATTT	ATAAAATCAT	195180
CAACTTCACT	TGGAGCAAGC	ACTGCTGTAG	GTTTCATCAA	AATAATAATA	TCTGCATTTT	195240
GATAAAGAAC	TTTCAATATC	TCTATTTTTT	GTTCCATGCC	AACACTCAAG	TCTTCAACCC	195300
TTTTTTCTAA	ATCTATCTTT	AAACCATACT	TTTCCGAAAG	AGAACTTATC	TTTTTTCTAG	195360
CTTGTTTGTA	ATCAAGAAAA	CCAAATTTTG	AATTTTCATA	TCCCAAAATA	ATGTTTTGAA	195420
CAGCAGTAAA	TTGCGGAATT	AACATAAAGT	GTTGGAAAAC	CATTCCAATC	CCATTTTCGAA	195480
TAGTTCGCTT	GAATCCTTAA	AGTTTATTTT	TTGACCTTTT	AAAATAATTC	GACCACTATT	195540
TACTTGATGA	ATCCCATAAA	TAGTTTTTCAT	TAAGGTAGTC	TTTCCAGCAC	CATTTTCTCC	195600
AAGAATAGCA	TGAACTTCGC	CTGCCTTAAA	TTTAATAGAA	ACATTATCAT	TGGCAACAAA	195660

ATCACCATAC TTTTTTGTAA TATTTTCTAA TACTAGTACA TCTTCTTTCA TCAAGCTTTA 195720
ATCCTAATAT AAATATCAAA CATAAATGAC TTACAATATT CTATTCTAAT GAAATATAAT 195780
AAAGCTTAAA ATTTATATTT TCAATAGCAT TTTAAATTTT AATAAACAAA ATAAATTATC 195840
TATAAAAATT AATTGCTAAT AAATAAAAAAT GCTTAAAATA TAAAAACCTT AATAAAGAGA 195900
GCAAATTAAT GTTAAATAA AAGAATAAAT AAATTATTAC AAAAGAGAGT ATTATGAAAA 195960
TCAAAGCCTG CATTTTGTAT ATGGATGGAA CACTGGTAAA TAGTATAATG GATATTGCAT 196020
TCTCAATGAA TTCTGCTCTT TCAAACCTAG GATACAGTAA AATAGAACTA AGCAAATTCA 196080
ATGCCCTTGT TGGCAGAGGA TTTAACAAGT TTGTAATAGA CACTCTAAAG CTATTATcTC 196140
TTGAACATGA TAATCCTAAT TTACAAGAAA AACTTTACAA AGAATTGTGTT AAAGAATACA 196200
ATAAAAAACCT TTCATTCCAA ACAAACCAT ATGAAAATAT AAAACCCCTT TTAGAAACTA 196260
TGAATAAGCT TAACATTCCA ATTGGAATTT TAAGCAATAA GAACCACGAA GAATTAATAA 196320
ATTTGGTGAA AAATATTTTT GGAAATATAT TGTTTTTTGA AATCAGGGGT TATTCAAAAA 196380
ATTTTCCACC AAAGCCAGAT CCTGAAAATG CCCTTGATAT GATATTAGAA TTAAATGCCC 196440
AAAAAGAAGA AATTGCATAT ATTGGAGACA GCGATGTGGA TATGCTAACC GCACTAAACG 196500
CTGGATTTAT GCCAATAGGG GTTCTCTGGG GATTTAGAAG TGTTCAGAA TTTAAAGAAA 196560
GTGGAGCAAA ACATATAATA CACAATCCAC TTGAACTATT GGACCTAATA AAATGAATAC 196620
AAAACCATAT TTTCTTATT TATATCATT TCTATTCAAT CATGAAAGTA TAAAAAGTTT 196680
ATCTGCCATA GAAAAAGAAA TTGAAATACT CAACTATTTA AAAGAAAACA AAAAAACAAT 196740
TGCTACATTT ATCAAAAATG ATTTTGAATC AGAAATAAAA GACCTAATTC AATACGTCAA 196800
GGATAAAACA GATATAATGA TTACCCCAT TGTTTTATCT GGCATTGAAG CTATTGATTT 196860
TAACATTGTA AAGCCTCTTT TTAGTAAAGA ATTGACAAAA AACGACTTAA ATTTGATATT 196920
TAACTTTGTC AAAGTCAACT CATCTTTAAG AAAAGAATTC TTTTATAATT TTAATACCAT 196980
AAGCAATGGA TACATTACTT TTTATATAAA CAACTATTT GAAGGAAAAA ACTCTTATAC 197040
AATATACTTA ATACAAAAGG AAAATAAAGC ACTTTATTCA TCAGACATCA TAAAAAATTA 197100
TATAAAGATA CTACTTCTCT TAAAAGTATT GGTAATTAAA TACTGCTTTG AAAAAGGAAT 197160
AGAGCTTACT ACTAAAAACA TTGAATCCAC TTCAAAAGCA ATAAGCAATG ATACCGACTT 197220
TCTAGACGAA AAGACAGCTA AGCTTATAAT TGAAAGCTTT TTCAAATATG AGACCTTACA 197280
AACAATGTCT CCAATTTCAA CATTAATTGC CATTTTTTCA GCCAGAGCAA GAACTCCAAA 197340
ATACAAAAAC AATCCGGTTA AAGGTTTTAT TGGGTATGAT GAAAGTTGGT TTTCAATAAA 197400

ACAGTCGGGC	TCTAGAGAAT	ATGATTCAAG	AATAATTAAA	GAATTATCAG	AAATAGCCAA	197460
GGTAAATAAA	TGGTAAAAAA	ATTTTCAATT	TTCTTAAAAG	CAATAATAAT	TTTTTCAATA	197520
TTTGAAC TTT	TAATCGAAGA	ACTCTCAATA	ATTCTTTTTT	TACCATACAA	AATACGATTT	197580
GCACTAATAT	TTCTTGGGTT	TCTATTTGAC	ACAATTTTTA	TTTTCATTTT	TTTATACAAA	197640
ATAACCAAGG	CCTACCTTTC	CCAAAGATTA	GAAATCTACG	TCAGAAACAA	TCTATTCTTC	197700
GATATAATCC	ACTGCCTTAT	TCCTTTAGCG	TTTTATAGCT	CATATCAGCT	TAAAAACATA	197760
ATTGTCGCCC	ATGAAACAAT	ATTAAATCCA	ATAATGCTAT	CACTTTTCAA	GTTAAGATTT	197820
TTAAGACTTC	TTAGGTTTAA	TGACCTAATA	ATAGAAATAT	ATTACAATTC	AAAAGAAAAG	197880
AACCTAATAC	TAATAGCATT	TGCTAGGACA	TTTCAATGA	GCTTATTAAT	ACCATTTACA	197940
TTTTTTTATAA	TAATATCAAG	CTCAAAAATT	GTAAATTCAA	TACCAGAAAA	ACAAGAATTT	198000
AATATCATTA	AAAATATATC	AATAATAAAT	GAAAAAGCTT	ACATTAAAGA	AAAATATCCC	198060
TTCATCTTAA	TAATCAAGGA	AAAAGATGAC	ATAATATACT	CAAAATCAGA	CGAAATATTT	198120
GTTTACTACA	GTCCCAGTGA	ATATAGAGTA	ATAGAAATGG	AGAAAACAAA	ATTTTATATA	198180
GATAAATATT	TGCAAAGAAA	AAGCGATTCT	ATTCTTGGA	TTTTTCTATT	TACATTGTTT	198240
GCATCATTTA	CTATTTTTTT	AATGAATTTT	TATAAATTTT	TTAAAGCAAG	CTTTTTTAAAT	198300
CCTATTATTT	TAATGACAAA	AATTTTACAA	GACCCATTAG	AATATCGAAA	AATTCAAATT	198360
CCTTTTACTT	TAAGCGAAGA	AAAAGTATAT	GAAGTTGCAA	AATCATTTAA	CAATCTCTTG	198420
CTAAAAGAAA	AACTAAACTC	AAAGCGAAAA	AGCAAAATAC	CTTTAGAAAT	TGAAAAAGTA	198480
AAAAAAATAA	TTAATAAAAA	CCAGGAAATA	AAATGAAAAT	TCAAATAATT	ATAATGCTGC	198540
TTGCATTGTT	AGATTTTCCA	CTTAATGCCA	GACTTTTGGA	CATTTCAATT	GAAAAAAGAG	198600
CAGATGAAGA	AATAAAAAAA	TATTCGTCTT	ATAATTTAAT	TTTAGAAAAA	GAATACTATA	198660
CCAATTTTCC	AACAAGCGAA	ATAGAAAAAA	ATATTTATAA	ACTAACAGAA	CATTTTGTA	198720
AAAGCATAAT	GCTCAATAAA	ACTAACTACA	GCTTATTAAA	TTCAAAC TAC	AAAGAAGCAA	198780
ATAAATATCT	AATTCAAAGC	GAAGTCATTG	ATAAAAAATT	TTTAAATAT	AAAATATTTA	198840
AAATCAAAAA	TATAAATGGA	ATTTTTAAAA	GCCATTCACT	AATATATACA	AAAAAAGGAT	198900
TTTACAAATT	AGAACTTTAC	ATAGAAAATA	ATGCAGAACC	TCTAAAAATA	TTTAACCTTA	198960
ACATTACTTA	TTTTTTTAAAG	AATTTAGATA	AAATAAGTAA	TGAAATGATT	TTTTTCCCAA	199020
GGGAATGAAA	ATAATAAAAT	TAAAGCTTGA	ACTTTTTTTT	TAAATAATTT	ATTTAACAAA	199080
TACAGACATT	ACTCTTTGAA	GAACCTTTGC	CCTATCTAAT	GGTTTAACAA	TAAATGTTTT	199140
TGCTCCTTTT	ATTAAGCAAT	CCTTAACTAA	TTGTTCCCTG	CCTAAAGCAG	ATATCATTAT	199200

CACTCTAGCA	TTTTTATCAA	ATTCCATAAT	ATTAGAAAGA	CAAGTTATTC	CATCCATTTT	199260
GGGCATAGTA	ATATCAAGAG	TGACAATATC	AATATTAGGA	TAATGATTCT	TGTATTTTAT	199320
CACAGCCTCT	TCTCCATCAG	CTGCCGTATC	AATAATATTA	AAGCCCTCTG	ATGTAAAAAT	199380
TTGAGTAAGC	TGCTTTACGG	TAAAAACAGA	GTCATCAACA	ATTAAAACAT	TAAAAGGAAT	199440
GCCTGTATCA	TAATTGATTC	CTCTAGGCTT	AGATGAAGAA	TCTGCAGCAA	TTGTAGTCTT	199500
TTGAATCATA	TTAACCTCTC	TCTTCTAATA	AAAAGAATTT	TTTTCATATC	AAACCCCTCTC	199560
TCTTATTGCA	ATATTAACTT	CTATAATTTT	ACCATCAGGC	AAAGAAAAAG	GAACAATTAA	199620
AGCCTCAGAA	CCTTTATTAC	TTATTTTCAT	ATTTTCTCCA	TAAATAAAAG	CTGGGGGGGT	199680
TATATCAAAT	ACAAAACCCCT	TGGCATGCAA	AGTGGTAACA	AAATTTCCAG	CAATAATATT	199740
GCCAACCTCA	GTTAGAGTTG	CAGCAACCAT	CTCTTTTGTT	TCTTCATCGT	CAAAATCATC	199800
ATACTCTTCA	AAATTTAATT	TAGAAGCAAC	AAAAAGAGCT	GTTTCTATGT	CCATATCAAT	199860
AATTATACTG	CCCTCAACAG	ACCCAGCAAG	CCCTACTATT	ACAGAAACAC	CTTTTATCTT	199920
TTGATTTATC	GACTTAAGCC	CGGGCTTACC	CATTTCTATA	TTCTCAACAA	GCAACATATC	199980
TCTTAAACC	GAAGAAGCAG	CATCCAAAAA	TGGCTCTATA	TAATCTATTC	TCATTAATTT	200040
CTCCTTTAGA	CTTTCCTGTA	CAAGTTAAAA	TATTTTGTGG	ATTTCTCTTT	TATAAAAACA	200100
TCATTATTTT	TAAGCTCTTC	GTTATCTCCC	AAAACCAAAA	GAGCCCCTTT	AATAGCTTTG	200160
GAAGCAATGA	TATTTAAAT	TAAAATCTGA	TCTTTACTAT	CCAAGAAACA	TAAAACATCT	200220
TTTAAAAAAA	CCATTCCCAA	ATTATCAGGC	AAATCTGAAA	AAAGAGCATC	GGAATATTCA	200280
AACAAAACAT	TACTTAGGAT	TTCTGACTTA	AATTTATAAA	CTCCGGGACT	TTGTTCAAAA	200340
GAATTCCTAC	TATAAATTTT	ACTAATGCCA	ATTTCTGACT	CTGAAAACAC	CAACCTAGAA	200400
GTTTCAACAA	CTTTTGATAA	ATCATTATCA	ATGGCCGTCA	ACTTAAAAGG	TTTACATAA	200460
TATTCAGACA	AAGCATTGGC	TAAAGCCATA	GTCTCCTTTC	CACTACCACA	ACCAATTTCC	200520
AATACATTGA	AAATAGAATT	TAAGTTATTC	ATAAACTTA	AGCGACTCTC	AACAATTTCA	200580
TTTTTAAATT	CTTCCAAACA	ATCAGCTCCC	CACAAATTTT	CCGATGATTT	TGAATAAAAT	200640
TCATTTAAAA	AACTATCGCA	AGGCAAGTAA	TCAGTATCAA	CCATATTAAA	TTTACTCCA	200700
ACTTTTTCCA	AAAACACATC	ATTTACCAA	GAAGCATTAA	ACGAGTATTT	CAAAAGATTT	200760
TTTTTAATAT	TTTCCAAATT	AAAAGCTGCA	GTATTGTTTA	GAGTTGAATT	TTCATTGTTA	200820
CCATCATTTT	TTGAAGAAAC	CTTATTGGAA	AAATCATTCT	TAGAATTTTC	TAGTATATCT	200880
AAATTATCAC	AATCGCTTAC	AAAGTCGCTT	TTTTCAACAA	AATTTTGACC	AGGTTTTAAT	200940

AAC TTTTCTT	CTTCACCATA	ATTAAAAAT	TTAAAAACAT	TAAGAAGTAT	ATAAAGCTTT	201000
TCGTTATAAT	CTACAACGCC	TTTTATATAG	TTTATTAAAG	AATCCTGAGA	TAAAAC TGG A	201060
TGTGGATCTT	GAATAAGGCT	AGAATCTATT	GAAAAAACAT	TATTAATTTT	ATCAACAATT	201120
ACCCCTATAA	GAAGGTCTTC	GTTTTTTAAA	ACCATAATAT	CTTCAATATC	TTTTTTATTA	201180
AATTCTAAAT	TAAACATTAT	TCTAAGATCT	ATAATAGGAA	TTATTT CACC	CCGTAAATTA	201240
TCAAGCCCAG	CAACATACTT	TTTGGCATT	GGAACATAAG	TAAAATTACT	AGATTTTCTA	201300
ATTTCTTTAA	CCTGCATAAT	GTCTACTAAA	TAATGATCCG	ACCCAAGCTC	AAAAGAAACA	201360
ACTTTAAAAT	CAAAATTGGT	CAATTTAGAA	TTAGAATTTT	TATCATCTAA	AATTTTGGGT	201420
CCAAAATAAA	TTTCTTTTAT	CTGCACAAGA	GATCACTCCT	TAGTATCCTT	TTGTAAATCA	201480
AAAAGTTTAA	AAACATCAAT	TATCAATACA	ACCTTACCAT	TGCCAAGCGT	AGTAGCCCCA	201540
ACTATACCCG	CGCTTGATGA	AAATTTATCC	TTAATAGGCT	TTACTACAAA	ATCTTCCTCA	201600
CCAAGAATAG	AGTCTACAAC	AATTGCTATC	TTCATGTTGC	TAGTATTAAC	AACTATTAAA	201660
AATTTTCTA	TTAATGAATC	ATCCCTTGTT	ATGTTAAAAA	GTTTATCAAG	CCTGAGAACA	201720
GAAATGACTT	CATCTCTTAA	ATTATAAACT	TCATGATAAT	TTTCAAGCAA	TTTTATATCA	201780
TGTT CAGTTA	TTCTATGAGT	TTCAAGAACA	TTATTTAAAG	GAATAACATA	AGTCTCAGAC	201840
CCCGACTTTA	CTAAAAGACC	TTGTATAATC	ACTAACGTCA	ATGGTAGTTT	AATTTTAAAA	201900
ATTGTTCCAA	GACCAATTTT	TGATTCCACC	AAAATAGTTC	CATTAAGCTT	TTCAATGCTT	201960
TTTTTCACAA	CGTCAAGACC	AACTCCTCTA	CCTGAAAGGT	CTGTCACTTG	AACTGCTGTT	202020
GAAAACCCAG	GAGCAAAAAT	TAAGTTAATA	AGTTCAAAAAT	CAGAGTAAAT	TGCATCTTCT	202080
TTTATTGTTC	CCTTTTCAAT	TAATTTGCGC	CTAATGACCT	TTGGATCTAT	ACCAATCCCA	202140
TCATCTTCAA	TCTCAATTGA	TATTACATTA	CCTTCATTCT	TGGCACGCAA	AATTATAGTA	202200
CCTGCTTTGC	TCTTTCCCTT	TTTAACTCTC	TCTTCAACTG	TTTCAAGGCC	ATGATCCATT	202260
GAATTTCTAA	CACAATGCAT	CAAAGGATCT	ACAAGGTCAT	CTATAACAGA	CTTATCAAGC	202320
TCAGTTTCTT	CCCCTTCCAT	TTTAAGATTC	ACAATCTTAT	TTAATTTCTT	TGAAAGATCT	202380
CTTACGACTC	TTGTAAACCT	TGAAAATATA	TTAGATATTG	GTAACATTCT	GGTTTTTAAA	202440
ACACTCTCAT	GCAAATCTGT	AATTATTCTT	GACAGCCGCC	CAGAGGTCAT	TTTAAAATTT	202500
TGAAGAAGTC	TGAAAAAAGA	ATTTCTCAAT	TCAGATATAT	CCTTAAGAGC	CTTTTCCATT	202560
TTAAAAC TCA	TCAAAGAATT	AATATGTGAT	TCGATCTCAT	CTTCTAATGT	TAAGCCTGCA	202620
TCTTTGAAAA	CTATCTTTAA	ATCAATTAAA	AAGTTTCTCT	GAAAAC TTTT	TTGATAATCA	202680
TAAAAATAAT	TAAAATTATA	AAATAATGTA	ATCATTTCTG	AATTTATTTG	ATTATAAGAT	202740

GATTTACTTA TTACAGCCTC ACTGACAAGA TTTAATATGT AATCTATTTT TTTGCTATCT	202800
ATTCTAATTA AATTAACACT AATTGGACTA TTTTCTTAA TATTTTATT TTCCTTAAAA	202860
GGTGCTTCAT CATCTTCTTT TAGCCTTACG CTCTTTAAAG ATTCTAAATT AACATTTTGT	202920
ATTTCAAAAT GACTAACAAC ATCTGGTAAA TTAATCTTTT TAGCAATACT TTCTTCACTG	202980
GTATTTGATA TTAAGTAATA TATTACAAAA TCAAAAACT TATCTGCCAA TAATTCGCTA	203040
GAATCTGGGA TAGACTTGAA AATTTTACCA AGACTTTTTA ATGCTTGAAG CATTTGAAGC	203100
CCACTAATAG TAGCCATAGG ATTGTCTTTT ACAAATCCA ATCTAACTTT AAATAACTTT	203160
TGATTTTCAA CCTCAAGTAA TAAATCAGAA ATCTCATCCT CTGTAAAATC AAAATTATCA	203220
TTTAAAACAA AATTGGAATC TAAATCAACA TCTTTAATCT CTTCATCTGC AAGCTTTTTT	203280
AATTCTTCTT TTACGTTAAA TTCATCAACC AAATAGCTTT CAATTAAATT TAAAGAATCT	203340
AACTTTTTT TCACGCCTTC TATATCTGAA TATATCAGAT AATAATCAAC CCTTTTTAAA	203400
AATTTATCCT CTATGATTG CTCATATTTA GGAATTGTAT GAAGTACAGA TCCTAAATTT	203460
TTTAAAATAT TAAATATTTT TAGCCCACTA TTTTCAACTT CAGAATTGCT ATTTGAATTA	203520
AAAACAACAC TGATCCTTAA AACCTTTTGT CCAATTCCTA GCCCTTCTCT TATCTCCTCA	203580
AGATCTGATT CTGAAAGACA AAAATTGTTT TTAATTGAAT TTCCATCAAA TCTCTTAATA	203640
AAAGTCTGAT CATCAATTAC TAAAAATTGC TTTAATTTGC TTTTAAGATC ACTTATGTCA	203700
TTTAAATAAA CCTTGCCATC AATACGAAGC GCAAGCATTT CCTTGATAAC ATCTAATGAA	203760
CTTAAAAGCA GATCAACAAG ATCATTATTT ATATTTACCT TACCATCTCT AATAGCATCA	203820
AAAACATCTT CGACAATATG GGTAATCA GATAACTCCA TCATATCAAG AGAAGCAGAG	203880
CTTCCTTTTA AAGTATGAGC TGCCCTGAAT ATTTTCATCA TAGTATCAGA ATTATTAGGA	203940
TCATCCTCTA ATGACATAAT ATTCTCTTCA AGGATATCTA CAAGATTTTG AGCTTCTTCA	204000
AAAAAACTC CTAAAAGCTC TTCATTTTCC AAATCTAATA TTTCCATATA CTATTCCTA	204060
TTATTTTAAT ATGTAAAGCA AACCTTTTAG GTAGCTTTAC ATATTAATTT AAACCTAATT	204120
TTTCGGAGAT GATTCTTCAG GTTTTTCACT CTCAATCTTT TCTACAAAGT TTTGGAAAGA	204180
GCCTTCAGGC ATAGAAATTT TTTCTCTAAG CTTTAAACT CTTTAAAG TTTCGTGTGC	204240
CTTTAATTTA CGAAGGGATT CAGTCCGCT AGTCTCATAA ACTTTAAATA CAGACTCACT	204300
GTCAATATCA GAATCTATTG AAACACTCAA CTTATCATAA AGAACTCTTA AATCTTTAAC	204360
ATAAAAGATG AAATTTTGCT CTTTGAACGT GTGTGACTTT GAAACTCTAA AAGCCTTAAA	204420
TCTCATTTTA CTTGAAGCAA GAGGATAATT TGGAACATCG TCTTTAATAA TTCTGGATGA	204480

TATATTAGGA	ATATAGTTAG	GATTTGACCA	AATTAAATCA	CCCCACCCTT	TAAACTTTAA	204540
AGTACCCATA	GAATAAGCAT	ATTCCATGCC	ATTCATATCT	TCAAATAAAA	CCTCAAGATC	204600
TATCTCATAC	CCTAAACTAT	AAACAGATAC	CTTAATTTCT	TTCATGGTTT	TAATGTTATC	204660
AATAAGACCT	TTGCCTAAAA	ATTGATTGCC	ACTTTCCCCCT	GAATAAAAAG	GAATTTTAAA	204720
TGGTGGCATA	ATCATAGCAG	ATGATTGAGA	ATAGCTTGGA	AACAAAACCTC	TTACCCCTAA	204780
AATAGTATCA	CCTGCGTACC	TTTTTGACTC	ACTCTTAACA	ACAGCGGGCG	CAACAACCTGA	204840
ATTTTAAACG	TAAGCCTGCA	ACCTTGCGA	AGGAGTAAGT	AAAACGCTCC	AATTATTTAT	204900
CCCAAGATCT	ACAACCATAT	CTTCCGGCTT	AACAATACCA	GAAGCGCCCG	AATATACATA	204960
ATCAACATAA	TTTGTAAGAT	CAAGTCTAGT	TGAACTTGGA	TCTCTTGCAA	GCTCGGCAAA	205020
ATCTAAAACT	AATTCTCCAG	GCTCTGCCCT	TTTAGAACCC	TCTGCTAATC	CATCAGTCTC	205080
TTGAGCAAAA	AGAACAGTGG	ATAATAAAAA	AAATAAAATA	CTTTTAGCTT	TCCTTTTTCAT	205140
GTAACCAAC	TCCTTATATA	TATAAATCTT	TTATAAAATT	TTCGTTTTTTT	AATTATTTTTT	205200
ATTAGTAAAA	TTTAATTTAT	CAACTTTGCT	CCTTTAAGAT	ACACCCTTCA	ACAAGAATAA	205260
CAATCTTTTT	TATCTTACCA	GGATAGTTAA	AGCGCATTGT	TTTTATTAAA	GACATAGCAA	205320
AAAGATTGAC	CTTAACATCA	AAAGATTTCAT	TAGATTTCATT	ATAATCACCA	TTATTAAAAG	205380
AATCATAAAA	TTCTCTTGAA	AGATTTACAT	AATAAACTCC	ATTCTTTAAA	AAAGAATATA	205440
AAAATCTTGA	ATCACTTAAT	AAAAACCCAA	AAGAAAACCC	TTCATTGCTT	CCTAAAAGAA	205500
AATCTTTTAC	TAAAAGATCT	AAATTATCTT	TCAAATTTTG	TTCATCTCTT	AAATATCTTA	205560
AATTAGCAAC	AAATCCCTTG	CTAGAATGAA	AATAAAAAAC	CTTTTTTGAA	AAAAGATTAT	205620
CATAATTTAA	AAAAACCATA	CAAATAGAAA	ACAAAAAGCT	TACTGCCAAA	GACCCCAAAA	205680
GCACCCTAAT	CATATGCTCT	TTTTTTGAAT	TTAAAAATTT	ATAAATCACT	ACATTATATT	205740
TAAAAAATAT	ATCCGAAATA	TTATTTTTCA	TAAAAATTTA	TAAATTCCAT	TAAAGCTTTA	205800
AGTATTAGAA	TATTAAACTT	GCTCATGTAA	TTATAATCCA	AAATTAATTT	AGCATCTAAA	205860
ATATTGGATA	AAAACCCCAT	TTCAATCAAC	ACAGCAGGCA	TACTGCTGTT	TTTTATTACA	205920
AACCATTGCT	CTTTTCTGAT	TGGCCTAATA	TTAGTTTCGC	TTAACTCATT	TTTAAACACT	205980
TTATACAAAA	TTTCAGCCAA	TCTTTTTGAT	TCATATTTAT	ATTTAATATC	TAGTATATCA	206040
TTAAGCTCGC	TTAAGTATCT	ATTACCTTTA	ATATCATATC	CCTTAAATC	TTTAATAACT	206100
TCTCTTTTTG	AATCCTTAGG	AAGATACCAA	AACTCAACTC	CTCTAGCTTC	ACCGTTTGGA	206160
GCATCATTAG	CATGTATAGA	TAAAAATATA	ACATTATTGG	GGAAATTTGG	CTTTATTGCA	206220
TTTGCAAATT	CCGACCGTTC	TTTAAAGTT	AAATAACAT	CATTTATACG	AGTTAACAAA	206280

ATATTTTTAT	TTACAAAATA	ATTACTTAAA	ATTTTAGACA	AATATATAGA	ATAGGTTAAT	206340
GCAAAATCTT	TTTCCTGAAG	CACAACGTCA	TAACCATTTA	TCTTTAAAGT	CACAACAGCA	206400
CCAGTATCAT	GCCCGCCATG	TCCAGGATCA	ATGATTATTG	AAGTAATTCT	GGGTTTATTA	206460
TAGTCTTTAA	GAGAACTAAA	ATAATTTTCA	ATTTGTTTTA	ATACCTTTTG	ACTTATTAAA	206520
ATTTCTCCAC	GAATGTCAAT	AATTGGGTCT	ACAAACATAT	AATAACCAGA	AGATGTAAGC	206580
GCATATTCAA	AGCCTACCCT	AAACTTCAAA	TATCCCTTAT	CATTTTCAAT	TGTAAAAACA	206640
TCATTTTCAA	TGTAAAAATC	AAACCTAAAA	ACATTAGTAT	CAAAAAAATC	AAGAACATTT	206700
AAATAATCGG	GGGTCTTAGA	ATACAAGCTT	AAATATGAAA	ACAAAATCAA	ATCAATCAAT	206760
AATATCATTT	TCCCAAAGCT	CAATGGCACT	CTTTAAGTCT	CCTTTGAATC	TTAAGCTATT	206820
TTTAGTAATC	TCACCTTTTA	TCTCCTTAAA	CTCTTTTGG	AAGAGAAAAG	GATTAATTTT	206880
GTATTTTAAA	CAAATTTTGC	AAAACCTTAA	AAAAGAAAAA	ACAACGCCAT	TTCCAACAAA	206940
AATTGGGACA	TAATTCTTAA	GCAAAAAAAT	CAAAAACTT	TTGCTTTTGG	TTAAATTTTC	207000
TGGCGAATTT	AATGCAGTAT	ACTGGATTCT	CAGCTTCTA	TAAATATAAA	CATGCTCCCC	207060
AAAATAAATA	GCTCTTAGTC	CAAAATCTAT	TCTTTGAAAA	TATTCATTTT	GAATTCTTGC	207120
GTCAAAACCT	CCAAGCTGTA	AAAATTTCTC	TTTAGAATAA	AGTCCGCAAT	AATCCATGGT	207180
AATCAAAGTT	TTTTCATAGT	CTTTCTCAGA	ATTTACTAAA	ATTACCTTAA	ACTTTTGCTT	207240
TTTATCTATG	CTGGGAAGAA	AAATTGAAGG	AATCATTTCC	TCTTCTTTAT	CAAAAACTC	207300
CCCACCAACA	AGAAGAACAT	TTTTTTTTTAC	TATTTCATCG	AATATATTTG	GAATCCAAAA	207360
GGGATTTAAC	AAGTACATAT	CACTTTGCAA	AACAAAAACA	AAATCACAGC	TGGATTCTTT	207420
CATTGCTAAA	TTAACCTTTT	CCCCAGAATT	CAAATCGTCA	GAAAGTAAAA	TAAATTTTAA	207480
CTTACCATAA	CTTTCTGAAA	TAAACTGCAA	AGAACTTCTA	TTGCTCTGTT	TTTCAATTGA	207540
AATTATTTCT	CTTATAAAGT	CAAAATTTGA	TAAAAATTCA	AACAAATCTT	CTCTAAAAAT	207600
TTTTGTTCCT	CTGCTTAATA	TTACAAAAGA	AATTCCAAAA	GAAGATTTTT	GTGAATAATT	207660
ATTTTTAGAT	TGAATAACAG	TATATGAATA	GCCACTACCT	GGAAGACGCA	TAAATTACTT	207720
TTAAAATCCT	TATAATTAAA	TTATAATAAT	CATATGTTAC	ATAATACAAT	GCTAATTGCA	207780
AGAATAATGA	ATATTAATAC	ATTATTCTAC	GGCATGATCA	TTATCATTTT	TGCACTCATT	207840
TCTTGCAATC	ATAAGAATAT	ACAGTACGAC	AAGAGAATTA	AAAAATTTTT	AGATAAAAAAC	207900
AAAATTGAAT	ATAAAATAGA	CTCAGAAAAT	GACTTTATAG	CATTTAAAGA	TATAACAAT	207960
AACGAAAAAG	AAGAAGTAAT	CATCAGATCA	AGACTAAACT	CATATAAAAA	TTCAAAGATA	208020

AGAGAAATAT TTGGAATTGT TAAAGTATTT GATATAAACA CACCAAAAAT AAAAGAAATA	208080
TCTGACTCGC TTATGAGCGA TAGTTATAAT AACAGAGTAT TTGGATCGTG GGAGATTATT	208140
CATAATGCAG AAAGAGGAAT CAACTCTTTG GTATATATTG TAAAAGCAGA AGAATTTGCA	208200
AATGATACAT TTTTGCTTGA TGCAATTGAT GAGATTGCCT CAACAATAAG TATTTTCAAA	208260
AAAATAATAA CAACCAACAA CGAAAACATT GATAATAATG AAGAAAATAA CAATACAAAT	208320
GAATCAAATG AACAGCCCAC CTTAAAGCAA GAAAAACAA ATTCAACAAA AGAATCTAAT	208380
AACGAACTTA AAGAAGATCA AATAGAAGAA GAACTTCAAG AAATCAAAGC CCAATAATTT	208440
CAAAATCATT CTACTAATAA AGAATTAACA TCAAAGCAAA AATGAACCTT GTCACCTATT	208500
TTTATTTGAA ATTTAGAAAA TGAGCCCCTT GGAAGCTCAA GAGCATACCT TACCTTATAA	208560
AGAGAATTAA CATTTGCCCT AGAGTACGGC TCTAAATCAT AAATCTCTTT AATAATTCCA	208620
CTTGAATCAA TATAAGCTAT TTCAAGCAGC AAAGGTGTAT TTTCCATCCA AAAAGACAAA	208680
TTTGATCTT TTTTAAAAAC AAAAAGCATT CCATTGCCAT ATTCAACTTT TTGAGCACCC	208740
ATGTAACCTT TTGCCCTATC AAGCTCATTG GATGCTATTT TTACAAAAAA CTTAACCCCA	208800
TTTATCATAA TTTCTTTATC GTAAAAATGA TCAGCAAAAG ATAAAAAAGA CATCGACAAA	208860
ACTAAAAACA AAAACCGTTT TAAAATTTTT TTCAATTATC AGCCTTATTA AAAATCATTT	208920
ATTATAATTT GAAATATAAG ATTTTAAAGT AATTCTTAAA ATATTTTTTAT TTAAACAAT	208980
AATAGAATCA CCAAGATCCC ATAAATAATT CAAAGGCGTT ACTAGTGTAG CCTCGCCAAA	209040
CTTTTTCTTT ACCTCAATAA AAATTGCATA CTGAGATATT AATTTTTTAT CAAAAACAAA	209100
AGTGACGAA AACATTTTAT TTTTGTCAAA ATTAAAAACA GCATATTTTA AATGGGTTTT	209160
AGCAATAAAT TGTAAGTCT GCTTCCTAGC ATAAGGAAAT TCAACTTCTT CAACATCATA	209220
ATAAAAATA GTGCTCTTGA GAACATTCTC TTAAACAGAA TCCATGCTAG AACCCAGAAC	209280
AAAAGATGCA AAAATAGAAA ATAAATAAAA AACTGTAATA CCCATACAAA GCCTTTAGCC	209340
ATAACAATA TAAAGAAAA GTATAACAAA TAAAAAATT GAAAATAAAT AAAGCAAAAT	209400
ATCAATATTA ATCCCAAAAT GGAAAAGCCT TACAAAGGTC TTAGAAGCTG CTCTATCACT	209460
TACCATTCTT GCTCTTTCTT TTCTTTTAAA GGGCTTTTCT TTAAGTTCTT GAAAAGGACT	209520
GTAGTGACAA TTAGGACAAC CTTCTCCAAA AGCAGAAACT GGACCTACAT GCCTACAATT	209580
TGGACATTCG ATATCACCAA GCTTAGCAGC ACAGTTGGGA CAAACAGATC GATTAAGTCC	209640
AACTTTTTCG CCACATTGCT CGCAAAAAAC TTCAAATTTT ACCTTTGCCA AACGAAAATT	209700
CCTCAAATTT TACTTAAAA TAAGTATTTA AAATACTATA TAATTAATTA TAATAAAAAA	209760
TATATGAATA TTACATATTT AAGGAATACT AAAACATGAA ATCGGGATTT GCAGCAATAC	209820

TTGGTAGACC ATCAACTGGA AAATCTACCC TTTTAAATTC AATATGCGGA CATAAAATAT	209880
CAATAATATC CCCTATTCCG CAAACAACTA GAAATAATAT AAAAGGAATC TTTACGGACG	209940
ACAGAGGACA AATTATTTTT ATAGACACAC CGGGATTTC A TCTGAGTAAA AAAAAGTTTA	210000
ATATTGCAAT GATGAAAAAT ATCCACTCTT CAATAGGAGA AGTTGAACTC ATTTTATACA	210060
TAATAGACAT TCAAGACAAA CCTGGAGAAG AAGAAAAATAA AATGTTAGAA ATAATTAAAA	210120
ACTCTAAAAT TAAATTTTTA GTAATACTTA ATAAAATTGA CCTTAAAAAC ACAAAAATAA	210180
AAGAAATAAC GCAATTTCTA AAAGAAAAAG GAATAGAAGA TAGTAATATA ATTAAAATAT	210240
CTGCTGAAAA AAAAATTAAC ACAGAAGAAC TAAAAAATAA AATTTATGAA AATTTTTTCAG	210300
AAGGCCCACT TTATTATCCA CAAGAATACT ACACCGATCA AGAAATAAAT TTTAGAATTA	210360
GTGAAATAAT AAGGGAAAAA GCTATTGAAA ACCTAAAAGA AGAACTCCCC TATTCTTTGT	210420
ATGTGGATAT TGATACCTTA GAAAATAAAA AAGGAAGTCT TTTTATCAGA GCAAATATTT	210480
TTGTAGCCAA TGAAAGTCAA AAAGGAATAA TTGTAGGAAA AAACGGAAAA GAAATAAAAT	210540
CAATAGGAGA AAGGGCAAGA AAAACAATTG CAAAAATTTT TGAAACAAAA TGCAACCTAT	210600
TCTTACAGGT AAAACTTAAA AAAAATTGGA ACAAAGAAGA TAAGCTAATA AAAAGACTTA	210660
TAAATTAACA AACATTAAAC TGCATTTTTT TAAATTCCTG AAAGTTGAAA AACAAAATGC	210720
TAAAATTTAC CTAAATTTAA ATTAGGAATA AAATGTGAAA ACAGCACACT GGGCAGATTT	210780
TTACGCAGAA AAAATAAAAA AAGAAAAAGG TCCAAAAAAC TTATACACAG TAGCATCGGG	210840
AATTACTCCA TCTGGAACTG TGCACATTGG CAATTTTAGA GAAGTTATTT CGGTAGACCT	210900
TGTAGCAAGA GCACTAAGAG ACTCTGGATC AAAAGTAAGG TTTATTTATT CTTGGGATAA	210960
TTACGACGTA TTTGAAAAAG TTCCCAAAAA TATGCCAGAA CAAGAACTTC TTACAACCTA	211020
TTTAAGACAA GCAATAACAA GGGTCCCTGA CACAAGAAGC CACAAAACAA GTTATGCAAG	211080
GGCTAATGAA ATTGAATTTG AAAAATATCT GCCTGTAGTT GGGATCAATC CTGAATTCAT	211140
CGACCAAAGC AAACAATATA CCAGCAACGC TTATGCAAGC CAAATAAAAT TTGCACTTGA	211200
TCATAAAAAA GAACTGTCTG AAGCATTAAG CGAATACAGA ACCTCAAAGC TTGAAGAAAA	211260
TTGGTATCCA ATCAGTGTAT TTTGTACAAA ATGCAATAGA GACACAACAA CTGTAAATAA	211320
TTATGACAAT CATTACTCTG TTGAGTATTC ATGTGAATGT GGAAATCAAG AATCTCTAGA	211380
CATAAGAACC ACATGGGCCA TTAAACTTCC TTGGAGAATA GATTGGCCTA TGAGATGGAA	211440
ATATGAAAAA GTTGACTTTG AGCCTGCAGG AAAAGACCAC CACAGCAGTG GCGGCAGTTT	211500
TGATACATCT AAAAATATTG TAAAAATTTT TCAAGGTAGC CCTCCTGTAA CATTTCAATA	211560

TGACTTTATT	TCAATAAAAG	GACGTGGTGG	AAAAATATCC	TCCTCATCGG	GAGATGTCAT	211620
ATCGCTCAAA	GATGTTCTTG	AGGTCTATAC	ACCCGAAGTC	ACAAGGTTTT	TATTTGCTGC	211680
TACTAAACCA	AATACTGAAT	TTTCAATCTC	ATTTGATCTT	GATGTAATTA	AAATATACGA	211740
AGATTACGAC	AAATTTGAGA	GAATCTACTA	TGGAGTAGAA	GATGTAAAAG	AAGAAAAAAA	211800
AAGAGCATTT	AAAAGAATTT	ACGAACATC	TCAACCATAC	ATGCCAAGCA	AAAGAATCCC	211860
TTATCAGGTC	GGATTCAGAC	ATTTAAGTGT	AATCAGTCAA	ATATTTGAAA	ATAATATAAA	211920
TAAAATTTTA	AATTACTTGA	AAAACGTTCA	AGAAGATCAA	AAAGACAAAC	TAATAAATAA	211980
AATAAATTGC	GCAATTAATT	GGATAAGAGa	TTTTGCACCC	GAAGATTTCA	AATTTTCATT	212040
AAGATCTAAA	TTTGATAATA	TGGAAATACT	AGAAGAAAAT	AGCAAAAAAG	CAATTAATGA	212100
ACTTTTGGAT	TTTTTAAAGA	AAAATTTTGA	AGTTGCCACA	GAACAAGACA	TTCAAAACGA	212160
AATATATAAA	ATTTCAAGAG	AAAATAATAT	AGAACCTGCT	TTATTTTTTTA	AACAAATTTA	212220
TAAAATTTTA	ATTGACAAAG	AAAAAGGGCC	CAAATTAGCT	GGATTTATCA	AAATAATTGG	212280
TATTGATCGC	TTTGAAAAGA	TTACAAGCAA	ATACGTTTAA	GCCTTAAAAAT	TAATAAAAAA	212340
TAAGTCATAA	TTATATGACT	TATTTACACT	TTAATACAAA	TAAATCGTTA	CTTTAACTTT	212400
CCTTGACTAG	CAACAGATTC	CATTGCCTTT	TTAATTTTGC	TCTCATCACC	TAGATAGTAA	212460
TGTTTAATGG	GATTTAAATC	TTTATCTAAT	TCGTAAACTA	AAGGAATGCC	TGTGGGAATG	212520
TTAAGCTTTA	AAACATCTTC	TTCACTTAAA	TTGTCAAAAT	ATTTAACAAG	CGCTCTTAAA	212580
GAATTACCGT	GAGCAGCAAC	AATAACTTTT	TTACCTTCAA	GAACTTCTTT	TGCAATCTCA	212640
TCAGTCCAAT	AAGGAATAAC	TCTTGCAACA	GTATCTTTAA	GGCACTCTGT	TGAAGGAAGT	212700
TCCCTTTTGG	GGATATGTTT	ATATCTTGGA	TCTTTTATGG	GATGACGATC	ATCAGACTCA	212760
TCCAAAGACA	TTGGGGGCAC	ATCATAACTA	CGTCTCCAAA	TTAAAACCTT	ATCTTCCCCA	212820
TATTTTGCAG	CTGTTTCTGA	CTTATTTAAA	CCTTGCAAAG	CTCCATAGTG	CCTTTCATTT	212880
AATCTCCAGG	TTTTTTTTTAC	ACTAATATAA	GATTGCCCTA	ATTCTCGCAA	AATAATATTT	212940
AAAGTGTCAT	TAGCTCTTGA	CAACAAAGAA	CTAAAAGCAA	TATCAAAAGA	ATAGCCTTCT	213000
TGTTTGAGAA	GCAAACCCGC	CTCAACAGCC	TCATCGATAC	CCTTGTCAGA	AAGTTTAACA	213060
TCTGTCCAAC	CAGTAAAAAG	ATTTTCTTTA	TTCCACTCAC	TCTCTCCGTG	TCTTACTAAA	213120
ACTAATTTAT	ACATAAAATC	TCCTAGCATA	TTATTTTATT	TACCAATACT	AATAATTATA	213180
AATTAGCATA	AAATCTAGTC	AAGATTTAAA	CCTTAGTAAT	TAAATAATGA	TATACTTTAA	213240
AATACATTAA	GCTTTAAGTT	TATCAAGCAA	GGAAAAGAAT	TTATGGAAAA	TCAAAAAAAT	213300
TTGGTAGCAA	AACATGCAAT	TGATCACTAT	ATCAAAAGCA	ATATGAACCT	TGGAATCGGA	213360

ACAGGTACAA CTATTTATTA TGCAATAAAA TATCTAAGCG AAAAGATAAA ATCGGGTAGC 213420
TTAAAAAATT TAAAATTCTA CACAACAAGT AGTGATACAA AATATTTACT CTCAAAAGAA 213480
CAAATTCCTT ATGAATCAAA TTTTTCAAAA CTTAATAAAA ATCTAGACAT TGCAATTGAT 213540
GGAGCTGATG AAATTTTATT AGAAAAAAA AGCTTAATAA AGGGAATGGG GGGTGCTCAT 213600
CTAATGGAGA AAGTAATAGC CTACAATTCA GAAACATTGC TAATAATAGC AGATGAAACC 213660
AAAATTGTTA AAAAATTAGG AACAAAAATG CCTATTCCCA TAGAAGTTGC CCAAATGCT 213720
GTTGGATTTA TTATGACTAG ACTTGAAGAA ATGAATTTAG AGGCAACCTT GAGAATTTGT 213780
AAAGAAAAGA AAGGCCCCAC TATAACTGAT AACAATAATT ATATCTTAGA TGTAAAAATG 213840
CATGTGGAAG ATCCTGAAGG AACAGAAAAA TACTTCAAAC TATTTCAGG TATACTTGAG 213900
ATTGGAATAT TCAACCATAA AAACACAAGA ATAGTTTATT ACCAAGACAA ACAAATCAAG 213960
GAAGCCTAAG CTTAACTTTA AAAAAGTTAT CATTAAAATG GTTTATAATT TTTACTAAAT 214020
AAAAATTTAA CTAAACCTT TCTCTCCCTT TTAATAGCAT AATATTATCA TCAAAAACAA 214080
ACTTTTTACT TAAAGTTGAG CAGTAATTAA TAAACTGAAA AAATTGTTTT TCATTATACT 214140
CAAATCTAAG CCTAAGAGCC CTCAAGCTGA CACCTTGAAT GGTCCAAGC CTTGAATAA 214200
AATGATAAAC AAAAACTCC AAATCCTCTA ACAATTCAAA CGTTACTAAG TGATTATTTG 214260
CTTTGACAAA ACTACCAGTT TTTCTAATCA AAGCTCTTAC ATTATTATTC TTGTCATTAC 214320
AAAAAAGCAA ACTTACAGCA TACAATCCTA ATCCTAAATG CGGCTTTAAC TCCCAATTTA 214380
GCTTATTGTG CCTGCTCTCA TGCCCCTTTA ATGCAAAATT AGTAATTTCA TAATTAATGT 214440
AGCCATTGGA TTCTAGACAC TCCAGAGCAC AAAACCACAG TTTTCCGAA TCAATACTGT 214500
TATCAAAATC TCTCAAGACA AAGCCTTCCT CTTACATAT AAAATCGCTA AAACAAATAT 214560
GCTCAGGCAT ATATGAAAGC AATTCTTTgc AAATCTCGCT TGAGATGAGA TTTTTTTTGC 214620
AAAGGCATAT TGACAGTCAT GTCAATATTC AAATCAAAAG GAACTTTCT AATATTGTTA 214680
ATCAAAATAT TCAATTTTTT ATAAGAAATT TCGGGTATCC CCACAATCTT TCTAACTCT 214740
AAAGAAAAC TTTGAACATT AAGATTAATT CTAGTAATAC AAAATTCATC CAAAAGTTTG 214800
AATTTTTCAA AATCAACATA ACCCGGAATA ATTTCTAAAG TAAATCTTC TAATAACTCC 214860
AAATTAATAT ACTTGACAA AGAAGTGAAA ATAAATTTTA AATTATCTTG CCTAGATAAA 214920
CAAAAATCTA CGTGCTTAAT GTAAAGTGTT TTTATAATTG GATGACCCAG CAAGATTAAA 214980
TGACATTTTA ATTCCTCTAA AATTCTATTA AAAATGCTAA AATCTTTACA ACAAATGAC 215040
AAATTAATAT AAAGACTTAA CTCGACAAGA GGTAAGAT CTACTCTCAT AATTGGTCTT 215100

TTAAAAATTT	AGGTTTAATT	ATAACATATA	TAAAGTATAA	ATATTAAAAT	ATATTTAAAA	215160
AATACAATAA	ATAAGGTAGA	TTGAAGGAGA	TTTTTTAATG	ACCAAAGACT	ACTACAATAT	215220
ACTTGGAATA	CAAAAAAATG	CTAGTAATGA	GGAAATAAAA	AAAGCTTACA	AAAAATTGGC	215280
AATAAAATAT	CACCCAGACA	AAAACAAGGG	AAACAAAATA	GCTGAAGAAA	AGTTTAAAGA	215340
AATAAATGAG	GCTTATGAAA	TTTTATCTTC	TCCTGATAAA	AAAAGAAATT	ATGACTCTTT	215400
GGGTAACACA	AATTTTAATG	GCAACAACGA	CCATTTTGAA	AGAGAATTTA	GCAGCACAAG	215460
ATTTGGCAAT	TTTGAAGATT	TAGATTTTTT	TTCCAAAATC	TTGGCGGAT	CCTCAAGAAA	215520
AACAGCAGAC	AGAGAAATAA	TTATAAATAT	TTCACTTTAT	GATGCTTATA	TGGGAAGTAA	215580
AAAAATAATA	CTTATAAACA	ACAAAAAAT	CGAGGTAATA	ATTCCAAAAG	GAACATTAGA	215640
AACAAC TACA	ATAAAAATAA	ACAACAAAGG	TCCCATTAAT	CCAATTTCTG	GAATAAAAGG	215700
AAGCTTAATA	GTCAAATTTA	ATATATCAAG	TTATAAAAAT	TTTAAACTGA	ATGGAAAAAC	215760
CTTAGAAACA	ACAATAGAAG	TTTACCCCTG	GGAAATAGCT	TTGGGTTGCG	AAAAGCTATT	215820
TGAAACAATT	GAAGGGAAAA	AAATAAACT	TAAAATCCCA	TCAGATGCAA	AAAATGGAGA	215880
AATTCTAAAC	TTAAAAGGAT	TGGGGATGCC	TATAATTGGA	AGCAGCTCAA	AAAGGGATCT	215940
TAAAGTCACT	TTGATAGTAA	AAATTCCTAA	AATAATAAAT	AATGAAGTAA	AAACTATTTA	216000
CGAAAGATTA	AAAGAGATAT	ACAGCTAAAG	TGTTTCTGAA	AATAAATGAC	CAAATTTTTT	216060
TAAATTTGCC	TCCCAACCCG	ACCTATATTC	ATTAAATTTA	TTTATTTTAG	ATTCATATTC	216120
TTTGATTCCA	TCCTCAATAT	TATCAAAATT	TTTAGCAATA	TCCACTGAAA	ACTGAAAAAC	216180
ATCCCTTGT	CTGGGAGCAA	GAGTAAAAAA	AGCAAATTTT	CAATTTCCAG	AATTTATAGT	216240
AGATACAATC	CTTTTTTTGA	AAACATAATC	GGAGATTAAA	ACAAATTTTT	GAAACTCTTT	216300
TCTTCGCAAA	TAAATAAGCT	CATTCCACTC	ATTAAAAATA	GCATCCGGTA	ATTGTTTAA	216360
ACCAATCTCA	ATTATATTAT	TAATAGATAA	AAGAATTTGT	AAAATTTCTA	ATAAATTTAA	216420
ATAATAGCTA	TCAAAACATT	GAATTGTAAT	TTCAAGCAAa	GCAATTTTTA	TAAGTAGTTT	216480
AGAAATGTCA	AGACTATGAT	CTTTCATAAT	TTTATCAATT	CTCTCTTTTG	TGTGATCTAT	216540
AATAAATTTT	TTATGAGTTT	CTTTAATATT	GCTACTTTTT	TTAATTTGCT	CTACTTTTTT	216600
ATAATAATCA	TTAATTTCTT	TATTAATTAC	ATCTAAATTA	TTACTATTGG	CCTCATTGGA	216660
AAAAAATCC	AATGAATTAC	TAAGTCGATC	TAAAAATTCT	TCTTGAATAA	AAAATGTGGC	216720
AATTC TTATG	CAAGAAAATG	GAGCCTTGCT	CTTTTTTTCA	AAATTTTCAA	TTTTTTGTTT	216780
AAGATCTACT	CTAAAATTTA	AATATTTAAG	CTTGTCTAAA	AATTTATTAA	AACAGGAAAC	216840
ATCTTCTAAC	AATTCATCTT	CATGAATGTC	TAAAAATTGG	GAATTAGGAT	GATATTTTCT	216900

TATCAAATTT	TTAATAATAA	GTAAAGTATC	TAAAAAATA	GCTTTATTGG	CACCCCAAGA	216960
TTTATTGATA	CTGGGATTAA	AATCCCTATA	AATCTTATCC	AAAAACAAA	GTTTATCTTT	217020
TAGCAAATTA	GCATCGTTAA	TAAGGCTTGA	CTGTTCTCGA	TAAGAATAAT	AATTTATTAA	217080
ACTATACCTA	AAAATGCTAA	AATTAAGATA	TTTTTGAAAA	TCAAAAAATC	TATAAAATCC	217140
TAATGAACCA	AAATCAAAA	ACTTCATGCC	ACAATATCAT	CTTATTTAAG	ATCTACTTTA	217200
TCTTTTTATA	CAGGTTTAA	AGTATTGGAG	ACGCTATGAA	TACAGAAGAA	TAAGTTCCAA	217260
CAATTACCCC	TACCATAAAT	ACCAAAGAAA	AATCTTTTAT	AGATCCTTCA	GTAAACACAT	217320
AAATAGAAAA	TACTGCAACA	AATGTTGTAA	CTGACGTCAA	AACAGTTCTT	GATAAAGTTT	217380
GACTAATACT	TATGTTTAAT	ACATTTAAAA	ATGTGTTATC	GGTTAATCGC	TTAACATTAT	217440
CTCTAATCCT	ATCAAAAATA	ATTATTGTGT	CGTTTAAAGA	ATATCCAATA	ATGGTAAGTA	217500
TTGCCACAAT	AATATAGCTA	TTAATCTCTA	TTCTAAATAC	CCCTAAAAAA	GCAACTATAA	217560
AAAATATATC	ATGAAATATT	GAAAGTATGG	AAGCAATAGC	ATAACTTAGT	TTAAATCTTA	217620
AAGTTATATA	AATCAAAATC	AGGATAAATG	TTCCTAATAC	CAAAAAAATT	GACCTAATTC	217680
TCAAAGTAGA	AGAAAACTT	GAATCAATAA	AATAAGAATC	CAAAACTTCA	ATATTAGCAT	217740
CAAATGTTTC	TTTAAGTTTA	TCTAATATTG	TTTTTTGAAC	TTCTGTTTTA	AAAGCATAAT	217800
CAATCACATC	AGACTTTACC	ATAATAGAGA	ATTCACTTTT	ATTCTGATCT	GGTGAAAAAA	217860
TACTATTAAC	ATCTAAAGTC	TTATAAATCG	GAGAGAATAT	TTTTTTAATT	TCATTTTCTT	217920
TAATATTTGA	TTTTTCTATT	GAAAGATTAA	TATTAACCCCT	AGAAGAAAAA	TCTATTCCCC	217980
AATTGTATCC	ACCATGATAA	AAAAAAGTAT	AAATAAGCCC	AACCAAAATC	AAAACGGCAC	218040
TAACAATTAA	AACATTGCTT	CCATATTTTG	AAAAATTAAT	TACTCTTTGC	ATATTTTGAA	218100
CTCCAAGATA	TACTTATAAA	TTTGCTTTTT	CTAACAGATA	TGATAAATTC	CAAATAAAT	218160
CTTGAAAAAA	TCAAACACT	AAAAAGGGAT	GCCACAATTC	CAACAGAAAG	AGACCAAGCA	218220
AAACCTTGAA	TAACTCCTGT	CCCAAGAAGA	GTTAAAAAAA	GCACCGCAAT	AAATGTTGTT	218280
ATATTTGCAT	CCATAATTGA	TAAAAATGCC	TTTTTAAAC	CAGCTTCAAA	AGCATTTTCA	218340
AATCTTCTGC	CTTCTCTAAT	TTCTTCTTTA	ATTCTCTCAT	AAATAACTAT	ATTTATGTCA	218400
ACGGCCATAC	CCATTGTCAA	AATAAGACCT	GCAATGCTTG	TTAAAGTTAA	AGTAAAATTA	218460
AAGGCCGACA	ATATCGCTAA	AATTAAAAAT	ACATTATAAA	TAACAAGTGA	AAATCCAGCT	218520
ACAACACCAC	TCAAACCATA	ATAAACACAT	ATAAACAAAA	AACTAAACA	AAGAGCAAGC	218580
GCAGAAGCTT	TAATGCCAAG	ATCAATAGTC	CTAGCACCAA	GAGTAGGCCC	TATTATTCTC	218640

AAATCATCTA	TTTTAATATC	AACTGGAAAA	GCTGCAGTTT	TAAACACTAA	AGCAAGATCT	218700
TGAGCCTCTT	TTTTATCAAA	AGAGTCACCT	TGAATTGAAA	CATTGCCCCC	AGTGATAGCA	218760
TATCCAATTC	CTGCCACAGA	CTTAATTTTA	CCTTCCATAA	CAACGGCCAA	AGACTTTCCA	218820
ACATTTTTTT	GAGTAAATTT	AAAAAATTTT	TCACTTCCAT	CAACATCAAG	GCTAAAAGCA	218880
ACAGTATCTC	GGCCTGTTCT	AGGATCGTTA	GAAACCCAG	CATCTTTAAT	GTGAGCACCA	218940
TCAAATGAAT	TTTCAGGGCT	TGCATCAACT	ACATAATAAC	GAAC TGATGA	CTCATCATCC	219000
ACACCATAAG	AATCTTTAAC	ATACCAAGGA	AAAATTTGTT	TACTATCTGG	AAGGTTTATA	219060
CTTGCCCTGAA	TTTCAGGAAT	AGAAAAAAGA	GAGCCCGCTT	CTAATATTTT	TCTATGCAAA	219120
AGAGATGTAG	ACTCATCATC	AACCACATAA	AAAGTCAAAT	TGCCTTTACC	GCTCAAAAGA	219180
GTGCTTACTC	TACTCTCATC	TTTTTCTCCA	GGAATATCTA	AGAAAATTTT	ATTTCCCCCG	219240
GCTTCTCTTA	CAATTTTAGG	CTCTGTAAGC	CCGAACCTAT	yTACCCTATC	TTTAAGAATT	219300
TGCATTATTC	GATAAATGGC	ATCCTCTCTC	TCAGCAAAAAG	TCAAAGAACG	ACCTAATTTT	219360
TTTTCAACAC	TTGAATAATC	AAGAGAAATG	GTAACACTCA	TCCCTCCAGA	CAAATCAAGC	219420
CCAAGATGTA	TTATTCTGCT	TTTGCCCTTC	TTTATGTTCT	CATAATATCT	ATAAATCTCT	219480
AAGCTTACTT	CTCCCATATC	CGAATCAGTC	AAAAATCCTT	CACGCAAGGT	TTTAGCAGTA	219540
AAAATATTAG	GTGGAATTTT	CATTGAAGAC	CTATAATTAT	TTTTTGCTAT	TGGAATTAAA	219600
TAAGACAAAC	TAGCTGGAAT	ACTGCTATTG	GGATCTTTAT	TATACAGTTC	CTTAAGCTTA	219660
ACAAGATCAT	TCAGGGCTTT	TTTCTTTGAA	TAATCCCTTA	AGGCCTCTTG	TGAATATGAG	219720
CTTATTTTTT	TATCCTCAAC	GCTCATTTAA	AAATACCATT	TTAAAGTCGG	AAATATTTAA	219780
AGACATGCAA	AAAACGTCAC	CAACAATATC	AATATAAGCT	TAGATCCTTT	TTTCATTATA	219840
CAAATCCTTA	AAATTTTTTA	AAAATACCAT	TATTAGCTAA	CAGTTCTAAT	TTTACCTTTA	219900
AACAATACCT	TTTTTTTTAA	TTCATTTTTT	TTTCAAGAAA	ACTTTATCAA	TAGAGTTTTT	219960
TATAAATACT	GCTTCGTTAT	TTGGACTTAA	TTCTAAAATA	ACATCCGTAT	CGCCTAATTT	220020
TTTCACAAC	CCAAAAATTC	CACCTATTGT	TAATACCTTA	TCGCCCTTTT	TTAGATTTTT	220080
TATCATTTCT	TTTTTATTCT	TCTCTTCCTT	ACGCTGAGGA	GATATCACTA	AAAACCAAAA	220140
TATAGCAATA	ACAGGCACAA	AAACTAATAA	ACTTCGTAAA	AAGCTACTAT	TGCCGCTAAA	220200
TTCTTGCAAT	AAAAACACAA	AACCTCCCAT	ACTATACATA	TGTCACTTTT	ATCTTATTAA	220260
TATCATCAGG	ATAAACTACT	CCAAATAAAA	GCTTAAAATC	ATCTTTTTTG	GTATAATTAG	220320
AGTTACTTAT	TTTATTATAC	TCTTCAATTA	AATAATTAAT	AAGACCATCG	TCATTCCCTAT	220380
AAAGAGCTTT	GCTAAAGGCA	CTTCTGTAAA	GTCCAAGTTC	AAAAAGTTCC	TTAGCACTTT	220440

TACCCTTATT TTCTCTTAAA AGCTGCCTAT CTACTATTGC CTTTGAACAA TCATAGCCTA	220500
TACAAAAAAC AAATTCATCC TCACTCAAAA TAATTCCTTT GAATAATAAA ATATTCACCG	220560
GCAAAAAACAC AAGCTTGCCG GTGAAACTTT AATTACATC ATTCCCATTCT CTGGGTCCAT	220620
AGGATAACCA CCACCACCAG AAGTATTTTT CTCTCTTTA ATATCTGTGA TTGCACATTC	220680
TGTTGTTAAT AAAAGTCCAG CAATTGAAGC AGCATTTTGA AGCGCGCTTC TTGTAACCTT	220740
AGCAGGATCA ATTATTCCAC TCTCAATCAT ATTTACCCAC TTAAAGCTGG AAGCATCAAA	220800
CCCAAGCCCT TTTTTTCTG TTTTAATTTG ATGAATATAA ATAGATCCTT CAAAACCAGC	220860
ATTTGAAATA ATCTGTCTCA TTGGCTCTTC AAGACTTCTT TTTACAATCT CAAAACCTTG	220920
CTTTTCCTCA TAGCTTAATT TACTTGATC TATTGTATCT AAATACATAG CAACTTCAAT	220980
AAGAGTTGAT CCACCGCCAG GCACAACACC CTCTTCAACA GCAGCACGAG TTGCAGAAAG	221040
AGCGTCCTCA ACTCTATGCT TTTTCTCCTT AAGCTCTACC TCAGTAACAG CTCCAACATT	221100
AATAACAGCA ACTCCGCCAA CAAGTTTTGC AAGACGCTCT TGAAGTTTTT CTTTATCATA	221160
TTCAAGATGTT GAATCTTCAA TTTGCTTTTT AATAAGCTCT GAACGCTCCT TTATTTGCTC	221220
TTTATTGCCG GTATTAATAA TAGTGGTATT GTCTTTATCA ACCTTAATAG TTTTAGCCTG	221280
TCCAAGTTGC TCAATTTCAA CTGTCTCAAG AGTAAGGCCT AGCTCCTCAC TGATTAAAAC	221340
ACCGCCGGTA AGCACTGCAA TATCCTCAAG CATTGCTTTT CGTCTATCAC CAAAACCAGG	221400
AGATTTAATT GCACATACCT TTAAAGCTCC TCTAACGCTG TTTAAAACAA GAGCAGCAAG	221460
AGCATCCCCC TCAATATCCT CAGCAATAAT TAATAAAGGT TTATTTGTCC CTAAAACTTT	221520
CTCAAGAACT GGTAAAAGCT CTTTAATAGA ACTAATCTTT TTCTCATATA TCAATATGAA	221580
AGCATCGTCA AAATTAACAC TCATATTTTC TTTATTGGTA GAAAAATAAG GAGAAAGATA	221640
TCCTCTATCA AATTGCATAC CCTCAACATA AGAAATCGTA GTATCAAAGG TTTTGTACTC	221700
TTCAACTGTT ATAACACCAT CTTTCCAAC TTTATCCATT GCCTCAGCAA TTTTTCACC	221760
TATATAACTG TCATTATTAG CAGAAATTGA AGCTACTTGT GCAATCTCTT CTTTGTGTGT	221820
AATCTTTTTT GCAGACTGAC GAATTTTCTC AGCAGCCAAA TTTACAGCGT GATCTATTCC	221880
CTTTTTTATT CCAATAGGAT TGATTCCTGA AGACACATTC TTAAGGCCTT CTCTTGCAAT	221940
AGCATAAGCA AGAACAGTAG CAGTTGTTGT TCCATCACCA GCAACATCAT TTGTTTTAAT	222000
AGCAACTTCC TTTAAAAGCT GTGCCCCCAT GTTTTCAAAC GGATTTTCAA GCTCAATCTC	222060
ACGAGCAACG CTAACCCCAT CCTTTGTAAC CGTTGGAGAG CCGAACTTTT TATCAATAAG	222120
GACATTTCTC CCTTTTGGCC CAAGAGTTAC TTTTACAGCA TTGGATAATT TTTCAACGCC	222180

ACTAAGTAAG CTTTTTCTAG CATCCTCATT AAAATATATG TCTTTAGCCA TAAAAATTTT	222240
ACCCCTTTCT ATAAATAAAA ATAATTTACA TATAACAATA TAAGATTAAC ATAACTTAA	222300
TACATTGCGT ATAGTAGCGT ATTACTTCTA TGCATCAAAA AATACAAAAT ATACAAAACC	222360
AGTAAAAATT TTTATTATAT AATGTAAATA TTGACTAATC TTTAAATTAT AAAGACAAAG	222420
AATTTATGTT TAGAAAATA AAAAATTGA AACTTATAT TATTATTATT TCAATAACTA	222480
AATTTTCAGA AGATAACCTG TTATTAATAA TATCAAATAT AAAATATTTG ATTGAACACA	222540
AACAGCTAGC TTACAAAATA CATTGGACAT TTCCAATATA CTTTTTTGAA ATTCTAAGAG	222600
AACATGAGGA ATTAAATAAA TGGCTATTTG AAAGATTCAA AACCAATACA GATATATATA	222660
TGCCTGGAAC TTACAGTGGA AGCCCTCATG AATACATGCT ACACGATGAA ATACATTTAG	222720
ATTTGTATTG GGCACATAAA AATCCATTCA AAAGTGGATA CAAAGACATA TTTCAAAATA	222780
CGCCTATTAT GTTTTATATA TACAACATAG AAAAGTTTAG AAAAAAGGTG ACTGAGCTTT	222840
ACAGAAAGCT TAATTTCAAT TATACAGAAG GAATAAGGCA GAGTAAAAAT AATAAAAAAT	222900
ATTTAATTTT TTATAAAAAAT AACTGCCAAT ATTTATATGA AGTACAAAAA ATAGATTCTC	222960
CAAAAAGCAA CGTAGAACT CTTATTTATT TTTATGAGAT CAAAGAACT TATGATAATC	223020
AAGAACTAAA AAATTTTSTA CTTTATTTAA AAGCCCTAGA AAACAACTTA CACAGCATTA	223080
AAATACAAAA TCTAGAAGGA TCCAACTTA CCACCGAACT ACTAGAGATT CCAAAATTTA	223140
ACTCCCTTAA AGAGCAAGAG CCAATAATAA ATTTTCAAAA CAAAGACTC AAAGATTATC	223200
AAATCAACGA AAAAAGCTTA AGAGAATTTT TAATAAATAA ACACCAAGAT GAAATCATTA	223260
AAAATTCAGA ATCAATTGTG CCTAAAAATT TAGAATACAA TATGGAAGGA AATTTACGC	223320
TATCTCACGA TCAATACAAC ATCAAATTCG AAAATGGAAA ATTAAATAAA ATAAATTTA	223380
AAGATAAAAA AGTTGAATTT TTAAACACAT CTAGAACCTA TTTTAAAGTT TCATCAAAAA	223440
AAGAACTAAT AAAAGAAGCA TCTATTGAAA GTTCATTTTC ATTCTCAAAT GAAAAATTT	223500
TAGGAATAAA ACAATATTTA GCTTTTAACT CTGCCAAAAA ATCAACAATT GATTTTTTTA	223560
TAGATGAGAC TATCTCTAGC TTCTTTATAT CGATTAAAAAT AAAATGGCCT TCTAAAATAG	223620
ATCTAGATAA AAAACATTA AAAAATGCA ATCCTGATTA TCTTCTTGAA TATTCAGCTC	223680
TTGAAATACC TGTTTTTGAA ATTACAAAAG GCACTAATTT AAAAATAACA GCAAAATACA	223740
GCGATCTTGA TACTTATGAA AAAATAATAA TAACTAAAAA CAATCCCAA GGCTACATTA	223800
ATGGCACAGA ATTTTTGATA TCTAAAGGAA ATGATAAAAA CAGCAACTTT TTTATAAGCT	223860
TTTTAAATGT TGAAAAACAT ATCATTCATA CAATTAATTA TAAAATTGAA AAAATAAAT	223920
CTAAGAAATG GTTAATTTTA AATATAGGGG GTTCTTATAA CACAGTTAAG ATCCAAGATG	223980

TAATAAATTA CTCTCAAACA CTAAATTTAA TGATACTACC ATTAAATAAT AATTTTGATA	224040
ACAAAATAAA ACTGAATTCA AAAATAAAAA ATTTAATTTT TTATACTAAT ATAAAAAAAT	224100
ATGAAAATAA ATAAATAATA AGTAGTAAAA TATTAATAAC TGGGTATAAA ATTATCCTAA	224160
GAAGAACATA AAAAGTATTT AATCTTTAAT TTAAACAAAA AAGGTATAAT CATATGAACG	224220
ACAACATAAT AGACGTACAT TCCGCATTGG AAAAAGTCGG CATTACAAAC GATCCTGTAT	224280
TATTGAAAAA TTTAACATCA GAATTAGGAA TGAAAGCATC TCATTGAGA AACAGAATCA	224340
TTTTATACAT AGCATCAAAC CCAAAGAAT ACTTTACGGC AAAAGAAGTT TATAACAAAC	224400
TTATAAAAGA AATTCCAAGC CTATCAAAG CAACAGTATA TAACACATTA AATATTCTAA	224460
AAGAAAGAAA TATACTAAAA GATATAAAAA CTA CTGATCA AAAAGAAACA AAATTTTATC	224520
TAAGCTTGGC TTCCACAATA GCTCACTTTA AATGCAATAA ATGCAATCAA GTCCACCCTA	224580
TTCAACTTGA CGATATTAAA GATATTTTGA AAGACAACT TGGAGAAAAC TGGGAAACAA	224640
AATCTATTGA AATCATTTAC TCAGGGCATT GCAATAATTG CTACAAAAAA GATACCCATA	224700
ATAACAATAA TGTCCCAGAT GAGAACAAGG AAATCACTTT ATGAATATAA AAAATATCAT	224760
TTTTTACTT ATATTCTTAT TACTCTTAAT ACTGGTTAGT CCGAGGATAA AATTTAAAAA	224820
TGAATTTTCA AAAAACTGA TTCCTAAAAA CATAGAAGAA ATTGACAATT ACTTATTAAA	224880
AGAAGAATTG CAATTTAATT TAGAAAGCAA TACAAAAAAA GAAATAATCT GGTATAAAGA	224940
AAAAGCACAA AAAACAAATT ATTCTGTGGT CTATATTCAT GGATTTGGAG CATCAAAAAA	225000
TGAAATTTAT CCGGTTCCAA ATAATATTGC AAAAGCTCTT AATGCAAATA TTTTTTTTAC	225060
AAGACTTAAA GGACACGGAA TTAACAATAA AAATGCATTT CGGGGAATAA CTACCCAAGA	225120
TTGGCTGAGA GACATTGATG AGGCTATTAA CATTGGCAAA TTAATAGGTG ATAAATTAGT	225180
ATTAATTGGA ACCTCTAATG GGGGCACTGC CAGCATCTGG GCCTTGGAAC ACTATCCAAA	225240
TGAAATAAAC TCGGCGGTAT TAATTTCTCC TAATATATTC CCTTATGACA AGAGAACAAA	225300
TATCGTTTAC TATCCTTGGG GCGGACAAAT TGCATATCTT ATAACAGGTG GCTACAATAA	225360
ATTCGAAACA AAAGAGTATA AACGAAAAGA ACACCCGACT ATAAAAAGCC ACTCTTCAAG	225420
AGTACAGCAT GTAGACGCAA TTATTGCAAT GATGGGCCTT GTCACATTAT TAAATTCATA	225480
TAATTTCAAC GAAATCAAAA TACCTTTAAT AATAACCCAC ACACCAAATG ATCATAACGT	225540
AGACCCAATA AAAATAAACG AATTTATAAA AAATTATGGG GGTGAAAAAA AGGATATTCC	225600
CATCATACTT CTTGAAAATT CACACGCTCA CTTACCTATT GGAAACCAA GCTACAAAAG	225660
CGCCCCAAAC ACATCATACT TCACAAAGTA TGTATTTGAT TTCATAAACA AGATTAATAA	225720

GTAATAGCCT TAAGCTATTA CTTATTAAAA AAATCAAGCC TCTAGCAATT CTTCTATTTTC	225780
ATTCTTAAGA AACTAACAC CTGGTCCGTA AACTACCTGA ACCCCATTGC CTTTAATAAT	225840
TACTCCTTTA GAACCAGTTT TTTTAAAAAT TTTTTCAGAA ACTTTAAGAA CATCCCTTAC	225900
TGTAATTCTA AGCCTAGTTG CACAACAATC AAGCTCAACA ATATTTGAAG CACCACCAAG	225960
CCCAATAATA ACCTTAGTGG CATAATTTTC TTCAAATTCA CTACTCTTAG AACTTGGAGA	226020
ATCTTCAGAA TTAAATCTT GCGTTCTACC CGGAGTTTTA AAATCAAACCT TATTTATTAA	226080
AAATATAAAA GTAAAGTAGT AAAGAAAAAA CCAAACAATG CCTATAACTG GCACCAAAAAG	226140
CCAATTAGTT CTTGAATTTT CCTGCAAAAT GCCAAAAAGA ATAAAATCGA CAAACCCTCC	226200
AGAAAACGTT TGACCTATTG TAATTTGCAA AATATGCGCT AGCATGAAAG CAAATCCATC	226260
AAATGTAGCA TGAACAACAT AAAGAATAGG GGCTACAAAA AGAAAAGAAA ATTCAAGAGG	226320
TTCTGTTATA CCTGTAAAA ATGACGTTAG CGCTGAAGAC ATCAAAAGAC CAAAACTTT	226380
TGTTCTCTCC TCGCGCTTTG CAGTGTAATA TAGAGCAAGT GCAGCTCCGG GCAAACCAA	226440
CATCATGGTA ATAAATCGTC CACTCATAAA ACGGCTAGTT CCGATAAAAA ATCTATCTGT	226500
ACCTTGGGCA GCAAGTTCTG CAAAGAAAAT ATTCTGAGTT CCTTCAATTA ACTTTCCATC	226560
AATAATAACA GATCCCCCAA GGCCTGTTGT CCAAATGGC AAATAAAATA TATGATGAAG	226620
ACCAAAAGGT CCAAGCATCC TTAAAAAAT CCCATAAATA AGTGTTCCTAA TATAACCGGT	226680
TGAATCTACT AAGCCCCCTA CTTTATTAAT TCCACTTTGT ACAAATGGCC AAACAAGAAA	226740
CATAATAACA GCAAGAAAA TACTAGAAAA AGAAACAATG ATCGGAACAA ATCTAGATCC	226800
AGAAAAAAT CCAAGAACCT TAGGTAAATC TACTTTGTTA AATCTAGAAT GAAGATAATA	226860
AGTCAAAATA CCAACTACAA CCCCGCCAAA ACCCCCGTT TCTAAAGTCT TAATTCCAAG	226920
AACAAAACCC ACAGCACCAC TAGAGAAAGA CTCCGCTCTG CCTGACACAT CAATTAAAC	226980
TCCAATAGTA GCATTCATTA CAAGGTAGCC AATAAATGCT GCGATTCCAG ATGTGCCTTT	227040
ATCTGATTTT GCAAGTCCAA CAGCAATTCC AATAGAAAAT ATTGGCGCTA AATTTGAAAA	227100
AATAATAGAA CCGACGCAC TCATTATTTT GAAACCTGAT TGTAAGAAGA ATATATTCAA	227160
AAAAGAATAC GTCCTAACGG TTTCTGGATT AGAAAGAGAG CCTCCAATTC CTAAAAGCAG	227220
CCCCGCTGCT GGCAAAATAG CAATTGGAAG CATAAAAGAA CGTCCAAATT TCTGAGCTTG	227280
TTCAAAACCC TTAAACATAA AACCTCCTA AAATAAAAAA TAAATTAACC CTTAAGTTTA	227340
AAATTATTTT TTAATCTGAT TTATTTTTTC TACAAATTTT TTAGTAATCT CAGCGGGCCT	227400
TGTAATAGCA CCCCTACAA CCACTAAATC AACCCCCATT TCAAAGCATT TTTGAGCTTT	227460
TAAAGGGGTG TCTATTTTTT CTTCCACTAT TAAAGTAGAT TTCAAATTAG AATTAAGCAA	227520

GGTTCTTAAA AAATTTAAAT CATTGTCTGC AATATTCAAA CCATTGGTAT TTTTGTATA 227580
GCCATACAAA GTTGTTCCTAA TAAAATCAAA TCCCAATTTA TCGGCATTAA TAGCTTCATC 227640
TAAAGAAGAA ATATCTGCCA TCAAACACTG CTTTGGATAT TTTTTTTTAA TATTTTCAAA 227700
AAAATCATCA AGTAGCACGC CATCAGGCCT ATTTCTAAAA GTGGCATCAA GGGCAATTAT 227760
ATCTACCCCC TCATTACAAA GCTCATCAAT CTCTTTCATG GTAGGAGTAA TAAATACGTC 227820
GCAATTATTA TAATTTTTTT TAATAATACC TATTATTGGC AAATCAACTT CCAACTTAAT 227880
CTGGCTAATA TCATTAACCT CGTTGGCTCT TATTCCAATA GCTCCACCTA TTTTGGCTGC 227940
CAAAGCCATC TTAGACATAA TAAACTACT ATGTAAAGGC TCGTTCTCAA GAGCTTGACA 228000
AGATACTATT AACCCCTCTTT TGATTTTTTAC AATAATAATC AAACCTCCTG TAAAATTTAT 228060
TTTCTTAAAA AATATAAAAA CTAAATACA GATTATATTT TTTATTTAAA AAAAAACAAT 228120
TCTTTTAAAG AAAACTAACA TAACTAAAA ACAAAAACAA TTTATCATTC AATACACATT 228180
AAGCTATAAT TTAGGCATGG CAAATAAAAT CAACTGGTTT CCTGGACATA TGAAAAGGGC 228240
CTTAGATCTG ATAAAGAATA ATTTACAAAA AGCTAATATT GTGCTAGAAA TACTTGATGC 228300
TAGAGCTCCA TTTAGCAGTA AAAATCCATT AACTGAAAAA ATTACTAAAA ATCAAGCTAA 228360
AATAATTCTT CTACACAAAT CAGATGTTGC TCAAATAAAT GAAATTATAA AATGGAAAAA 228420
ATATTTTGAA AATCTTGGCA ATACTGTAAT AATAAGCAAT ATTTACAAAA AAGGAATGCG 228480
TAAGCAGATA ATAGATATTA TTAAAAAATT GGCCATTGTT AAAAAGATAA AAAACTATAA 228540
AGAAAAATA AAGGTTTTGA TTATTGGAGT TCCAAATGTT GGAAAATCTT CAATAATAAA 228600
TCTATTATCC GGCAAAAAGA GCGCAAAAGT TGCCAATAAA CCTGGATATA CTAAAAATAT 228660
ACAAATAGTA AAAATAAATG AAGAAATAAA TCTTTTTGAT ATGCCAGGGA TTTTATGGCA 228720
TAATCTAGTA GACCAATCGA TTGCAAAAAA ACTTGCAATA TTGGATATGA TCAAAAATGA 228780
AATAGTAGAT AACACAGATC TTGCATTGTA TTTACTTGAA ATAATGGATC AAAATAATAA 228840
AAATATTTTA CTAAAAAAT ACGAAATATA TCATAAAAT TCACTTGATA TTCTACAAAA 228900
TTTTGCAAAA GCAAGAAAAT TAATCGGTAA AAAAAATGAA CTTAACCTTG AAAAAGCATC 228960
AAAAATATTA ATCAAAGAAT TTAGAGAGGG TAAATTTGGC AAAATAATTC TTGATAAGAA 229020
TTATAATGCC TTTTAAAAA GGCATTTACA TAAATAATAA TATTAAGTAT AATCTTGATT 229080
TGTATTAATA CAGCCATAAG GAGGTTGGAA TTAGTTGGAT AATTGTATCC TAGAGATTAA 229140
AAATCTAAGT CATTATTATG ATAACAATGG AAACAAAAC TTAGATAACA TAAATTTAAA 229200
AATTAaaaaa AATGAGTTTA TCACACTACT AGGCCCATCC GGATGTGGAA AAACAACATT 229260

GATAAAAATA TTGGGTGGTT TTTTAAGCCA AAAAAATGGA GAAATTTATT TCTTTTCTAA 229320
AGAAATATCT AAAACCAGTC CAAACAAAAG AGAAATTAAT ACTGTATTTT AAAATTATGC 229380
ACTTTTCCCA CATATGAATG TTTTGTGACAA TATTTTCATTT GGACTTAGAA TGAAAAAAC 229440
GCCAAAAGAT ATAATCAAAG AAAAAGTAAA AACATCGCTT TCGCTGATAG GAATGCCAAA 229500
ATACGCATAC AGAAATATTA ACGAACTATC GGGGGGGCAA AAGCAAAGAG TTGCAATAGC 229560
AAGAGCAATG GTAATGGAAC CTAAGCTTTT ACTCCTAGAT GAACCACTTT CCGCGCTTGA 229620
TTTGAAAATG CGACAAGAGA TGCAAAAAGA ATTAAAAAAA ATACAGCGTC AGCTTGAAT 229680
CACATTCATA TATGTTACTC ACGATCAAGA AGAGGCATTG ACAATGAGTG ACAGAATCGT 229740
TGTAATGAAT GAAGGAATAA TTCTGCAAAT AGGAACACCT GAGGAAATTT ACAATGAGCC 229800
TAAACAAAG TTTGTAGCCG ATTTTATTGG AGAAAGCAAT ATTTTGTATG GAACATATAA 229860
AAAAGAGCTG GTTGTAAGTT TGCTTGGTCA TGAATTTGAA TGCCTTGACA AAGGATTTGA 229920
AGCTGAAGAA GCAGTTGACC TTGTAATACG CCCAGAAGAT GTAAAACTAC TTCCAAAAGG 229980
AAAAGGACAT TTAAGCGGAA CTATAACATC AGCAATTTTT CAAGGAGTTC ATTACGAAAT 230040
GACTCTAGAA ATCCAAAAAA CAAATTGGAT AGTTCAAAGC ACAAGACTTA CAAAAGTTGG 230100
AGAAGAAGTT GATATATTTT TAGAACCTGA TGATATTCAT GTTATGCATA AGGAATAATG 230160
GTTTTGAAAA AGTTGATATT AATCATATAC TCCATATTCC TACTAACATT TAGTATTCTT 230220
CCCTTACTAA TAATAATATT GCTTGGATTT TTAAATGAAA AAAACGAATT TACCATCTAT 230280
AATTTTCATTG GACTTTTAAA TCCAAGCTAT CTTAATATTT TTTCAAGAAG TCTAAACTC 230340
GCAACAATAG CAACAATTTT TTGCATTTTA ATAGGCTATC CTGCCGCTTG GCTAATTTCA 230400
TTATCAAAAA AAAGTGCTCA AAACAAATTA ATAATCATGA TAATACTTCC TATGTGGATA 230460
AATACATTAC TTAGAACTTA TGCCTGGATG AGAATACTTG GAAAAACGG ATTCATCAAC 230520
AACTTATTTG AAAAGATCGG AATTGGAAT TTAGATCTTC TTTATAATGA ACAGGCTGTT 230580
ACAATAGGCA TGATATACAA TTTTTTGCCT TTTATGATCT TGCCAATATA CACGGGGCTT 230640
TTAAAAATTA AGCCAGAATA TATTGAAGCA TCACAAGATC TTGGAGCAAG AATGTGGCAA 230700
ATATTACTTT ATATAAAAAAT ACCACTAACA CTCTCTTACC TGGCAACAGG AATAATTATG 230760
GTATTTATTC CTTCAATTAC GGTATTTATC ATTTTCAGATT TGCTAGGAGG CTCTAAACAA 230820
ATTTTAATAG GAAATCTAAT AAGCAAACAG TTTCTCTTTA TAGAAGACTG GAATACTGGG 230880
GCTGCAATTT CATTTATTTT AATGTTAGTA ATATTAATTT TTAATTTAAT AATAATAAAA 230940
TTAATGCGAA AAAATAATGG GGAGTAAAAT ATGTTTAGAG CCTTTAAAAA CATTTTCTTA 231000
TTTCTAATAC TCAGCTTTAT TTACCTTCCA ATAATAATCT TAATAATTTA TTCCTTTAAC 231060

TCTGGTGACA GTGGATTTAT ATGGCAAGGA TTTAGTCTAA AATGGGTATAA AGAAATTTTT	231120
GCCTCAAGTC AAATCAAATC AGCAATATTT AACACCATTT TAATAGCCAT AATCTCATCT	231180
TTGACTTCTG TTGTTATTGG AATTATTGGT GCTTATGCAA TTTATAAATC AGAAAACAAA	231240
AAATTAAAA CAATACTATT ATCAGTAAAT AAAATAACAA TAATTAATCC TGACATTGTA	231300
ACAGGAATAA GCTTAATGAC ATTTTATTCT GCAATAAAAA TGCAATTGGG ATTTTCTACA	231360
ATGCTAATAT CACATATAAT TTTTCAACA CCATACGTAG TAATAATAAT TTTACCCAAA	231420
TTATATTCTC TTCCCAAAA TATTATTGAT GCTGCCAAAG ATCTTGAGC CTCAGAAATT	231480
CAAATATTCT TCAATATAAT TTATCCGGA ATCGCAGGAA GCATAGCAAC TGGGGCCCTT	231540
ATTGCCTTTA CATTATCAAT AGATGATTTT TTGATATCAT TTTTACCAC TGGACAGGGA	231600
TTTAATAATT TATCTATCCT AATAAACTCG CTAACAAAA GAGGCATCAA ACCCGTAATA	231660
AATGCTATTT CTGCAATATT GTTTTTTACA ATATTGAGCC TTTTGTTTAT TATTAATAAA	231720
TTTATAGGAA TTAAAAAATT GACAACAGAT GCTGAGCTTT AAAATGAAAA AAAGGAGTAC	231780
TTATGAAAA AATTTTTATA TTAATAGTAA TTCTTACAAC TTTTGCTTGC ACTAACAAAG	231840
ACACAATAAC TTAAACGTA TTTAATTGGG CAGAATATAT TGACAAAAC TTATTAGATC	231900
AATTTGAAAA GGAAAACAAT ATAAAAATTA ATTATGAAAT CTTTCACAAT AATGAAGAAA	231960
TGATGGCTAA ATTTAACAAC ACAAAGAATT ACTACGATAT AATAGTCCCA TCAGAATATT	232020
TAATCCAAGA ATTAATCGAT GAAGGCAAAA TTGAAAAATT AGACTACTCA AAATTGCCAA	232080
ATGTAACAAA AAATATTACC CAAAATCTTA CAAACTTGGA ACATGATCCT GGCAATCTTT	232140
ATTCAAGTCC AGCCTACTGG GGATTAATGG GCATACTTTA CAATAAACT AAAATAGATT	232200
TAAATGACAT GCAAGGTTTT GACATATTAT TTAATAAAAA ATATAAAAA GAGATTACAA	232260
TGCTAGATTC CCCTAAAGAC AATATTGGGG TTGCTTTAAA AAAACTTGGA TACTCAATAA	232320
ATGAGCATGA TACAGATAAA ATTAAAGAAG CTGGGGAACT TTTAAAAATC CAAAATCCAC	232380
TATTAATCGG ATATTTTTCA GATGTGCCTG CAAAATCATT AATGCTAAAT GGAGAAGCAT	232440
CTATTCAACT CACATGGAGC GCGAAGCAC AAAGCGCTAT GCTAAAAGAC AAAAATTTAG	232500
ATTTTTATGC ACCTGAAAC ACCAATCTAT GGATAGACGC ATTTGTAATT CCTATTGATG	232560
CTCCAAATAA AAACCTGGCT TACAAATTCA TAAACTTTTT ATACGAGAAT GAACCATCTT	232620
ATAAAAATTT CAAAGAACT AGATATAATT CTCCAAACAA AAACGTAATA AAAAGAATAG	232680
AAGAAGAGGC AAAAAATAAC CCCGAAATGA AATTATATTT AGAAGAAAAA TTTTACCAC	232740
AAGATTTTTTC CAAATTTGAA ATTTTAAAA AAATACCTAA AAAAATAAAA GAAGAAATCC	232800

TTAAAATATA TTTAAATCTG TCTTCTTAAA TATTTAAATT CAAAAAAAAC TTAAAAGCTT	232860
TTAAAATTTA AAGCTTTTAA GTTTTGTGAC TATTTTAAA AAAGACTTAA ATATTAACCT	232920
AATATCAAGT CCAATTATAG ACAAAGCAAT CAATAAGATC AAAAATCCTT GATAAATTAA	232980
AAATGAAAA ATGTCAAAAG GAGAAAGCTT GCCTTTTGTA AAATCTACAA GAGCTATAAC	233040
ATGCATACTA TGGGGCAAAA TACTTAAAA AAAGCACGAA GACATACAAA GTAAAGCCGC	233100
AATACGCTTT GAGTTTAAAT TATTTTCCTT AGTTATTGAT CTTACAACAG AACCCTCAT	233160
TAAAATAGCA AGCCCATTAT TTGCAAGAA CATGGTCAA ATGCCAACTA AGACAACAAT	233220
GACAAATTC GAAGTTCTTT TAGACTTTGA CATTTTTTGC AATTTTAAGA GCAACCAATC	233280
AAACCCCCCA TACTTAATTG TCATATAAGA AATTCACCA GTAGAAATA CAAGAATAAA	233340
CATTTCCCCT AGGCCTAAAA ATCCTTCATT GATTTTTTTA GCCAGCAATA AAAAAGTAAT	233400
ATCTGAATAA TAAATTCCTA TAATACCAGC AACAACAATG CCTAAAAACA AGGCTAAAAA	233460
TACATCAAAG CCTGAGATTG CAAAAACCAT AACAAAAATA TACGGAATAA TTTTGAAAAA	233520
ATTTATCTCA CCAGGCTCAA TAATAAACT ATCGACCTTG CAATAATAAG AACCTAAAAA	233580
TGCAAAAGCA ATGCTTGCTA AAATTGCTGC TGGAAACGTA TAAAAAGCTC CATTTTGTAA	233640
AACATCAACA ATATTAACCT TTTGAGTATG ACTTGAAATA ATAGGAGTAT CTGATATCAA	233700
AGACATGTTG TCCCCAAATG CACCAGCGCT AAGAATAGCA CCAGCAATCA ATGGAAGGGG	233760
GATGTTTACC TTATCTGCGA GCTCCAAAGC AATAGGAGCA ACAGCAACAA TAGTCCCCT	233820
AAACTTCCA GTGGAAAAAG ACAAAAAAAG AGTAATTAAA AAAATGCCAC ATACTATTAA	233880
ATTCAATGGA ACATATTTAA GACCAATATT TACTACAGCA TCAACACTTC CTATTTCTTT	233940
ACAAACAGCA GAAAAAGCAC CGGATAACAT AAATATTAAA GATATAAAAA TAACATCTTG	234000
CTGAGCGCAT CCCTCAATGA ATTTATTCAT TTTTGCTAAA AAAGATCCTC TAAAAATAAT	234060
AAATGTCAA ACAATAGCAA TAAACATAGC AACTACGGGA GGCATTTGAT AAAATGCCCT	234120
TTCTACACCA TTAAAATAAA GAACGAGTCC TGTGCCAATA TAAATCCCTA TAAAAAGAAA	234180
AAAAGGCATA AGCCCCCAA AATTTGGAAC CACATTAGTT TCTCTTTCTA ATTTCAAATC	234240
TCTTTCCAAT TTAAACCCTC CTAAATCATA TAATTAAGAA CAATTTATTC TAAATAAAAT	234300
CAAAAAAATT AAACAATGCA AATCTTAAAA TTTTAAAT TTTTATTTTT TTAAAAAAA	234360
TAAAAAACT TTTTATAT CAAGGCCCAA AATAGATAAA ATAACAAAA ACAATAAAAA	234420
TCCAAAAATA ACTAAAAATG GCAAAATACT AATTGGCGAC ACAAGTCCAT TTGAAAAATT	234480
CACTAAAAATA ATCATTTGCG CACCATAAGG AATAATGCCT TGAAAAATAC AAGAGAACAT	234540
ATCTAAAAATA GAAGCACTTC TTTGAACACT GATGTTATTT TCAAAAGCTA TCTTTTTTGC	234600

TACTTTGCCG CAAATAAGTA TGGCAATTGT GTTATTAGCA AGAAAAACAT CAACTATTGA 234660
AACAAAAGCC CCAATAGAAA ATTCCGCTGA ACTTTTTCCT CTAATCAAGG ATTTTAATTT 234720
AATAAGTAGC CATTTAAAGC CTCCATTATG AATCACGGCA AAAGAACTC CCCCTGTTAA 234780
AATTGAAAGA AAAATCAAAT CCGCCATATT TAAAAACCCT TTATTAATGT TTTTCATTAC 234840
ATCTAGAAAG TATAAATTAC CATACAAAC GCTAATAAGA CATATAGAAA GAATACCTAA 234900
AAAAAGAAGT ATAAAAACAT TCATTCCAGC TAAAGAGAAA AATATAATCA TTAAATAAGG 234960
CACAGTTTTC ACTAAATCTA TTGAACTTTC GTGTAAAAAG TTTGTGGCAT TGGACAAATT 235020
TTCAGAAAGA AAGAAAAAAG AAAAAAAGT TAGTATGGCG GATGGAAAAG CATAAAACT 235080
GCTACTAATA AAAACATCTA AGATGCTACT ACCTTGAGTT CGACTAGAAA CAATAGTTGT 235140
ATCTGATATT AAAGAAAGAT TATCTCCAAA CATAGCTCCA CACATTACAG ATGCTGCTAT 235200
TAAATTCGGA TTAATGCCGC TTTTAACAGC AATATTAAAA GCAATAGGAG CAATTGCAAC 235260
GATAGATCCA ACAGAAGTGC CGGCAGAAAA AGAAGAAAG CAGGTTACAA AAAATATACC 235320
AGAAACAATC CAATTAGGAT TAATATATTT AATTCCTAAA TTTGCTACAG TTTCAACGCA 235380
GCCTATTTCT TTACAAAGAG AAGAGAAAGC TCCCAGAAAGC ATAAAAATAA GACACATTAG 235440
TATAATATCG TACTGAGCTG CTCCTTTAAT AAATATGTGA ATTTTGTCGG AAAATTTTCC 235500
TTTAAATACC AAAAAACAAA CAATGGAAGC AAAAAACATT GCAACACTAG CCGGCAGTTG 235560
ATAAAAGGCC ATTTCTACAC CAATAACTCC CAAATAAATC CCCGTGCCTA AATAGATAAT 235620
AATAAAACA AAAAAAGGAA TAAGCCCAAA AAAATTTGGC TGCCCTCTTA CTTCAATATT 235680
TTCCATATAC ATCCTTTAAA TATAAGCATT GTTTTATATA AAAAATTACT TATATCTTTT 235740
AATCATAACG CAAATTATTA ATCGATGCAT AAATTTGCAA TCAAATCAAG AATAAAAATC 235800
CTTAAACTC TTAGCTAGAT TAAAATAATA GAACACAGAG TTGGGGTTGG GGGCTCAAGT 235860
ATTAAAAAGG GATAGGAATA AATTATATAA AAATTCTATC TCATTTATCT ATTTAAAAAA 235920
TATCTTTTAA AAAACTAGAA AATTAAATTT TACGCCAAAA ATGATCTTTT TCTAAAAATAG 235980
AGTCTATCTC TTTTGGTCCT TCAGAGCCAT AAAAATAATT ACAAATTTCA ATATCTGCCC 236040
ATTTATTTGC AATATCTGAA ACAAATTTCC AAGAACTTTC AATCTCATCA CTTGTGCGAT 236100
ATAAAGTACC ATCTCCTAAA AAAGCGTCTA ACAATAAACG CTCATAAGCC TCATCAAACA 236160
ATCTTTTAAA TGCTCCGTGA TATGAAAAC CCATATTAGC AGTTTGAATT TCATAATTAT 236220
ATCCGGGCTT CTTGGTATTG AATTTGATTT CAATTCCATC CCTTGGCTGA ATTCTAAATA 236280
TCAAAGCATT AGAAAAATCA ACAGAAGTAT TGTAAAAAG AGTAAAGCTC GGTTTTTTAA 236340

ATTGAATATA TATTTCTGAA AATTTCTAG CAAGACCTTT CCCAGTTCTA AGATAAAAAG 236400
GAACCCCAAGA CCAACGCCAA TTATTAATAA AACTTTTCAT AGCTAAATAA GTTTCGGTAT 236460
TTGAATTTCC CAAAAATTCT GTTTCATCTT TATAGCCTTT TTTAAAAACC CCTTGAACCTT 236520
GTGAGCCTAT ATATTGACCC TTAACAATGT AATTCTTAAT ATCTTCTTTG CTAATTTTCC 236580
TCAAACTTTT TAAAACTTTT ACTTTTTTCAT CATGAATAAA CTCAGAATCA AATTTAATAG 236640
GAGACTCCAT TGCAACAAGG CTTAACAATT GTAAAATATG ATTTTGAACC ATATCCTTCA 236700
AAGCGCCAAC AGAATCGTAA TACTCTACTC TTCCATCAAG ACCTAATTCT TCTGCTACCG 236760
TAATCTGAAC AAAATCTACA TAACGATTAT TCCAAATATT TTCAAAAATA GAATTGCCGA 236820
ATCTAAATGT AAAAATATTT TGAACCGTTT CTTTACCCAA ATAGTGATCT ATTCTATAAA 236880
TTTGATCTTC TTTAAAAGCA GAATAAAGCA AACTATTTAA TTTTTTTGCT GTCTCAAGAC 236940
TAGAGCCAAA AGGCTTCTCA AGAACTATTT TTGACAAAGT CAATTTTTCG CTTAAAAAAT 237000
ACTTTTTCAA ATGATTAATT ATAGGTCCAT AAAATGCAGG AGACGTCGAA AGATAATATA 237060
TCGTTTCTCG ACTTCTATCT AAAAATTTAA ATAAATTTTT ATAAGACTCC TTTTCATTAA 237120
AATCGCCAAA TACATAAACA AAAAAATTTA AAAAAATCTC AATCAACGAA TCGGTCTCTT 237180
CCTGCCATAA AGAATCTTTA ATATACAATC TAAATTCTTT ATCTGTAAAA ATCTTACGAG 237240
AAAAACCAAT AACCTTAAA TTGCTAATAC ATTTATTTTT AAATAAATTA AAAAGTGAAG 237300
GAATAAGCTT TTTTCTAGAC AAATCCCGG TAACCCCAA AATTACAATA TCAAAATTAG 237360
AAACACTTCT TTCTTTCATA GAATTTAGTC CAATCTGGTC AATTTATTAT ATATCACAAA 237420
AAACATATTC ATAAAGATTA GCAGACAAAA ATTAAGCTCA AATTAAATAT CATTTTTTTA 237480
TAAACAAAAC TAGTATATAA TAAGGAGAAT GAAAAATCTA TCACTATTTA CAGATTTTTA 237540
TGAAATTTCA ATGATGAACG CTTATTTTAC AAAAGGAATT AATCCTAAAG CAAAATTTGA 237600
AGTGTTTTTT AGAAAAACAC CCTTTAAAAA TGGCTATATT GTTTTAGCTG GAATGCATAC 237660
ATTGATTAAT GAATTAAAA ATATTCGTTT TGGAGAAAAT GAACTTAAAT ATTTAAAAAG 237720
CTTTAATATA TTAGATAAAC AATTTTTTAA CTTTCTAAGA GAATTCAAAC TAAACGTAAA 237780
AATAAGCTCA ATAGAAGAGG GTCGAATAGT TTTCCCCCAA GCACCAGTAG TTGTGATTGA 237840
AGGACACTTA ATAGAATTAT TATTAATAGA AGGGTTAGTG TTAAATATAA TAACTTCGA 237900
AAGTTTGATA GCAACAAAA CCGCTAGAAT AAAAGAATCT GGTGCAAAAA TTTTAGCAGA 237960
ACTTGGGCTA AGAAGAGCTC AAGGAATAAA TGGAGCACTT TCTGCCAGCA AAGCCGCCTA 238020
CATAGGGGGA GCAGATTTCA CAAGCAATAT GCTTGCTGGA TATAAATACA ATATACCACT 238080
TACAGGAACA ATGGCTCATA GTTGATAAT GAGCTTTGAA ACCGAAGAGC AAGCATTCAG 238140

AGAATATGCA AAAACATATC CAAACAAAGT AAGTTTGCTA ATCGATACTT ACGACACGCT 238200
TAACAGTGGA TTAAAAAATG CCATTAAAAAT ATTCAAAGAA TTAAAACATG AAGAAAAAAA 238260
TAATTTTTCATAAAGAATTG ACAGTGGAGA TCTTGAATAT TTAAGTAAAG CAGCAAGAAA 238320
AGAATTAAAC CGAAATGGAT TAAATCATGT AAAAATTATT GCATCTAATG AGCTTGACGA 238380
AAATATTATC ATGTACTTAA ATTCAATAAA TGCTCCAATT GATATTTGGG GCGTTGGAAC 238440
AAATTTAGTT ACAGCAAAAG GAGATCCAAG CCTTTCAGGA GTATATAAAA TGATCTCTAT 238500
AGAAAAAAT GGAAATTTA TACCAAAAAT AAAAATATCA AATAACGCAG AAAATCCAC 238560
ATTACCTGAC CAAAAAGAAG TTGCAAGAAT CTATTTAAAT GACCAAATGA TCCTTGATTT 238620
TATATTTTTA AAAGAAGAAA AAGATAAAAT CAAAGATCAT CTGAATTCAA GAAAAGAATT 238680
TACCGTTTTT CATCCAATAC AAGATAACAT TTTCAAAATC ATCAAACAAT ATGACGATTT 238740
TGAATTTCTA ACGCACACTG TCTTAGAAAA TGGAAACTT CGCAAAGGCT ACGAGTCTAG 238800
CTTAACCAAT ATTAGAAATA AAACCAAACCT CGACTTAAGC AAACCTGAAC ATACGTACAA 238860
AAGAATAATT AATCCCCACA TATATAAAGT AAGTATCAGT AAAAAGTTAA GAAAGTTAAA 238920
AAACAACTC ACAAAGATA TCAAAAACAA TTAATATATG TATATATATA AAACAACTA 238980
AGTAAATAAA ATTTATAATA AAATTAAAGA ACTAACTCAA AAAGACAATA TTTTAAAAA 239040
AGAAACACTC ATCATAGTAA AAAATGATCT CTTAAGAGAA GAAATTAAAA AAACCATAGC 239100
AAAACTAAAT GGGATTTCTT ATAATCTAAA TATTAAAAA AATGCCGCAA AAAGCATATA 239160
TGAAATTTCT TTTAAAAATC CCAATATAAA AAAATACATA GAAGAGAATA CTTTTTCATT 239220
TTACTTGGA ACAGAAAAAT TTATTTTATA CAACATATTG AAACTGAAA AACTAAAATA 239280
CATAAAGAT TTCAAATCCA CAAAGAATAG GTACTTTTTT GCATCAAAAA TAATAGATTT 239340
ATTCCACCAT TATTACTCAA AATTTTCAAA ATTAATTGAA ACTTGGAAG ATAATGGATT 239400
TTTATTCCAA GAAGAAAATT TAAAACCCTA CGAAAATATG CAAAAAGAAC TATTAAAAA 239460
GCTCTTTGAA AAACAAAAA ATATTTTAA CTTACATAAA AAAATAATTC AGGAAAAACC 239520
AACAAAAA ATAGAAATTG AAATTAAAA AATAATATTT ATTGGCAACA ACAGAGAGAT 239580
TGAGAAAAA ATTCTCAACT CTTTAGAAAA AATTTTGTAT TTTGAAGTGC ATGTGTTAAT 239640
TTTTGAAGAT TTAATAAAT ATGAATCTAC TCTTGTTAAA GAATTGTTGT TAACAAAAAC 239700
AAAAATCAAC CCAATAAAT ATCAAGCTTT AGAAAAAGTA GATATTGAAT TATTAAAGG 239760
TGAAATTTT TTAACAAGCA TTAAAAATA TATCATAGCA AAACTCCA TTTCAACATT 239820
AGACGATAGC TTTAAATA TAGAAGCTAA AAATCAAAA CGTGAAGTAG AAATTTTGAC 239880

AAATCAAATA GTACACTCAA TGCAAAAAAA TAACCTAAAA TTAAGCGACA TAGCAATAAC	239940
TTGTTTGCAA GAAAAATTTA ATGAATATTT GCCATATATA GAAGAATGTC TAAATAAATA	240000
TGAAATCGAA TATAGCGTTC TATGTTATAA CAATTTGTCA AGAGGAGAAA GTATAATAGC	240060
TTTAAAAAGG CTAATGGATC TTTTCGTATC AAAAAACGGA ACAATTAGTA ATTTTAGCAG	240120
AAAAGAAGTA TTTGACCTAC TAAGTAACAA CAAAGTAATG AAAAAATTTA ATATATCAAC	240180
ATCTGAATTA AACTATTTAA TAGAATTTAG CGATACGATG AACATTAGTT TTGGTGCAAA	240240
CAAACTCAC AAAGAAAATC TAAACTATGA TCAAACTTT TTAACTCAT GGAAGATGG	240300
ATTTAATCGA TTTTAAATGT CTGAAATATT TGACGAAAAA TACGAAGAGG AAACCCAAAA	240360
AGAAAGCACA AGATTTCAAG ATCAAGAGTC AATAATGAAA CTTATAACAA TAGTAAAAAG	240420
TTTGTATGAA GATATAAACT ATTTTAAAAA TAAAGCATAC AAAGTATATG AATGGGCAGA	240480
AATCATAGAA ATTTTATTC AAAAATATAT TGATCTTGAA GATTTTAATA CAACCGATGA	240540
ATATTTACAA AATAAGATAA AATCCTTTAA AAATTTCCCC AAAGATTTAA ATGACAATCT	240600
TTACAAAAAC TATTTAAAAG AAATTAATGA AATAAAATT GAATTTTATC TTTTAAAGAT	240660
TATGCTTGAA GAAAGTCTG AAAAAGAAAA ATACGGAGTA ATGTATAAAA AAAATGGGAT	240720
ATTGATTGCC AATTACAAAG AAATAGAATA TCTTCAAAAA AAAGAAATTC ATTTTTTGGG	240780
ATTTCAAAAA TTCAACTCTA AGATAAATTA TGATAATATG AATTTATTAA ATGAATACTA	240840
TGAACATGAG AATACTGAAA AAGAGGAAAT AACGGCTCTT TTTAATTTGA TTTTGTCAAC	240900
ATCAGAAAAA TTTTATCTTT ACTGCTCCTT TCAAGACAAC TTAAGCCCAG AAATTAATAC	240960
ATCAAAAACA ATAAACAAAA TACTTGAACA CATACAAAAG TATGAAAAA ATTTTCAAAT	241020
AGAAAAGCAT CCAAATGAAA ACCACGACCC AGTATATTTT AAAGATGCAA AAGAAAATTA	241080
TTTAATAAAC TATGATCCAG AAGCCTATAA TATCGCAAAA ATACTACAAA ATCTTAAACC	241140
AATTGGATTC AAGCAAAATA AAATTAAACT AGAAAGCCCA ATTAAGCTAA ATTTATACGA	241200
ATTAAAAAAC GCCCTTTCCA ATCCTTACAA GCACTTTTAC GAAAAAATT TAAACGTTAA	241260
AATACAAGAC ATAAGATTGG AAAATGAAAT CAAAGAAAAA CAAGAAGAAC AAATTTTCAG	241320
TGTTATTGAA ATTATTTACA GACTTATAAA AAATTCAACA CTACTGCATG AATACATAAT	241380
GGGGAAAAA GATGATGTAA GAAAAGCAAT AGAAATTATT AAAAACCACA TTAGATATGA	241440
AATACAACAA GGAAGCATTC CTTTCAACAT AGATCAAAAA ACGACTGTAA ATGAAATCTT	241500
AAAAAAAATA AATAAATTAA AATATAATGC TGCTGAAAGC TTAAAAAGC TTTTCAGCAAT	241560
GACAAAAAGC AAAATTAAAT TTTGCAAAAA AATAAACTA AATTTTCAAA ATAAAAATAT	241620
AGAATTTGAA TTAAAAAAG ATATCGAGAA TGTATATAAG GTCGAAAACA ATTATTTTAA	241680

TTTAAATTTT GTAAAAAAG ACTATTGCAG TATCCCAGAT AAAATAAAAA ATGAAATAGA 241740
TTTATATATA ACAGGACTGC TAATAAAAAA AGAAATACAA AACTTCAATT CATTAACAGA 241800
AGTAAAAATT GATCTTGAAA GCTTAACTGC AAAAAACAAC TATTTGCTAT CATCACAAAG 241860
AAATAATAAT TGATGACATT GAAAATATGC TTATGCAATT TGCATACATA TCAAGCTATC 241920
CAACTCCAAT TTACCAAAGC TTGATAATTA AAATTTTAAC AAAAATAAAT CAAAATAATT 241980
TTTCAAATTG TTTTAAGAAT TTAATAAAAA TGCAGATAAA AAATCCTTCC AAAGCTTATT 242040
TCACAAGCAA AGCACACGAG AGATTTTTTA AAAC TAGCGA AATAACACTC TGCGATTACT 242100
ATAACAGATT TAAAGACACT CATGATTTC A GTTAGACAA AAATTTATTA ATATTGATAG 242160
AAAAATTTTA CATTAATTC GTAAGGACAA AAAATTAAAA TTCATGAACA AAATCCTAGA 242220
AAAAATTCAA AATAACACAA CAATATTAAT AGAAGCATCG GCGGGCACCG GAAAAACTCA 242280
CATACTGGAA AATGTGGTTA TAAATTTAAT AAAAACCAAG CTATACTCCA TAAATGAAAT 242340
CTTGGTATTA ACTTTTACAA AAAAAGCCAC AGAAGAAATG CACACAAGAA TACTAAAAGT 242400
AATAGAAAAT GCTTATTCTA ACTCAAAAAC AAATGAAATC TTAAAAGAAG CTTATGAGCA 242460
ATCAAAAAAA CTCTTTATAT CAACAATCAA TAAATTTGCA TTACATGCCT TAAATAATTT 242520
TCAAATTGAA ACAGAAAATT ACTCCAAATA TAAACCTAAA GAAAAATTTT CAAAAGAAAT 242580
AGATGAAATA GTTTATGACT TTTTAAGAAA ATCAGATAGC TTGATTCAAG CTCTTGATAT 242640
TAAAGACTAC GAACTTAAAG TGTTTAAATC TGATGCTAAA AAAACAGAAG AGATTGTTTT 242700
AAAAATAAAA AAAGCTTACG AAAGAGATAC GACTCAAGAG CTTGGAGATT GGCTTAAAAC 242760
CCAAACGGCT TTTGAAAACA TTCTTCTTAA AAAGGAAGAG CTGATCAAAG ATTACAACAA 242820
AATAATAGAA GACTTAGATA AAATGACAAA AGATGAAATA TTAAGTTTTT ATAATAACA 242880
TATTCAAACCT GGCAAACCTG AAATAGAATA CTCTAAAGAA AACGACATAT TCAAATAGC 242940
AGAAACATTA TTAAAAAATA AATTTTTTTC AACTCTAATA GAAAAAGAAA CTAAAAAAA 243000
TTCTAAATTA TCGCCTAAAG AACTTAAGAT TAAAAATGAT TTAATCTGTT TGGAATTAA 243060
TATTAAACAT GAAAAATATA AATCAGAAGA CAATAGAAAT AAAAATAGAA ACAATTTAAA 243120
GCAATATGTC ATTTTAAAG TTGAATACAA AATACTAAAA TATATAGAAA AAGAACTAAA 243180
GAAACTATT AAATCAACAA ACACAATAGA TCAAATTAC ATAATTCAA ATTTAAAAAA 243240
TTACTTAAAA TCAGAAGACA AAAAGCTTCT AAATGCAATC AAAAATCGGT ACAAATCAT 243300
TTTAATTGAT GAAGCGCAAG ATTTAAGCCT AATACAAATT GAGATATTTA AAATATTAAA 243360
AACAGCAGGA ATAAAATTGA TATTCATAGC CGATCCAAAA CAGATAATAT ATTCCTTTAG 243420

AAAAGCAGAC ATTTTCATTTT ATAACAAAGA AATAAAAAAT AAAATCAATA CAGACGCTAG 243480
AATTGTACTA AAAATAAATC ACAGATCAAG TAAAAAACTC ATAGGGCCTT TAAATAAAAT 243540
TTTAAATAAT ATATACAATA ATGCAATAGC CGATGAAATT GAAAAAATTG ATTTTACCAA 243600
TTCACTTCCA AATCAAAAAA ACGACAATAA TAAAATTGTC ATCAACGGAC AAGAAATAGA 243660
AGGAATCAAT ATAATAACCA CAAATACAGA AAGCGAAGAA GACATTTACC AAAAAACAGC 243720
ATTAACAATA AAATATTTGC TTGCATATGG AAAAATTGCT GAGAACAATA AAATTAGAAA 243780
TATTAAATG CAAGACATTA AAGTACTTTG CAGAGGAAAA AATGAAATCA ATTTAATAGA 243840
TAAAGCATTA AAAAAAGAGC AAATCCAAAC AAACAAAAC CAAGAAAAAT TTTTAAAAAC 243900
CAAAGAATTT AGCGAAATTT TTTATATTAT TAAGTGCTTA GACCGAAAGC AAAGTTTTAA 243960
AACTCTAAAT TATATTCTAA GCAGCAAAAT ATTAAATGTG CCGTGGAATT TACAAAGAAT 244020
TTTAATCAAA CAAGACAAAA TTTGCCTTAT AGAAGAATTT ATTGAAAATA TAATAGTTTT 244080
GCTTGAAAAA AATGAAATAA CATTAATAAA TGCAATTAAC AAAATTACAT TCGAAAAAAA 244140
CCTGTGGATC AAAATTGCAA ATATCACCAA AGATCAAAAA ATTATTGAAT GGGCAAAAAA 244200
TAAAATAAAT TACAAAGGTC TTCTTATTAA AGAAGGTAAG CTTGAAAATT TAAAAACCTA 244260
TGAAACAACA CTTGAGATCA TCTCTAAAAT ATATCATAAA GAACAAAACA TACAATCTCT 244320
AATCTCTACT TTAGAAAGCC TAATAATAAA CGAAGAACCT GAAGAAATAG AAGAAAAAAT 244380
AAATAATATA AATAATGATA ATGAATCTAT AGAACTCATG ACAATACACA AATCAAAAGG 244440
GCTTGGCATG AATATTGTAT TCTTACTAAA TACAACTCCA ATAGAAAATA GCAATTTTTT 244500
TTCAAAAAAA AATCAATTTT ACAAATTTTA TCAAGACGGA AAAATTGAAT ATGATTTTTT 244560
TAAATTGGAA GAAAATAAAA AATACGCAAG ACTAAAAATA CTAAGCGAAG AAAAAAATAT 244620
ATTTTATGTG GGAGCAACAA GAGCTAAATT TGCTCTTTTT ATTATAAAAA TAAATAGCAT 244680
AACTAGCAAA TTACTAGAAA TAGCAAAAT TTTTACTATC GATGATATTA AACATGACTT 244740
TAACATACAT GAATTTATTG GCCAAAAGAG ATTCAATAAA AAAAAATACA ATACAAATGT 244800
AAATACAAAA TTAATTCCGC CAAAACCAAT AATTAAAAAC ATGTTTAAAA AAGAATATAC 244860
ATCTAGTTTT TCAAGTTTAA CAGCGCAAGC TCATCATAAA GAATTTTACG AAAACTATGA 244920
TTTTAAAAAT ATTAACCTACG AAAAGAAAC AGAACTTGAT TATGAGCCTG GATTAGAAGA 244980
GACTCTGCCC AAAGGAAAAG ACATCGGAAA CATTTTACAT GCAGCAATGG AGGAAATAAT 245040
CTTTAGCACA GCAAAAGATA CATTTGATAA TTTTAAAAAA AATAACATTG AAATTATTGA 245100
AAAACAAATA CAAAAAATTA ACTCAAATCT CAATACAATA GAAATACAAA ATTCATTAGC 245160
TAAAATGATT TATAATATAC TAACTTATAA TATAAGAGCA ATTAATACTC GTCTGTGTGA 245220

TATTGAAGAA TTACAAAAAG AAATGGAATT TTTAATAAAA ATAAATCCTG AATTTCAAAA 245280
ACAAAAATAT CTTTTTGACA AACACTTTGA AGATCTTCAC ATAAAACTAA GTGATGGATA 245340
TTTAAAGGGA ATAGTAGATC TTATATTTAA AGCTAATAAT AAAATATATA TCCTAGATTA 245400
CAAAACAAAC TATCTTGGA AAAATAAGGA AGATTATAAT ATAACAAATT TAGAAAAATAC 245460
GATAAAAAAA GAATATTATG ATTTGCAATA TAAAATATAT GCCCTTGGA TAAAAAAAT 245520
ATTATTTAAA AACAAAAAG AATATAATCA AAAATTTGGT GGAATAATAT ATCTTTTTTAC 245580
AAGAGCATTT GAAGACAATA TTGAATGCTT AAAATCAAAA TTTGAAAATG GTATTTATTT 245640
TAATCTTCCA AAATTTAACG ACGTGATTT AGATAAAATC ATCTTAGAGT TAGGCATTAA 245700
AAGACACTTA TGAGAGATTT TTTAGTATTA AGAGAATTTT TAAAAGATAA AAACAAAAAA 245760
TTCTTAACCC CCGAGCTTAA ACTTTATGAA ATAATTGAAC TTTTAAATAT CAATAAAAAA 245820
AATTGTTATA AAGCACAAC ACTTGCAAGA TCCACAAACA ATGAAAATAT TGTAATATTT 245880
TTAATATTTT TATTTAACTA CTTTGATAAA GGCCATTTAA GAGCTGACAT AAATCTATTA 245940
GCAAAGATA TTCAAAATAC AATAATATTC ACAAAGACA ACCTAGAAAA AACCAATAAA 246000
AGTTACAACA AATTAATAAA AATACTAAAA GGGCTAGAAA CATTTGGAAA TCTAGAACT 246060
ATTAAGAATA TAGTTTTACT TTAAAGAAA AACACATAC TAATGGAATT TAACAAGCTT 246120
AAAATTACAA CTCCCCTAAT CCTGGAAAAC AATATTTACA TTTATACTCA AAAAACTAC 246180
AGAGAAGAAG AAGAATTAAT AAAACAAATT ATAAAAAGAT TAGAAAACCA TAAAAGCGAA 246240
TTAAATGACA ATAAAATACA AAATATAATA TCAAATTTAA ATACCAATAA TTTAAATAAA 246300
GAGCAAATTA CATCAGTGAG AAAGGCATTA AAAAGCAACT TCTTTCTATT AAGCGGAGGC 246360
CCGGGAACAG GCAAACAAC AACTGTTAAC TATATCTTAA AAGCAATTAA TAAAACATTA 246420
AACATAAAA AAAAAGGATT AGTAGCCATT ACAGCACCTA CAGGAAAAGC TAGCCTAAGG 246480
CTGCAAACAA GTATCGACTA TTCATTCAA AATTTAGAAA TAGAATGTAA TACAATCCAA 246540
AACTATTGG GAATCAAATT CATAACAAA AAAAATCTAT ATGATGAAGA AAATCAATTA 246600
AATTTTGACG TAATAATAAT TGACGAAGCT TCAATGGTAG ATGCACATAC TTTTTTAAAA 246660
CTACTGAAAG CAACTCCAAT AACCCTAAG TTAATAATGG TAGGAGATAA AAATCAACTC 246720
CCGTCAGTAA ACGAAGGAAA TGTATATTCA AGTCTTTTGG GAATACAAAA AATAAATAGC 246780
GATAATGTAG AAGATCTTAA AGAAAATTTT AGAAGCAACA AAGAAATAAA TTTACTCTCA 246840
AAGGCAATAT ACAAAGAAGA TAGTACTTTG ATTTGCAAAT ACATTAATAA TAATAAAAAT 246900
ATTCAACTGA AAGAAATAGA AAAAATAAAC TTAAAAAAG ATCTAATAGA ATATACAAAC 246960

AATTTATACA	GAAAAATACC	CACTTTTAAAT	CTTAAATTAC	TAAAAGAATC	AAAAATTGAA	247020
ACAATACTTG	AAACTTTACT	TGAAAATATA	ATTTTAAGTT	CAAAAAATTT	TGGCAAATTT	247080
GGAACTAAAA	CACTAAATGA	AATAATAAAA	ACTTACCTGA	AAAAGACCTA	TGGAAGCTTT	247140
ATTGGCCAAA	TAATAATGAT	AACTAAAACT	GACTATAAAA	ATAAATTATT	TAATGGAGAA	247200
CGGGGTGTTA	TTTTTAATGA	AAATTCTAAA	TTTATGCTT	TATTCCAAAG	AAAAGATGAA	247260
AAATATAAAA	AAATAAATTT	AGATTTACTA	ACAAATTATG	AATTCAGCTT	TGCCACAACA	247320
ATACATAAAA	GCCAAGGATC	TGAATACAAA	CATATAAAAAG	TAATATTAGA	AAATAACCCCT	247380
TTTTTGACAA	AAGAACTTAT	GTATACTGCA	ATAACAAGAG	CCAAGGATAG	CTTAGAAATA	247440
ATTTCTAACA	AAGAGACTAT	TATTAAGTTA	AGCAAAAAAT	CTAGCAAAAAG	AGATTCAAAA	247500
ATACTAGAAC	ACGTAAACTC	ATTTAAAGAA	ATTGACAAAT	AAATTAAAAA	CTACTATAAT	247560
CTTTTTTAAA	GAATGGCTTT	GGGGGCGTAG	TTCAGGTGGT	TAGAACGCCT	GCCTGTCACG	247620
CAGGAGGTCG	CGGGTTCGAG	ACCCGTCGCT	CCCGATGATG	AATTTTACAT	TTTATTGTGT	247680
CAGCAGCTTT	TCTTAGAGAA	TCTATTGATG	CTCTAGCAAA	TTTTTAATAA	AAAAATTACA	247740
AATCTTTAAT	TTAAAGGTTA	TAATTTAAAT	AATTAAAAAA	AAAATCTATA	AGGAGAATGT	247800
AAAATGAATC	TACAAAAATA	TCTATTTTTA	ACTGCTTTAC	TATTAATTTT	AACATCTGTT	247860
TTTCGCACAAA	CCAACACAAT	AGCAAAAGAA	AATGTAATTC	CAAATGGGAA	CTTAAGCCAA	247920
TTTGGAGTAG	AAGAGATCTG	CCCAATATGC	GGATATGTTA	ACTGTATTTG	CGATGAACAA	247980
AGTACAGAAA	TCGCTGCAAA	AGTCTCTCAA	TCAAATACAA	CAGGCTTTTT	TACAAGCATG	248040
GCTATACTTG	CATTGCTAGT	AATTACAGGA	TTAGCTCTAG	CAAAAAAGAA	ATTATATAAA	248100
TCAAAATTAA	AAATTTAAGC	AACTAAATA	CTGTAGCTTT	TAAAAGCTAC	AGTAAAGTTT	248160
CAAAATCAAT	CCTTCAGCTC	TATTTAAAAT	ATTAAGAAGT	GTAAATATCC	TCAACCCTAA	248220
TCTGACAAAG	CATCTTTTTA	ACATCTTGAA	ATTCACAAAG	ATTGCCTTTT	AATGCCGTAG	248280
CTGTACCAGC	TGCAACACCA	AATTTAAATG	AATCCTCTAA	AGTACTTCCA	TTATCAAAAAG	248340
CATATAACAA	CCCGGCAATC	ACAGAGTCTC	CTGCTCCAAT	GGTGCTAACA	AAATTAATCT	248400
TAGGAACAAA	GGCCCTAAAA	GCAACATTTT	TGCCGCCAAT	AAAAATAGCT	CCGTCACTTC	248460
CCATGGAAAT	TATAATGTTT	TGAACCCAC	TTTCTACAAG	ATTTTTTCCG	ATTTTAATCA	248520
ATTCTTTTGT	AGAATCAAAT	TTAGCATTAA	AAAGATCTTC	AAGTTCATAA	ATATTAGGCT	248580
TTATTAAAAA	GGGATTTAAT	CTAAGAATTT	TTGCAAAGG	TTTGCCACTG	GTATCAATGA	248640
TAAGCTTAAC	ATCATTAGAA	ATGCTATTAG	CTATTTTATT	GTATGCATCC	TCACCAAGAG	248700
CTGCGGGAAC	ACTTCCTGAC	ATCACTAATG	TACTATTATT	TGCTAAATTT	TTAAGTTTAT	248760

TTTTCAAAAG TTCAAATTCA TTCTCAGAAA TATCTGGAGA ATTGGCATT AATTCGTGTTT	248820
CTCTGCCATT TGCTATCATT TTAATATTTA ATCTGTATC ATATTTTATT TTAATAAAAT	248880
CGTTTTTTTAT GCCCCTAGAA TCAAGAGAAA ATCTTATATA ATCACCCGTA AAACCTCCCA	248940
AAAATCCCAA AGCCGTACTA GGTTCCTA AATTTTAAAG AACGGTGCTT ACATTTATTC	249000
CCTTACCGCC AGCAAAAAA TTGTTATTTA AAGCATAATT AAGACTTTCT TCCTGAAATT	249060
CTTTTAAAC TATTTTATAA TCCACAGAAG GATTGAGTGT TAGAGTATAT ATCAAGATAA	249120
TCTCCTTTGA TTTATAAAAT CAATTAAATA AATAGTAAAA TTTAATAAAT GTATATACAC	249180
TATATAATAT ATAAAGGTGA TTATTATGCA AAATTTATTT TCAAAAAACT TGATTGTTTT	249240
AAATTACAAT GCAACTAGTA AAGAAGATGT AATTAGAAAA ATGGCTAGCA TGTTCATGA	249300
AAATGGATAC TTAAATGACA TGGAAGCATT TATAAAAGAA ATTAAAAAA GAGAAGAAAC	249360
TAACGGAACA GGCATTGAAG AGCATATAGC TATGCCTCAT GCAAAGGCA ATTCATTAA	249420
AAAACACGGA ATTGCTATTT TAAGAGTTGT TGGCAATGGT TTTGACTTCA ACTCTTCTGA	249480
TCAAAAGCTT TCAAACTGT TTTTCATGAT GGCCCTACCC GAAGAACTC CAAGCAATGC	249540
ACACATAAAA GCTATATCAT ACCTAAGTAA TACTTTTAGC AACAACCTAT TAAGACATGA	249600
ACTTATGAGC ACAAATAATG AAGATAGATT TTTAGAAATA ATATTGAATA ATGACAATAT	249660
AAATGAATCT AACAAATTAA ATACAAAAA AGATTCATT CTTGCCGTAA CAGCATGTCC	249720
TGTGGGAATA GCTCACACCT ATATGGCAGC AGAAAGCCTT AAAAAAGCAG CTTTAGAATT	249780
AAACATAAAT ATAAAAGTAG AAACAAATGG ATCTAGTGGA ACCGAAAATC CAATAACAGA	249840
AGAAGAAATA AAAAAAGCAA AAGGAGTCAT TATTGCATCT GGCAAACTA TCGATAAAGA	249900
AAGATTTAGC GGAAAACCTT TAATCGAAGT GGGAGTAAAA GACGGCATA CAAAAGCAA	249960
AGAGCTTATC CAAACAATTC TTAAAAACGA AGCACCAATT TACAAAAA GCAACACAAA	250020
CAAAACCACC GAAACCCTCC AAAAACAAAA CAAAAAACG GGGATTTATA AACATCTAAT	250080
GAATGGGGTC TCATTTATGC TTCCATTTGT AGTCTCAGGA GGAATAATAA TAGCAATATC	250140
ATTCATGTTT GGAATCAAAG CATTTGACAT AAACGATCCA AGCTACAATA AAATAGCAGA	250200
TATTCTAATG CAAATCGGCG GTGGAAGCGC ATTTGCTTTA ATGATCCCAA TACTTGCTGG	250260
CTATATTTCA TTTAGCATAG CAGAAAGACC AGGACTTGCA CCTGGAATGA TTACAGGATT	250320
AATGATGAAC AATGGAAATG CAGGATTTTT GGGAGGCATC TTAGCAGGAT TTATTTCAGG	250380
CTACGTTACA CTAAGTAA AAAAAATATC TGACAAAATA ATTCCTAGCA ATTTAAGAGG	250440
AATAAATCCG GTATTAACCT ATCCTTTTTT ATCAGTTATA ATTCAGGAA TTTTGATATA	250500

TGGAATGCTT AGTCCAATAT CTGTTATTAA TGAATCAATA ACAAATATGC TAAATCAACT 250560
TAGCGGTACT AATATGGCAA TACTTGAGC TTTGCTTGA GGAATGATGG CAATAGATAT 250620
GGGAGGGCCT GTAAATAAAG CTGCATATGC ATTTGGAATT GCAATGATAA CTGCCAAAAA 250680
TTATATTCCT CACGCAAGCA TAATGGCAGG AGGAATGATA CCTCCCATAG GAATTGCTCT 250740
TGCTACAAGT TTATTTAAAA ATAGATTCTC AAAAGAAGAA AGAGAATCTG GAAAAGTTTG 250800
TTATTTTTTG GGAGCATGCT TTATTACAGA AGGAGTAATT CCATTTGCAG CAGCAGATCC 250860
TTTAAGGGTA ATACCCGCAT GTATACTAGG CTCATCTGTA GGAGGATTTA TTTCTGCACT 250920
TTTCAAGGTA GAGGTTATAG CACCACACGG CGGAATATTT ATTCTACCAA TAGTAGTAAA 250980
CCCATTAATG TGGATAACAT CTATCCTGGT AGGATCTATT ATAACAGCTG TTTTAATAGG 251040
AATCCTTAAA AAAGAATACA AGAATATAAA CGATTAAGTT TATATTCTTG AACCCAGTCA 251100
ATAAACTAAT CTAAGTTTTA TTGGTGTTTC AAGACTTAAT CCTTTAACCA TATCCATCTC 251160
AAACCGCAGT GTGTTTGAGT TAATTTGTTT GAATCCAAAT TGTTCCTGAA CATTTCTAGA 251220
AGTCTTAACT ACAAGATTAA GTTTGGAATT GTCAATAAGT TCACTTGCTT TGGAAGTAAA 251280
ATCCGATAAA AAATAAACCA AAACATCTTT ATATTCTTTG GCAGACATTG GGATCTCATC 251340
CGATGGCAAA AGAGCAGCAA GTGCATCACT AATATATTCT TTATTTTCAT TAATATTCTT 251400
AGTAGCGTTT TCCAAATTAA TATTAAGTTC AATAATATTT TTACCATCTT TTTTTTCTAT 251460
CTTAAACACA GATATATCGG GTTTTTTCAT ATAATCGCCT AAAATTTTAA TTAAATTATC 251520
AAACTTAACA ACTAAATTAA TAGAATCTCC TTGGGTTTTA ATACTCAAAA GCTTAAGCCC 251580
AAGCTTTTCC TCTCCATTTT TAAAGTATTT TTTTATTTCA TCTACAGGAA AAAGAGGCAT 251640
ATTTGCAATT TCTTCTCCCA CCAAAGTTGT TAAGAGTTCT TTTCTAATTT TTTCAAATTC 251700
TCTATTAACA TTAACAAATA TTGAACAAT ACCACTAATA TCATCATTTA ACTCAATTTT 251760
AACATTAGAG CTACAAGCAA AAAAAATCAA CAATAAACTC AaGCTAACAA AACACTTTCT 251820
CATAACAAAC TCCTAACTAA CAGTTAAAAA CTATTATAAT AGAATATATA GCTATAAAGC 251880
AATAAACTA AAGGAGAACA CCTATGGTGA mTGMtAAAC ACTAGAACCA AAATTTTTTC 251940
AAAGTCTGCT AGACAATAGC CCTACCCCTT ATCACTTAGT AAATATATT GAAGAGAAAT 252000
TAATAAATTA TTTTAATGCA CAACAATTAA AACTTAATGA AAAATGGAAA ATTAAACAG 252060
GATCATATTA CATAAAAAAA GAAGGAACTA GCCTTATTGC CTTTAATATT GATGTCAAAA 252120
AAAAATATGA ACCGTTTCTA ATAGCAGCAG CACATACAGA CAGTCCGGGA TTAAAATTAA 252180
AAATAGACGC AACAGAAAAA GTAAGTGGTG TGTTTTATAA CCATATTGAA GTTTATGGTA 252240
GTCCAATAAT TTCTACTTGG ATTGACAGAG ACTTAAGCTT AGCAGGAATT GTATATTTCA 252300

AAAAAATGA GAATATTGAA TCAAAATTAA TCAACATTGA AAACATAGGA ATTATTCCAA	252360
ACCTTGCAAT CCATTTAAAC CGACAAATTA ACGAAGGATT TAAATACAAT GCTCATGACA	252420
ATTTAACAGT AATCAGTAGC ACTAAAAAAG CAATAAAAGA TAATATCTTA GAACAACTTG	252480
GAATAGAGTG TGAAAATTTT CTATCTTGTG ATTTAATATT CACAGAATCA CAACCTTCTA	252540
AAATAATAGG AACTGAAGGA GAATTTTTGG CTTCTAAAAA TCTTGACAAC AAATCGGGAT	252600
GCCATGCAAT CATGAATTCT TATGTTTATA CAAGCAATGA TAAAAATAAA ATAGCTGTAT	252660
TTTTTGATAA CGAAGAAGTA GGTTCCTTAA CATCAAGAGG CGCTGATTCA AATTTTTTAT	252720
CAGAAGTTTT AGAAAGAATC GATATTGCTC TTGATTTAAC CAGAGAAGAG CATTTAATAA	252780
AAACAAACAA ATCATTTAAT ATCTCAATTG ACAGCGTTCA CGGCATTCAT CCGGGTTATA	252840
CATCTAAACA TGATCCAAAC TATCAAGCAA ATCTAGGTAA GGGCGTAGTT GTAAAAATA	252900
GTGCTAATTT CAGATATGCA ACAACTTCAA CAGGATTTGC AAAATTAAAA AATTTGGCTA	252960
TTAAAAACAA TATTAAGATT CAAGAAATAA TAATGAAAGC AAATGTTTCT TCAGGCACAA	253020
CAATTGGTCC AATCTCAAAT GCAAGAACAG GAATAGAAAC TATTGACATT GGAACACCAA	253080
TGTGGGCAAT GCATTCCCTG CGCGAAACAG TATCAATAGC TGACCACATA GAAGCAATTA	253140
AATTGCTAAG GGCTTTCTTT GAAAAAGGAA TTTAAAATTG GAAAAATAA AAGAAATAAT	253200
TGTAGTTGAG GGAAAAGATG ATCTTAAAAG AATCAAAGAA TCTTTTGA CTGCAGTAAT	253260
AGAAACAAAA GGATTTGCTT TAAAAATTGA AACTATTAAG TTGTTAAAAA AAGCCTTAAA	253320
ATACAAAGGA ATAATAATCT TAACAGACAG CGATAAATCT GGAAATATTA TTAGACAAAA	253380
AATAGTCAAA TATCTGGGAG AAAATAATAA AATCAAACAT GCATATCTTA ATACTAAAGA	253440
CACTGAGGTT GAATCAGTAA ATAAACAGA AATAATAAAA ATACTTAAGG GGGTTGGAAC	253500
TTTATCTAAA GATAATCAAA AAGATTTATT AAAATTAAGC GATTTGTTAG AACTTGGCAT	253560
AATAGGAGAA AACTCAAAG AAAATAGACA AAAAATACAA AAACACTTTT GTTTGGGGGA	253620
TGGAAATAGT AAAAACTCT TAGAAAGGCT GAATTACTTT AAAATAAAAA AAACAGACCT	253680
AAAAAACCAA TTGGCTTTAA CTAACCTCCC CAGAAGGACT TGAACCTCCG ACCTAGTGGT	253740
TAACAGCCAC CCGCTCTACC ACTGAGCTAT AGGGGAAATT GAACACTAAA AATATTATCT	253800
TAAATTTAAA AATTTTTGTC AATTATTTTC CAATATTTTT AAAATCCCAT TAGCAAGAAT	253860
TTTAGAATCT TGATCTCTAA GCTTAGAAGA TCTAATAGCC CAAGCTTCCT CTGGAAATGC	253920
CAAATTTCTA ACTTCTACTA AAAGCTTAGT CATTACTATA TTATTTCTTA AAACATGAAG	253980
ATTTTGACCC TTAATATAAA AACTTCTTTT CATTCCTTCT GTAATTTTTT CTGCTGCAGA	254040

CTTTGAATGA ATATCATATT TTTTATCGTC ATCTTTTGA TAATAAAACC CCATACTCTT	254100
AGGCGCTCCA ACACTATTAT CCGCATGCAA ACTAAAAAAG GCTATATCCT TATCTTTAAT	254160
ATGTTTATAT TTATTAACAA TGTTTTTAAC AACGACTAAT CTTTTTTTAA GGCCTGATGG	254220
AGTGCCGCTT ATCCAAGAAT CAACAGTATC ATTTTTATTT AGATCATAAT CATTGTAAAC	254280
CTCGTTTTTA ACATTAACAA AAGTATTGTT AGCAAAAAACA CTATTCTAA TTAAATGGTC	254340
GGGGGCTAAA ATAGTAAATT CAACATTGGC CCCCTCTTCT TTAAGGTATA CATAAAGCCT	254400
TAAGGCAATA TCATATACAT ATTCATCTTC AACAACAAAA ACTTCATTTT CAAGACCATC	254460
TCTAGATTTA ACAATAGCTC CAGGATCAAG ACCACCGTGA CCTGGATCAA GAATTATTAA	254520
TTTATCCTTA AGTCTTGATC CTTTATTAAA CCTAGAATTT ACCAACTTTT CAAAACTTT	254580
GAAAAGCTGG GTTGCCTTTT TATAAGAATT CAAAGGAGAA TGCCAATCTT CTGAATAAAA	254640
CTCACTTGGC TGACTTATCT TTCTTGGTCT ATACCAATAA TAGAAATCAC CAACAACCTC	254700
AAATATTGGT ATTTTGGAGT CTAAAATAAC CAAAGAGCTA ATATCAAAAA GATCTTGATT	254760
GGCAGTAATT CAAAAGTAT TTAAATTTAG TTTTTTATTT TTACTTGAGG GAAGATTAAC	254820
TATTGTTTGC ACTTTATTAG AAGAATTAGA GCCAGAATCA ACCTTTTTTT TAATATATAA	254880
ATCGTTTTTA GTTTTAATTA TAGAAGAATC AATTGAAAGT TTTTATCAA AAATTTTCAA	254940
TTTTTGATCG TGCATAATAT TATTGCTGCT TAAATTATTC CAATTTTTAA GATCCTCGAT	255000
TAAAACACCG TAATGTCTGG CAATGCTATA CAAAGTCTCC CCTACAGCAA CTGAATGATA	255060
GATAAACTTA TTATCTATTT TTTTCTCAAT TTTTAAATCT CTCTCAACAG GTTTTCTAA	255120
ATCATTATTT ACAATCTTTA AAACATTTAA CAATGAACCT GCTTTAAGAT TAATAGCCCG	255180
ATTGCCATTA AGGGCTACAA GATCCTTAGC AGTAACGCCA TAAATATAAG CTATCTGCC	255240
AAGAGTTTCC CCTCTTTTAA CATAATGAAA ATTAACATTC TTAGTGGCTT TCTTTAAAAA	255300
AAGTTGCTGG CCAATCTTTA ATTTATCATC ATTAAGAAAA TTAAATTTTA AAATATCCTT	255360
AGAACTAATA TCAAAATCCT GAGAAAGTTT TGAAAGTGAA TCACCTTTCC TAACCATATA	255420
AGGCTTTAAA AAATCAGGCT CGGTTAATAC AAGCTTCATT CCAACCTTAA GATCTTTAGA	255480
ACGCAAATCA TTCCAAGCAA TTATCTCTTC TTGACTTAGT CCAACAAGCT TTGAGATGCT	255540
CTCAATGGTG TCGCCTTCTT TTGCGGTGTA AAAAATCCC CCTTTACTAG ATTCTAGCAA	255600
ACTAAAAGAA TGATTGACTT TGTGGGTAAT GTTTTGACCT AAATTAGAAT CACTTGGAAT	255660
AATTAATATT TGACCCGCCT TAATATTGTC AACATTAAGT TTATTAATCC TTTTAAGATC	255720
GCTTACTTTG ACTTTATATT TAATTGCAAT TGAAAAAGA GTATCTCCCT TGACAACCTT	255780
ATACTCAAAA TCGGCATTAA GATTACAGG ACCTATTATT AAAAAATAA ATAATATAAT	255840

AAGATCTATA ATTTGCAAAA TACAAAAAGT TTTACTTTTC CTTAATGCCA GTATTTTGAA 255900
CAATGTAATC ATAAATTATC CAATAATAAT CATATTTTTT AAAGAAGAAA GTATATCTTT 255960
TGGAAATATA AAATTGCCCA TCGTCAAAAT ATAAATCAGC AATCACCTTG CCAGAAGTAT 256020
CAGAATAAGT AGTTTCAATA ATAGAAAATT TATTTGGTGC TTTTGAAATA TCCGAATTAT 256080
TAGAATTCCA CAAATATTCT TTATACTCTT CAACTACATT TTTATTGGGA ATAGGTGATA 256140
ACTTTTGCTT ATAAAGGTAT GCCTTGCCCT TGTCAATTAA TAACAAACCT TCAATATCAA 256200
GATATAAAAA GAACTTTTCT TTTTCCCAA GCTGCAATGC CTTTAACAAA TATTTAACAA 256260
TTTCATCGGG AGATAATTTT TTCTTTTTTCA AGATATCTTG AATATCATT TTTTCAGACA 256320
AATTAACAAG GTCATGCTA CCTGGATTTT CATCAAAACC ATCATTCAAA AAAAGCGTAA 256380
TAATATTGGA TTCTTTTTTC TTAGATGGAT CTGAAATGTC TGGGAAAAAA ATACCCTTAA 256440
CAAAATAAAC TCCATCTTTA CTAAACTTAA CAAATTGATT TAAGTTAATA ACTACAGAAA 256500
ATTTTTCATT AGGTCTCAAG CTCATATTTT TAACAGGAAT TGCAACATTT TTAGATCTCT 256560
TTTTAACATA TTCAATAGGT CTTTAACTT TAATATTGGT GGTATCAGTA ACATCAAAAT 256620
CAAAGCCAAA AGAATTAATA TCGCCTATTT CTAAAGTTAA AACACTCTCA GACGCATTAC 256680
TAAGAGAAAC TTCAATAAAA ACATTACTAT TGACACGATA AATAGATTGA TTAAAAAAT 256740
TGATTTTAAA ATCAAGGCC TGTAAATCTC CCGCAAACAA AAGAAAAGAA ATATTCATAA 256800
AAAAGATACA AAAAAGCAAT TTTCTAATAT TCATAAGCTC CCCTCAAAAC CTAAACACAT 256860
TATATATAAA GAAAGTAATA ATACCTATAG TATATTATTA TACTAAATTA ATTAAACAAA 256920
AAGGTAAAAA ATGAATATAG ATGAAGAACT AACAACAATA TTAAAGAATA ATTCTAATTT 256980
AAAAAAATG AAAGAATTTT TAGAACAAA TATATTTTTT TCATTAACAG GATATGAAGG 257040
ATTTTTCAG GCTTTTTTAA TTAAAAAAT CAAAGAATAT AGCAAAACCG GAAAAATAAT 257100
ATTAATAGTT AAAGACGAGC ACACATTAGA TAAATCAAA AACGATTTAC AAGTAATTAC 257160
AATCAAATC TTTGAGCTTA ACTATTTTAG CCCCTTGTA TACAAGGCA TTGGCTCAA 257220
AAGTACGATC TTTAACGAAA GAATCAAATT CTTATTCAAT TTTTATAAAA AAAATCCTGG 257280
AATATATATT ACAGTCTTGA AATCATTGCT TAGCAAAATA CCCGATAAAA ATACATTACT 257340
AAAGAATATA TATAAAATTG AAAAAAATAC CAATATTAAT ACAGCAGACA TTGAAAAAC 257400
TCTTATAACA TTGGGATATG AAAAAACATT AAGAGTAACA ATTCCAGGAG AATTTACAGT 257460
AAAAGGAGAA ATTATAGATA TATACCCTTT TGGAGAACAA AATCCAATAA GAATTGCACT 257520
AAACTTTGAC AAAATAGAAG AAATAAAAAA ATTTAATCCC TTAACCCAAT TAAACACGA 257580

TAATGAAATT	TTAGAATTCC	AAATTCTTCC	AAAAAAGAA	ATTATTTGGG	ACGATAAAAC	257640
TATTAACACC	TTAAAAACAA	AAATTAAATC	TGTTGAATAT	AAAAAGATTC	TTGAAGAGTT	257700
GGATTTTAAA	AAAGAAACAA	AAACAGAAGA	AATGTTTTAT	CCACTAGTAG	CAAATACTTA	257760
CTTAGGTGAT	GAGATTGAAA	AACACACACC	TATTGTAAAC	TTTGAAATTA	ACAATTTCGA	257820
AAAAGAAATT	GAAAAAATAC	ACCAAGAATA	TGAAAAGCTT	TACAAAGAAG	CAGAAGAAGC	257880
CGGTAAAAAT	ATAATTGATC	CAAAAAGAAT	TCTCTTAAAT	TATAAACCTT	TCAATCTAAA	257940
AAGCGATGTT	TTATTTTCAA	AAATTAAAAG	CCTTAAATCC	AAAGAAACTA	TAGAGTTTAA	258000
AATCGAAAGT	GAGAGAAACT	TTTTTTTCAA	TATAGCACTT	ACAAAAGAAG	AATTTGAAAA	258060
TTGGCTGAAA	AATGGATTTA	AAATCATTAT	TGCAGCAGAA	TCTGAATCAC	AAAAAGAAAA	258120
ACTTAAATAT	ATTTTCAAAG	AATTGCCAAA	AGTATCAATT	GAGGTTTTAA	AAATATCTAG	258180
CTCTTTAATA	ATAGAAAAAG	AAAAAATTGC	CATTATTCTT	GAATCAAACA	TTTTCAATAC	258240
GGGGCAAAAA	ATAAACAAAG	CCTTTGAATC	TTCAAAAACA	AAAGCTATTG	ACTCTTTTGT	258300
TGAGATTGAG	AAAAATAGTC	ACGTAGTTCA	CATAAACCAT	GGAATTGGTA	TATTTAGGCA	258360
AATAAGAGA	ATAAAAACAA	GCTCTCTTGA	AAAGGATTAT	ATTGAAATTG	AATACGCTGA	258420
AGGAGAAAAA	CTATTTATTC	CAATTGAACA	AACAAATTTA	ATCCAAAAAT	ACATTGGAAG	258480
TGATCCTAAA	AATATCAAAT	TAGATAAAAT	AAGTTCATAA	ACATGGATAA	AAAACAAAGC	258540
AAACGCAAAA	AAAAGAATCG	AGGAGATTGC	AGACAAATTA	ATAGAACTTT	ATTCAAAAAG	258600
AGAAAGCATT	AAGGGTATTA	AATACCCAGA	AGATAATGAA	TTACAATTGT	TGTTTGAATC	258660
TGAATTTCCA	TACGATGAAA	CTCCAGATCA	AATAAGAGCA	ATAAAAGAAA	TAAAAGAAGA	258720
TATGATGAGC	TTTAAAGTAA	TGGATCGCCT	TCTTTGTGGA	GATGTTGGAT	TTGGAAAAAC	258780
TGAAGTTGCC	ATGAGAGCTG	CTTTTAAAGC	CGTAATGGGA	AACAAACAGG	TTATTGTACT	258840
CTCACCAACA	ACTATCTTAG	CAGAACAGCA	TTCAATACA	TTTAAAAAAA	GATTTAAAAA	258900
TTTTCCAATC	AAAATCGAAG	TATTAAGCAG	ATTTATAAAA	AATAACGCAG	AAAGCCGGAT	258960
CTTAAAAGAA	CTTAAAAGTG	GAAAAATTGA	TATAATCATA	GGAACGCACA	AAATTCTTTC	259020
AAAAAAATTC	ACCTGCAAAA	ATTTAGGGTT	AATAATAATT	GATGAAGAAC	AAAGATTTGG	259080
TGTAAGAGAA	AAAGAAAAAC	TTAAAGAAAT	AAGAATTTTCG	GTTGATTGCC	TTGCTCTTTC	259140
TGCAACACCA	ATTCCCAGGT	CTCTTCACAT	GTCATAATT	AAGCTTAGAG	ATATTTCCGT	259200
TTTAAAAATT	CCGCCTCAAA	ACAGAGTAAA	AATAGAAGCT	TATTTAGAAT	CATTTAGCGA	259260
ACTTTTAATA	AAACATGCAA	TTGAGAGTGA	ACTGTCTCGA	GATGGTCAAG	TTTTTTTAGT	259320
AAATCATAAT	ATTGAAGAAC	TGTATTATTT	AAAAACACTA	ATTGAAAGAT	TAACCCCTTA	259380

TCGAAGAATT GCAATAATTC ATGGAAACT AACAGGAGAA GAGATTGAAA ATATAATGCA	259440
CAATTTTATT AAAAAAGCGT ATCAAATTTT ATTGGCAACA ACAATAATTG AAAATGGAAT	259500
AGATATTCCA AATGCAAATA CAATAATAAT AAATAATGCA AACAAAGTTTG GACTTGCACA	259560
GCTATATCAA CTAAAAGGAA GAGTTGGAAG AGGATCTCAG AAAGCTTATG CTTATTTTTT	259620
GTACCAAGAC AGCGAAAAGC TAAATGAACG CTCTATTGAA AGATTAAGAG CAATAACAGA	259680
ATTTTCAGAG CTAGGAGCAG GATTTAAAT AGCAATGAAA GATATGGAAA TAAGAGGTGT	259740
TGGCAATTTA CTTGGTAGAG AACAACATGG GGAGATTGAG TCGATTGGAC TAGATTACTA	259800
TCTAACAATG CTAAATAAAG CAATTGAAAA GAAAATGGGA AAAATCTCAT CAGATGAAGA	259860
AGAGGTTGAT ATTAAAATTA ACTATAGTGG ATTTATTCCT GAAAATTATG CAAAAATGA	259920
GCAGGATAAA ATACTAATCT ACAAAAAAAT CTTTAAATTT CAACTGAAG AGGAAAGTAA	259980
AAAAATAAGA TCAGAGCTCC ACAACGACTT TGGCCCAATA CCCGAAGAAA TAAACAGTCT	260040
ATTAATGTGA GCTGAACTTA AAATCTAGC AAAAGATTTA AACATAACAA AATTAAAAGA	260100
AAAAACAGG GCTTTGGAAG TAGAATACAA AAATATAGAA AGCATTCCCTA TGGAAAAAAT	260160
AATAGAAATA CTTCAAAAAC ATCCTAATTT ATTAATATTA AATCCCTCAT ATCAAAAATC	260220
AATATTTTTA AGCTTTAAAA ATATTGAAAA ATCTGAAAAA ATAAATTACA TATATAAAAA	260280
TATTAACCTA CTAAAAACAA GCACATAACT TGTCAAATAC AAAAGGAAAA AAAATGAAAA	260340
TATTAATCAT AAACACAGGA AGTTCTTCAT TAAAATTTGC TATTTATCAA TATGAAAATT	260400
CAAAAAAAT AATATCTGGA ATTGTTGAAA AAATAAAATC ACAAAAATCA ATCATAAAAA	260460
TTGTAAATAC TGACGGATCA ACAACAGAAA GATTTGAAAA AGGAATTGAA AATCACCAAA	260520
AAGCAATAGA AAAAATGTTT AAAATACTCA CAAACAGCGA TTAAAAATC CTTAAAACTC	260580
TTAGCGAAAT TAAATAATA GGACACAGGG TTGTACATGG AGGATCAAGC CTTAAAAATT	260640
CAGTAATTCT TAATAATAGT ATTTTAAATA AATTAAAACA AATTTCTGAA CTGCTCCAC	260700
TTCATAACCC AAATGCAATC ACCGCAATAG AAGCGGTGCT TAAAATTTA CCACACGCAA	260760
AGCAAGTTTT ATGCTTCGAT ACATCCTGGC ATCAAATAT AAAAGAACAT GCCTTCTTTT	260820
ATGCAATTCC ATATTCTTGG TATAAAAACC ACAATATTAG AAAATATGGC TTTATGGCC	260880
TTTCTTATTC GTACATAACA AAAAGATCCT CAGAAATTTT AAATAAAAAA ATAGATAGTC	260940
TAAATTTAAT AATATTGCAT CTTGGTAACG GAGCAAGTAT TAATGCTGTT AAAAATGGAA	261000
AATCTTATGA CACAAGCATG GGAATTACTC CGCTTGAAGG CCTTGCAATG GGAACAAGAA	261060
GCGGTGATAT AGACCCATCA ATTATTAATT TGATGAGCAC TATATTAAAC AAAACCACCA	261120

AACAAATTGA AGAAATATTA AATAAAGAAA GTGGCATACT GGGAATTTCT GAAAAATCAA	261180
ATGACATGCG GGATATTTGG AACAAAATTG AAGAAGGAGA ATATCAATCA AAACCTGCGAG	261240
TAGAAATAAT GACATATAGA ATAAAAAAT ATATTGGATC TTACATTGCC GCTCTTGATT	261300
TTAATGTCGA TGCAATAGTT TTTACAGGCG GAATTGGTGT TACTGATTAT GGAATAAGAG	261360
CTCTTGCACT AAAGGGGTTT GAAAAAATTG GAATAGAACT GGACCTTGAA AAAAATGAAA	261420
TGGCCCAAAG TAAGTATTTA GAATCTGAAA TATCAACCAT TAATAGCAAA CTAAAAATAC	261480
TGGCAATACC AACAAACGAA GAATCAACCA TTCTTGAAGA CATTTATAAT TTAATTCCAA	261540
AAAATTTATA ATTTACAATT TTAAAACTA AAATCTGGTT TATTTATTAT AATCATTTAA	261600
AATAGATTTA TATTTAACTC TTGCAAAGCA AAGTTGCTTT TTTAACATCT TCCATTATTT	261660
GTTTTCTTTT TACCATTTCA AGAAGAGTAA AAGCAAATTC AAATGAAGTT CCAACTCCTT	261720
TAGAAGTAAT AAAATTATTG CTTCTAACAA CATTTTCATC TACAACTCA CCATCAAGCA	261780
CATTTTTCTC CAAACCTGGA TAACATGTAA ACTTATTGAA TCCTAGAAGA CCTTTAGCAG	261840
CAAGCACTAC TACCGGAGAA GCACAAATAG CTGCAATAAA CTTACCTTTG GAATTCATAT	261900
CTTTTAAAT CAAATCCAAT TCTTTTGAAT TAAAAAGATT AGTAGCTCCA GGCATACCTC	261960
CCGGGAGAAT TATTAGATCA AAACAATTTT CCTTACAGTT TGATATTATA TCATCTGCTA	262020
AAAAAGAAAC GCCTTTTGAA CTTATCACAA CATTGCTATC ATTTGTGCTG ATAATTTGAA	262080
TATTAACATT ACCCCGTCTT AAAATATCAA TCGGGATTAT GGCCTCAATA TCTTCAAAGC	262140
CATTTGCAAG AATAATTCCT ACTACCATTT ACAACCTCTA ATGCTGATGG AGGGACTTGA	262200
ACCCACGACA ACTCGGATAT GAGCCGAGTG CTCTAACCAA CTGAGCTACA TCAGCTTAAA	262260
CTTTTATTAA GTGTATAAAT TCAATAATGC TTTGTCAATG TTATTATTCA AAAGTATTAT	262320
TATAAAGTAT AATACAAAAT GGCTTGCTAA TAAATATAAA TTACTAAATT AGCATTTATT	262380
ATTTATATGG TTAAATGAAA AGAAATTTTT ATCTCATTGT CCTTTTTATA GCTAATAACT	262440
GCTTTTCTAT TGATTTTTGG GATACGATGG AAAGAGAAAA ATTAATAAAT GAAATGGTAA	262500
GCAAAATGCA AGATCATGAA TTACTGGGGC AAATGTTTCAT GATAAGCTAC CCAAATCAAT	262560
CAATCACAAA TTTTGTCTT GATTTTATAA GTAAAAAAA TCTTGGGGGA ATTAAAATTT	262620
TTGGATGGAA CGCAAAAGAT TTAAAAAATT TAACAGAAAG TATTCATAAA GCTCAAAAAA	262680
CATCTCAAAA TAATAAATTT AAAATTCCTT TATTTGTAGC AACAGATCAA GAAGGGGGAT	262740
TGGCGCAGCA CATAAAATTA AATACATCAG AAACAATTGG CAATCTTGGA ATTGCAGCAT	262800
CGCTTTCTCC AAAAGATTCT TATAATACAG GATATTACAT AGCACAAGAG CTAAGGCAAC	262860
TTGGAATAAA TCTAACTTT GCGCCCATAG TAGATATATA CAGCCATGAA AATAATTTTG	262920

CAATAGGACC AAGAACATAT TCGGATAACC CCAAATAGT ATCACTTCTT TCTCTGGCCT 262980
TTTATAAAGG ACAAAGCAA GGAGGAGTAA TTTCTACTGC AAAACATTTT CCAGGACACG 263040
GCAATACCAC TCTTGACTCT CATATCAATA TTCCAATAAT AAATTCTAAT TTACTAGAAA 263100
TAAGCTTAAA TGAACCTTTA CCATATAAAA TATTAATCCA AGAAAACATC CCCGTAATAA 263160
TGACAGGTCA TTTAGCATAT CCAAAGCTTA CAAATGGAGA AAATATTCCT GCATCATCCT 263220
CAATAAAAT AATTAAAGAC ATACTTAGAA AAAAATTAAA ATATAATAAC ATAATAATTA 263280
CTGATGACCT ATTAATGAAC GCAGTAACT ACAATAATGA GAGCATTAT AATACGATTG 263340
AAAGAATAGT TAGAACCAA AGTGACATTT TTTTAATATC TTTAAATGAA AATATACAAC 263400
AAAATGCTTA CAACATGCTA TTAAATTTAA TGAAAAAAGA TTCAGAAATA AAAACAATA 263460
TTATTGAATC TAATAAAGA ATATTAAGAA TAAATTAAT GTACTTAAAA GAAAATAAAA 263520
ATAAATCTGA TCTTTATCCT AATTTAAACA AAAATGAGAA AATATATTCA AAAGAAGGTG 263580
AAAAATTTTT TGAACAAAAC ACATTAAGGA GTATTACAAA AGTAAGAATA GAAAAAGAAA 263640
TATCTAAAAC CAAAAAACA CTTATAATAT CTCCTTACTA CAAAATGATT GTAGAGGGTA 263700
AAAAAATATT TCAAAATACA TACGCTTATT ATTACAATA TTATCCCTTA AACGGAATTA 263760
ATCCCCAAAA ACTCGACGAA ATTAAAAAT TAATTAATA ATTTGAACAA GTAATATTTA 263820
ATTTATCCAC ACCTGGAAGC TTGAAATATT TAGAAAATTT GAAAGAATAC AAAGACAAAA 263880
TAAGCGTAAT TGTATCTCTT ACTCCTCACC ATATTAAAA ATTAATTTGG ATAAAAACA 263940
TAGTAATTAT TTATGGAACA ACACCCTTGG CATTTAAATC TGGATTTTTA AACTCACTA 264000
AAGATTTTGA TCCAAAAGGA ACCATCCCTT TAAAAATAT TATAAATAAA TATTATCCTT 264060
AATGTATGCT AGCATTGAT TTTTACAAT CTCTAGAGAA CCTTGTTTGA TTCTAAACCC 264120
ACTGGCATT TTAGCCAC CGCCTCCAAA ATCTTCTGCC AATTTTCCAA CATCAAAGA 264180
ATCTTTAGAT CTTAGCCCAA CTATAATCGA ACCATCCTCC ATTCCTTTA AAATGCCTAA 264240
AATTCATTA TTCTCAACAT TGCTTAAAT CATATAAAA AGCTCATTA CCCACTAAC 264300
TCCACCATCT TTGCCAGAGC TAGAAGAAGA TAAAAATGTA AACAAAACCT TTCCATTCCA 264360
ATAAGATTCA AGACTGTAA GCATTAACCT AAGAGTTTCT ATTGATTTA GGCTTTTGGT 264420
GGTTTCTATA TAGCTATAAA CTTCTTTAAG GCTTATTCCT TTTGAAACCA GTCTTGCAAC 264480
CATTTCAAAA GGCTCTGGAT CACTTCTTGA AATAAATTTA AAAAACCCAG TATCAGTACA 264540
AAATCCTACT AAAATATACC AAGCTTCTTC TTTTGTAAGA TCATGTCCAA ACTCTCTTAT 264600
CAATTTTCA ATTA AAAAG TAGTAGAAGG TGCAAAGGA TCAATATAGC CCTCACATTC 264660

TAATTTTTC	CCAGACATAT	GATGATCGAT	TACTAAAGTA	GGCATATTCT	TTACATAAAA	264720
GATAAATTCA	TCACCTATCC	TATCTAAAT	CGAGCAATCT	AAAATAATAA	CTGAATACTC	264780
TGAAATCTCA	ATATTGGGCC	ATTCAGATAA	AACTTATCC	TTAAAAGGAA	CTATTTCTTT	264840
TCTAATAAAA	GGACCTTCAT	TTAACAAAAT	AGAATTTTTA	CCAATTCTTG	AGAGAAAAGA	264900
GGATAAAGCT	AAAGAAGAAC	CTATACAATC	AAAATCAGGA	TCTTTGTGCC	CAATAATAAC	264960
AAAATTATTA	TATTTTAA	TAAAATTAAT	AACATCTCTC	ATAATAAAGT	TCGCAAACCT	265020
TCCGCAAAAC	AAGTTTTTAG	CTTATTTTAC	ATTGACTATA	TTACAATATT	TCAATAAAAT	265080
AAACCACAAT	GGCTAATAAA	ATATAACAGG	TGGGAAATTT	TGGAAAAACT	AAAACAAGAA	265140
GATATAGATA	AAGCATTTTA	TATGGCAGAA	AAAGCACGAA	ATAATTCATA	TTCTCCATAT	265200
TCAAAATTCA	AAGTAGGTGC	CTGCATTAAG	ACCAAAACAA	ACGATTTTTT	TATTGGAACA	265260
AATGTTGAGA	ATGCAAGCTT	TGGAGCAACT	TGTTGTGCAG	AAAGAAGTGC	GATTTTAAAT	265320
ATGATTGCAA	AAATTGGCGT	ACAAGAAATA	GATTTTTTAT	TACTTAATAC	AAGTCCTGAA	265380
TGTATTCCGT	GCGCTATATG	CCTGCAAGTA	ATGGCAGAAT	TTTTTAATCA	AGATACAAAA	265440
ATAATAATAA	CAGAATCTAA	ATCATTTAGT	GAAAACAAAA	CACCAATAAA	AATTTATACA	265500
TTAAAAGATT	TACTTAAATC	TCCTTTTGAT	AAAAAAGAAC	TACGAAGAGT	AACATACTCT	265560
GAGCTTGAAA	AAAAATTAAT	TTAATTTAAT	ATCTTTAGAG	AAACCAAAGC	ACTTGCAAAC	265620
TTATTTAATT	TGTTGCTTTC	AAGAGTATGA	GCAGATAAAT	CAAATACATT	TAAAATAAGC	265680
TTTTTCTCAT	CAGAATTAAA	ATTATATTCC	AAATCTTCAA	ATAATAAAAA	ATTAATAATT	265740
GGAACAAATT	TTTCTATAAA	GCTGTATAAA	CTATTATTAA	TATCATGGGT	TTCATAATAA	265800
TAATCAATA	TATCTTCTAA	TGACCTTCTG	TCAAACCTTT	TTAAAATCTC	GTAAAAAATA	265860
TTTTTAATAT	TATCAATTAA	ACTGTGCAAA	TCATTATTAT	TTAAAATAAT	TTTTTTACAT	265920
TTTTTCACAA	AAAAATCTGC	TTGCCGCATA	AAATATCCCT	CACTTTTGCC	CCCAACAAAC	265980
TAAGATTGAG	CTTAAATTTA	ATAAATGATA	AAATTTAACA	TTACTGCTAA	TATAGTAAAA	266040
TTATGCAACA	ACTAGGAGAA	TGTTACAATT	ATGGTCAAGG	TAATAAGCTT	AAAAAACATT	266100
CATAAATTTG	CTTATTTAAA	ACTGGATCCT	TTAAAAAAG	AGGATATCTA	CATTGTTTAT	266160
ATTGAAACTA	ATTCAAAATT	AATTGCAAAT	CTTAAAGCAA	AAACAAAAGT	TGATCAAATT	266220
GAAATAATTA	ATTTTATAT	TGATGATGAT	TTTAAATCGG	AAGGCATAGA	AAGAATAATG	266280
ATTAGCAATT	TAATTCACTA	CGGCAAAAAA	AATAAGTTTA	AAACAATTTT	ATGCCAAATT	266340
GCTGAAATAC	AAGAAGAGCT	TTTAAGCTTG	GGATTTGAAT	ATAACGATTC	TAAATATAAA	266400
AAAGAATTAG	CATCTGAAAT	AGAAGAAGAT	AAATTTGTAA	TGGGAATAGG	AATAATCTCT	266460

ATATTTACCG AAGTAGCATC AATATCTTCT AAGCTTACTG TTGGAATACT GTTTAATTCA 266520
TTTGCACTTA TTGCTGATGC TTTCCACGTA ATGGCCGACT TTGTTTTATC TACAATAACT 266580
TATTTTAGTT TGAAAATTAC AAGCAAGCCT GAAACCATTG ATTATCCCTA TGGACACAAA 266640
CTAATGGAAA GCTTAATAGC TTTTATCATG GGAATAATTA TACTTATGAC AGGATTTACA 266700
CTATTTCTAA ATACAACCGG ATTAAATAAA TTTATCACTC TTGGGGGAGA GTCTGGATTT 266760
AATCTACACA TACACCAGAA CAAAAATAAA AATGATACTA TATATGAACA TGACCATTGC 266820
CATTCACACG ATCACGATCA CGATCATAAC CACGACCACA ACGAAGAAGA CAAAAAAAC 266880
ATACTAGAAA TATTTTCAAA TAAATCTCTT AAAAAAGCT TGTGGATACC ATTAACCCCC 266940
TTCATTTTTT TTATAGTGAA AATAATAGAA TATTTGACAA AATTTCAAAT AGGAAAAAGA 267000
TACAACAATC AACTTCTCTT AGCACTAGCT TCTGCTGATA AAAACTGTAT ATTCTCACAT 267060
GGTGGGATTA CACTAAGTTT ACTGCTTGCA ACCTACATGT GGAGTGGCTT TGACAAAATT 267120
ATGTCTATAT TTATTGGCTT TATCATAATA AAAGAAGGGC TTAACGTAAT AATAAATAAC 267180
GCAAACAATT TGCTATCAAA ACAAATATA GATCTTAAAA GAAGCGTAAA AGACACGTTA 267240
AAAAATTCAA ATATAAACTT TAAAACACTC AATTTTCATA ATCAAGGCAA CAAACTTGTG 267300
CTTTATATCA AAATAAATTT AAATTCAGAA AATGACTTTA AAAATTTTAT AAATAAAACA 267360
CAAGATATTA AAAAAATCAT AAAACAAGAA TATAAAGAAA TAAATGATAT ATATTTTTTA 267420
GTCTAATTAA ATTAATAATA AACAAATAAT TGACACTCAT AATAAAGTTG TGTTAACATT 267480
TTAAATTGTA AGACGCAGGG TAGAGCAGTT GGTAGCTCGT CGGGCTCATA ACCCGAAGGT 267540
CATAGGTTCT AGTCCTATCC CTGCTATGCT TTATTTTTTA TATGTGAGGA ATTGATGAAT 267600
AGAAAACAAA TAGCTAAAGG CAAGCTGGTA AGGAGATTTG GTATCAACAT TTTTGAGCAG 267660
CCAAAATATG ACAAATCCT CAAAAAAG CCGCATCCTC CCGGAATGCA CGGAAAAGCC 267720
AGAAAAGCTA AAATCACAGA ATATGGAAAA CAATTAATAG AAAACAAAA GATAAAGTTT 267780
ACTTATGGTG TAAGTGAAAG ACAGCTAACC AACACTTTTA AAGAAGCAAA AAAACATCAC 267840
GGTGTTACTG GAGACAACTT GCTCTCAATA CTTGAAAGAA GAATTGACAA TGTTGTATAT 267900
AGGGCTGGAT TTGCCATCTC AAGAGCACAC GCAAGACAAA TAGTTTCTCA CGGTATTATT 267960
ATATTAAATG GAAGAAGAGT TACAATCCCT TCAATAATAC TAAGAGCAAA TGATCAAATT 268020
CAAATAAAAG AAAAGACAG CCTAAAAAA TTAATAAGAT CAAATATAGA AAAAATTCTG 268080
TCTCTTAGAA ATTTGCCAAC TTGGATAGAA GTAAATGCTG ATGATTTAAA CATAAAAGTA 268140
AAGCATGCTC CATCAAGGA CGAGATACCT ACGCTTGCTA ATGAACAAAT GGTGTAGAA 268200

TATTATTCTA	AGAGAGCATA	AAATATCTTT	TATTTCTGTG	TTATTAAATA	AAAAAAGTGG	268260
CTAATTAAAG	CCACTTTTTT	TATTTACCCC	TTTTTTTACC	CTTTGAAAAA	CTTTTACCCA	268320
AATTATTCTT	AGCAAAACAA	GAAAAACTAT	TATTCTTTCT	CAAGCCCTTA	ACATTAGGCT	268380
GAGCGCTAAA	AGACGCTCTA	TTGCCCCAAG	GCTTTCTAAC	TCCATCTTTC	ATAGATCTAC	268440
TCCTAAAATA	TAAATTTAAA	TATGTAAATT	TTTAAATAAT	ATTCAAATAA	TCAAAAACCT	268500
CTTCCAAGCT	GGAGACAAAC	TTAACATCTA	TATTGTCCTT	AACTTCTTCT	GGAAGCTTAG	268560
AATAATCTTT	TTTATTATCT	TTGGGCAAAA	TAACTTTACT	TATACCGTTT	CTATAGGCTG	268620
CTAAAACCTT	TTCTTTAATG	CCGCCCCACAG	GAAGAACAAA	GCCCTTTAAA	GTCACCTCAC	268680
CAGTCATTGC	AAGATCCAAA	GGAACCTTCT	TGTCAGACAA	TATCGAAGCA	ATTGCCGTTG	268740
CAATGGTAAT	ACCTGCAGAA	GGCCCATCTT	TTGGTGTTGC	TCCTTCTGGA	AAGTGCAAAT	268800
GAATTCAGG	ACTTTCCTTC	ACATCAAAAT	TAAGCTTAGA	AGAATAGGTC	TTAACTATAG	268860
AATATGCAAG	CTGTGCACTC	TCTTTCATAA	TAGCTCCAAG	ACTACCTGTT	AGAATAATGT	268920
CTCCCTTTTT	CTCAAACTTA	GTTGCCTCAA	CAGGAAGAAC	TGTACCACCA	TAATTTGTCC	268980
AAGCAAGCCC	ATAAACAAAC	CCCGAAGAAT	CAATCTTAAT	TAAATCCAAG	TTATCCTCAG	269040
TATCAACATA	ATTATAATAA	TTATTAATAT	TGATTATTTT	ATAAATACCT	GGAATATCAG	269100
GATCATGAGT	AAAAAGCGAA	TTATTCCCAT	GTATCAAAGA	ACTTGGTGAA	TAAAAGTTGC	269160
CTTTGATGAT	TTGATCTTTA	GAATACTCAT	AAAGCAGCTC	CCTTACAAGT	CTCCTAATCA	269220
AATTAGTCAA	AACTCTCTTT	AGCCCCCTTA	CACCAGATTC	CATAGTATAG	TTTCTAATCA	269280
AATTAAAAAT	AACATCATCT	TCTATTCTTA	TATAAACTTT	GTCCAAAAAA	CTCTCTTTAA	269340
TTATGCTTGG	AATCAGAAAA	ATCTTAGCAA	TCTCTAACTT	TTCAATATAA	GAATAACCCT	269400
CAACCTTAAT	TATTTCCATT	CTATCTAAAA	GCGGCTTTGA	CATACCATTA	AGAGAATTGG	269460
CTGTTGTAAC	AAATAAAACA	TTGGAAAGAT	CATAAGGAAT	TTC'TAAATAA	TGATCTATAA	269520
ACTTATAATT	TTGCTCCGGA	TCTAAAACCT	CCAAAAGGGC	AGATTCGGGA	TTTCCCTTAT	269580
AACTACTATT	AATTTTATCT	ATTTTCATCA	GAAGAATAAC	GGGATTGGAT	TTACCTGATC	269640
TTTTCATTGC	GCTAATAAAA	ACACCCGGAA	GAGAACCAAC	ATAAGTTCTT	CTATGCCCCC	269700
TAATTTCTGC	CTCATCTCTT	AAGCCACCAA	GAGATATTTT	AACAAATTCT	CTAGACAGTG	269760
ATCTTGCAAT	AGACTCCACA	AGAGATGTTT	TGCCAATACC	AGGAGGCCCC	ACAAGACATA	269820
AAATAGGAGC	TTTGACCTTA	GAATTAATCT	GATAAACAGC	CAAAAAATTT	ATTATCTTTT	269880
CTTTTGCTTC	ATCCATACCA	TAATGAGAAT	TTCTTAAGAT	AAATTCAATC	TCGCTTAAAT	269940
GATTTTTCAT	AACAGTATTT	TCATTCCATG	GAAGATCTAA	TATTAATTCT	ATATAACTTC	270000

TAATAATATT AGCATCAGGT GAATTCATCT GCATTTTAGA CAATCTAGAA ATTTCTTTTT 270060
CAATCTTAGA TTTAACATCT TCTGGAATAT CTTTAGAGTT TAATCTATCA ATATAATCGT 270120
TTTCATCTTT ACCTAATCTT TTTTGTATCT CTTTAACTTG TTCAGAAAGA AAATAATCCC 270180
TTTGCCCCCTT ATCCAACCTA GCTCTAACTT TAGAATTAAT ATCTTTTTTA AGATCTAAAA 270240
GATCAATTTT AATGCTTAAA TTAACAATCA ACTTTTCTAT TCTGGTTTTA ACATTTAGCT 270300
CTTGTA AAAAG TTCTAATTTT ATGCTATTTT CCAAATTTGA ATTAGAAGCT ATAATATCGA 270360
CAAGCTTACT TGGATTCTCA AAATAATTAA TTGGTTCATT ATCCGCATCA TAAGATTTTA 270420
AAGATAAGGA ATTTCTATAA GCTTCATAGG TTTCTTTTAA AAATTTAGAA TAGGTAAAAA 270480
GCTCTCTGTT TAATCCACTA GAATCAGGCA CAAAAGTAAC TTTAGCTCTC AAATAATCAT 270540
TTTTTTTAGA AACACTGTCT ATAAGAACCC TACTTTGACA CTCAACTAAA ACTTTTATTA 270600
CGTCTTTACT AATCTTTATA ACCTGAATAA GTTTAGAATA AGTACCCACA GAGCATAGGT 270660
TTTTAACTAC TCCCCTATCA GATTCATCAC AATTAGGCTC ATTTGAATAA GCAAATAAAA 270720
TCAATCTTTC CTCTAACATG GATTGCGCTA TGGAATTAAT TACATATTCA TTATCAAAGG 270780
TTACCCACAA TGTAATATTG GGAAAAAGAA CATTTTCTTT TAAAATAACA ATTGGAAGAT 270840
CTTCTTTTCT ATTTTTTATC ATATTTAAGA TTGATTTTCA ATAACTCTTT TGCCCAAGGT 270900
TTTTTAATTG CATTTCCAC TAAAATTAAT GGGTTAACAT CTGCATTTAA AACAGATTCT 270960
TTTGTAACAA CAACCTTCTT AGCCTTACTA ATAGAAGGAA CCTCGAACAT AACATCTTTA 271020
AGAAGACCCT CTAAAATAGA TCTAAGACCT CTTGCTCCAG TATTTTTTAA AATGGCTTCA 271080
TCTACAATTG ATTCTAAAGC ATCTTTTTTCA AATACCAATT CAACATTGTC CATTTTAAAC 271140
ATATGATAAT ACTGCTTAAC AATAGAATTT TGAGGATCAA CCAATATCTT CAACAAATCT 271200
TCTTTATTCA ACTTTTCAAG ATACGAATGC ACAGGAAGTC TGCCAACAAA TTCTGGTATT 271260
AAGCCAAATT TAATCAAATC TTCCATTTCT AAATACTTTA ATGAAGTATC TTCTCTTATA 271320
TTCTTTTTTT CAATTGCTGA AAACCCAATA GAACTTTTAT TTATTCGATT CTTAACAATG 271380
TTTTCAAGCC CAACAAAAGC ACCGCCACAT ATAAAGAGTA TATTTTGAGT ATTAATTTCA 271440
ATAGTATCCT CATAAGGATG CTTTCTACCG CCTCTTGGAG GAACATTGGC AACCGTGCCT 271500
TCAATTATCT TTAACAAAGC CTGTTGAACC CCTTCCCCAG AAACATCTCT TGTTATTGAG 271560
ACGTTTTTCAT TTTTTTTAGC AATTTTATCT ATCTCGTCTA TATAGATAAT CCCTTTTTCA 271620
GCTAAGCTAA CATCCCCATG AGCAGCATGT ATCAATTTAA GCAAATATT TTCTACATCC 271680
TCGCCAACAT ATCTTGCTTC TGTCAAAGTT GTAGCATCTG CTATTGCAAA TGGCACATTC 271740

ATCTCTGCAG	CCAACGTTTT	TGCAAGCAAA	GTTTTACCAC	TGCCTGTAGG	ACCAACCAAA	271800
AGTATATTAG	ATTTTTCAAT	CTCAATACCA	TTGTCATATT	TATTATTTTT	CAATATTCTT	271860
TTATAATGAT	TATAAACAGC	CACAGATAAG	ACTTTTTTAG	CATCTTCTTG	CCCAACAACA	271920
TACATGTCTA	AATGATCTTT	AAGTTGTTTG	GGAGTTGGCA	AACCGTTGGA	CTTAGAATCT	271980
AGCGGCTTAC	ACAACTTTTC	TTTAAAAAGA	TTGTGACATA	TTTTAGAACA	TTCCGGACAA	272040
ATCGCTACCC	CATTAGATAT	AACAACATTA	CCACCAAGCT	CAGCGACACT	AAGTCCACAA	272100
AAAGAACACT	CTTTTACTTT	TTGACCTTTT	ACTCTTGCCA	TAAAACTTTT	TACCGAAAAT	272160
AAAACACTC	CCTTACTAAG	ATACTATCAA	TAAGACCATA	TTTAAGAGCA	TCGCTTGAAG	272220
TCATAAAATA	ATCTCTTTCC	ATATCAAGAG	CCAGTTTTTC	CTTATCAACT	CCTATCTGAT	272280
TAGACATAAT	ATCTATTATT	AATTTTTTAA	GTCTTAAAAT	TTCATTAGCT	TGTATATTAA	272340
TATCACTAGC	CTGACCACTT	ATTCCACCCC	AAGGCTGGTG	AATCATTATT	CTAGAATAAG	272400
TTAGAGATTC	TCTTTTACCT	TTAGCGCCAC	CAGCAAGTAA	AAAAGCACCC	ATTGAAGCGG	272460
CTTGCCCAAT	GCAAATTGTC	CTTACATCAG	GCTTTATATA	TTGCATAGTA	TCATAAATCG	272520
CAAGACCTGC	AGTAATACTG	CCGCCTGGAG	AATTTAAATA	AAGATAAATG	TCTTTGCTTG	272580
AATCTTCTGA	TTCTAAGAAC	AAAAGTTGCG	CAATCACGGT	ATCTGCCTTA	GGATCATTA	272640
TTTCACCACT	CAAAAATATT	ATACGCTCCC	TAAGTAATCT	TGAATATATA	TCAAATACTC	272700
TCTCATAATT	TCCCGTATTC	TCTATTACAG	TGGGTATTAA	ATTATGCATA	AACTCCATTT	272760
TTCTTACTCA	CAAATTTTAT	AATTAACAAA	ATCTCTAAAA	TTTAGTTTTT	TACCCTTTAC	272820
CTCTTTAAGA	TTTTCCAAAA	TTTTTTTCTT	AGCTCTTTCC	CTTTTAATAT	CATCCTTTAA	272880
ATAAGAAATC	AAATTTTGAT	CTTCATAAAA	TTTTTTAATC	TCCTCATAAC	TTACACCTAA	272940
ATTCTTAGAC	TGCCTGGCCA	TTTCATCTTC	AACATCGCTT	TCAGTAACTT	TAATTGGGTC	273000
TAAATCTACC	ATTTTTTGCA	TTATCAGTTT	AGATTTCAAA	TTCCCAAGAA	TCTCATCTTT	273060
TAAATTATCA	CCACCAATAT	ATCCTGAAGA	ATAAAAAATA	CTTTTAAACT	CTTCAAGGCT	273120
CATATTATTT	TTATTTTGCC	TTTTAGCATC	CTTAAAAGCA	ATTTCATTTT	CAGCCTCAAT	273180
CATTGAATGG	GGAATATCTA	TTTCTAATTT	TTCAGAAATA	GTAGAAAAAA	ATTTATTTAG	273240
CTTTAAAGTT	TCTTTTTTTT	CTTCAACAAT	GTTTAAAAGA	CTAGATCTTA	TAAAATTTTT	273300
AAGATCATCT	AGTGTATTAT	ATTTATCACT	AATATCCTGT	GCAAACCTCAT	CATCTATTAA	273360
GGGGAGATCT	CTTTTTTTTAA	TACTCTTAAT	CTTAATCTTC	AATTTTCTTG	AAGAACCCGC	273420
AAGTTCTTCA	AATTTGTAAT	CTGCAATATA	AGATTTTTCT	ATAACTCTCT	CTTCATTTAT	273480
TCTCATACCA	ATTACATCTT	TGTCAAAATC	ATAATAGGTC	TCAGATTTTC	CAACCGTAAA	273540

AACAAAGCCT	TGTCTTTTTG	TTGATACTAT	CTCATTTGAA	AGGTCATCAA	GCTCAACAAA	273600
ATCCACTTTA	ACAATGCTAT	CTTCCTTGAC	AACTCCTTCC	TCATCTTCAA	TGATAATTGA	273660
ATTTTCTATT	TGAAGATTCT	TAATCTCATC	ATCAATATCA	GAATCATCAA	TAAAACTTC	273720
AGGGATCTCC	ACTTTAATAT	CAATCTCATC	AAAACCTGGA	ATTTTAAATT	CAGGATAAGT	273780
CTCATATGTA	AAAGTAAATT	CAAAATCTTT	GTCAAGATTT	AATTTTAAAT	TTTTTTCCTT	273840
TACAGTAGGA	GTAGCATAAC	TTAAAGGTAT	TTTGGACTCT	TCTTTGAAAA	ATTCCTTAAA	273900
AGAATTATTA	ATCACTTCTT	CTAAAACGGT	AGCTTTTAAA	CCCTCAGAAAT	ATTTATTCTC	273960
AATAACATTA	ATAGGAACTT	TTCCAATTCT	AAAGCCTTGA	ATCTTAAGTC	GGGAAGAATA	274020
ATCTTGCAAT	AATGAATTGT	ATTTTTCCTG	AATAACGTTT	TTTGAAACTC	TAATGACAAC	274080
CTCAACTTTT	GAACCTGGAA	GAAGCTTAAT	ATCTTTACTC	AAAATCACTG	TTAATGCCTC	274140
AATTAAATTT	TATTGATAAT	TATTAAAAAG	CGAAAGACGG	GATTTGAACC	CGCGACTTCC	274200
ACCTTGCAA	GGTGACACTC	TACCCCTGAG	TTACTTTTCGC	ATTTTACAG	AAGGTGGGAG	274260
TCGAACCCAC	ACGCCAAAGG	CACTAGATCC	TAAGTCTAGC	GTGTCTGCCA	ATTCCACCAC	274320
TCCTGGCATA	CTTCATACTC	AAAATAGTAT	ACAAAAACTT	AAAAGCTTTT	GCAAGTATGC	274380
CTAATCTACT	AAATAAATAA	TAATTTGCGA	CTCAGCAGGA	GTGGAACCTG	CAACCTTCGG	274440
ATTGGAAGTC	CGCCGCTCTA	TCCAATTGAG	CTATGAATGC	AGTTAAAAAT	AAAATTGATT	274500
AAAGGGTGAT	TGACGGGGCT	TGAACCCGCG	ACATTGCGAA	CCACAACCCG	ACGCTCTACC	274560
AACTGAGCTA	CAACCACCAA	TAAGTAGTGA	CTATGATTAT	TATAATATTT	TATAAATATT	274620
TAATTCCTAA	GTCAATAAAA	GATAAAAATA	ATAAAAGCCA	TAAGACTTTT	ATTAAAAAAT	274680
TTATAATAAA	ATATTAATTT	TTTTCAAAAC	TAAAATTTTT	GAAATCTTTC	TAAGCTTTTT	274740
TTCAAAAAAT	CATAAACTCT	AATAGTTGAA	GAAATATTTA	CTCTTCCCT	AGTAGTATGA	274800
GGCCATTCAA	TCCAAGGCC	AAGGGTAACA	GATTCTATAC	CTCCCAATCT	AGAAGATATT	274860
ATGCCTGTTT	CAAGACCTGC	ATGTATTGTG	GAAACATTAG	CATCTTCAAG	ATACATCTCT	274920
TTATACACTT	CTTGAAGATG	TTTTAAAAGA	TTGCTATTCT	TATCAGGCTG	CCAAGAAGGA	274980
TCATCATAAA	TTACACGCAA	ATTAGCTCCC	GACAAATCAC	TTATTGATTG	TAAATGATTG	275040
CAAACATACT	CTTTGTCTAA	ATCCAATAAA	GATCTTATTA	AAAAAGTAAA	AATATAATCG	275100
TCTTGCAATC	TCAAAAGACT	TGAAAAATTT	AAAGAGGTCT	TTATAAGCTT	ATTTTCATAA	275160
TTTTCTACTT	TTTGAAGTCC	ATGTAAAAAT	CCCATTCCCA	TATTTAAAAG	CTTATTTTTG	275220
CTATTTTCAT	CAAGAACTTT	AACTGATGAA	AATTCTCTTT	TATTAACAAT	AATATCAAAT	275280

TCATCTTCAA	GAGAATATGC	ACTTTTAACT	TTAAGTACGA	ACAGTTTAAG	CTCTTTATTT	275340
AATAAATCAT	AATCATTATC	ATCTATAAAG	ATTAAAGCCT	TGGCTTCAAT	TGGAATTGCA	275400
TTGCTACTAT	TTCCACCAAA	AATGCCTTCA	ATCTCAAAAT	TAAGATTTGC	CTTAATTTCA	275460
AAAAGAGCAA	AAAACATTAA	TTTTAAAGAA	TTTGCCAAAT	CTAAATGAAT	ATCTGCCCCA	275520
GAATGGCCAC	CTTTAAGCCC	TTTAAACAAA	ATTTCTACCT	TTGTTTTTTT	CGTTACAAGG	275580
CTATACTTAG	GAGAAAAAAC	AATTTCTACA	AGTCTTGATC	CCGCACAACC	AACTAAAAAA	275640
TAACCCTCTT	CCTCTCCATC	AAGATTAATG	AGGCTTTTAC	CACTACATAA	ATTAGAATCA	275700
AGACCAAGAG	CACCTATTAA	ACCTATTTCT	TCATCAACGG	TAAATAGAAG	TTCTAAATCG	275760
GGATGAGGAA	AATTATTGGC	TTCACTCATA	ATCCCCAACA	TCATAGCTAC	TCCAATCCCA	275820
TTATCAGCTC	CGAGGGTGGT	CCCTACTGCT	TTAAGATATC	CATCCTCTTC	AACAATTTCA	275880
ATTGGATCTG	TTTCAAATTT	ATGCAAACTG	GATTCATTCT	TTTCGCAAAC	CATATCAACA	275940
TGAGATTGTA	AAATAATAGG	ATGCATATCA	ATATTATTAT	TTGATTTTAT	CTGCACTACA	276000
ATATTACCAA	CACGATCTTC	TTTAAAAGAA	TAACCAAATT	TTTTGGCTCT	CTGCTTAATA	276060
AAATTAATAA	TTCCTTTAAT	ATTTTTTGAA	CATCTTGGA	TTTTTGATAT	CTCTTTAAAA	276120
GAATCAATTA	CAATACTCAT	AATAACTTTC	CTTTGATTAA	ATTAAATCCA	TAAATATACT	276180
TGGATTTAAT	TTATAATTAA	TAATATAATA	TACTAAATTA	ATCTTTAAAT	TCATTCAATA	276240
AATTCATAA	TATTGGTTAA	GCTTTGTTTT	CAACAAAATC	TGCATAATAA	TTAAAATTTA	276300
AAAATTCCTT	AGGAATTTCT	GAAATAAATC	TTGAAGGCAA	CTGATCAAAA	ATTTGCCTAT	276360
CTTTTTTACG	CTTATTAGCC	ATAGTAATAA	CAAGAGAATC	TTTTGCGCGA	GTTAACGCAA	276420
CATAAAAAAC	TCGCTCTCT	TCTTCTAAGT	CAACCTCACT	ATCTTCAATG	ATTCTATGAT	276480
GAGGAATAAT	ATTGTCTTCA	ACAGCAATAA	AAAATACATA	ATCAAATTCT	AAACCTTTAG	276540
CAGAATGTAC	TGTCATTAAA	TTAATATTAA	TATTTTCAGC	TTCTCACTT	ACTTCGTTAG	276600
ATTGAAGAAC	TATGTAATTT	AAAAAGCTAC	TTAAATCTCT	CAACTCACCA	AATTGTTTGG	276660
ATTCCCAATT	TTAATTATG	CTTAAAAACC	CTTCTATATT	TTGATACTTA	TATTCAGCCA	276720
CTTTGATTGA	ATTGGGATTT	TCACTAACTA	AAAATCCCCA	ATATTCAATA	CTTTCTATCA	276780
TTTCTTTGAT	TATATTGGAA	TACGTGTTTT	TTGTTATACT	AACTTATAT	TGATACTCTT	276840
CAATAAAAGA	TACAAAATCT	TCTATGCTTT	CAATGACCTG	CTTATTTAAA	GCCTTGTCAT	276900
AACTAGAAAT	ATTTGTAAAA	GAAAAAGTAA	TGTCACAAAG	AGCATCATAA	ATGCAACAAC	276960
CCTTCTTGTC	TGCTATATCT	CTAATTTTTT	TCAAATATTC	CTTGCCAATC	CCCCTTCTTG	277020
GAACATTAAT	GATTCTAAGA	AGATCATAAT	CACTTTTAGG	ATTTATTATT	ACATTCAAAT	277080

AAGAAATAAT ATCTTTTATT TCTTTTCTCT GGAAAAAAGA TGTTCCTCCCT GAAACTTTAT 277140
ATTTTATGCC TTGTCTTCTA AAAATCATTT CAACGTTTTT AAAAAGAGCA TTGGTTCTCA 277200
TAAGAACCCC TATCTTTTTA GACTTAAAAT CCTCTAGCCT TGAAAGCTGC ATGATTCTAT 277260
TTGCAACAAA CTCAGATTCT TGAATTTTCAAT CCTCAAATAT AAAACATCT ATAACTTTGC 277320
TACACATCTT TGAGGACCAC AAGGTCTTTT CTTTCTATT TTTATTATTT AAAATCACAG 277380
AATTGGCAAC ATCTAAAATA TTTTTTGCAG AACGATAATT TTGTTCAAGC TTTATTTCTT 277440
TAACGTTGTA ATCTTTTTCA AATTGCAACA TGTGTGTATA ATTAGCCCCG CGCCAAGAAT 277500
ATATCGACTG ATCATCATCC CCAACACAAC ACAAATTACT ATGATTTATC AAAAGGCGAA 277560
TAAAATTATA TTGAATCAAA GAAGTATCTT GAAACTCGTC AATCAAAAACA TATTTATATC 277620
TTTTAGAATA TTTATTTCTA ATATCAGAAT TATTACTTAA CAATTCTTTT GGCTTTAAAA 277680
TCAAATCATC AAAATCAAAA GAATTATAAA GCCTTAACCT CTCTTCATAA AGCCTGTAAA 277740
TATTTATATC TTCTTCCTTT AAATCATTAAG GAGTGAGAAT ACCGTTTTTT AAAAGTGAAA 277800
TAACATTGCT AAGCGAATTT AAAGAACTT TTTTATTAAA AAGACCCTCA TCAAGTAAAA 277860
TCTCTTTAAG AAGAGAGATT CTATCATTTGT CATCATAAAT ACTAAAGTTT TTTCTATATC 277920
CTAACAATTT ATAATTTTCT TTTAAAAAGT AAAGCCCAAA AGCATGGAAA GTTGAAACCA 277980
TAAGATTACT AAGAGGACTT TTTAAAATTT TTTTAATTCT GTCTTTCATT TCATTAGCAG 278040
CCTTGTTGGT AAAAGTCAAG GCTAAAATTT CCCTCTGAGC AATGCCTTTT AAAAGCAAAT 278100
ACGCTATTCT GTGAGTAACA ACCCTTGTTT TTCCACTACC AGCACCAGCA ATAATTAAAA 278160
GAGCGCCTTC AATAGTAGTA ACTGCTTCAT ATTGAAATTG ATTGAGAGAA TTTTTTAAAA 278220
AATCATCATT AGACAAAATT AAAAAACCTT TGTTCCTCTT GGATATTCCA CAATAACCTT 278280
AAAGTTTCA GGAAAAGCAA AAATTTTTCG CGACTTAGAT TGATCAAAAT CTTTAGCTAA 278340
GATTGGAATA CGATACTTAT TCAATGTATT AACGGCAAAC TCTGAATTTT CAAGCCCCAC 278400
CTTAACCGAT CCTTTTGCCA TAAAATTAGT TCCACCAAAA AGCTTAGCCT TAAGATTACT 278460
TTTGCTAGCT CCATTTTCGA GCATTGCATT TATTAACATA GGAATAGCAT AAATCCATA 278520
TCTTCCCCTT TGATCAGGAG ATATGTCAAG ATCTGACTTA ACTAGAACAT AATGATTCAT 278580
TCCAATTAAA TTGTTTGATT CGTCGCAAAG CACAACAGCA ACACAAGAAC CAAGAATTGT 278640
AGAAATCACT CTTTGTGTTG AAACAAAAGC TTCACCAGGA ACTATTATTG TAACATCGCG 278700
TTTTAATTTA AAATTAAAAT GATTTAACAT AAAATTAATA CTCTCTTGAA AAAAGATTTA 278760
TAAACTCTT ATAAAGACCT TGCCAAAACC CTAATCTTTT TACCTTGCCA CTAAACAAAG 278820

CAACATCCCC TATTTTTTCA TTTTCTAAAA AAATCATAGC CCTCCCAACA GGCATATCCC	278880
CACTAAGTGG AGCAACCAAT TTATCAACAG TATAACTTAT ATTAATTTTA TCAAATTCAT	278940
CTTTAGTTAA AATATAATAA AAAGGCTCTT TAGAAAAAAG AGCAACTGTA TCCACTGTAC	279000
CATTATAGAC TTTTCTTTT AATTTTACTA TTAAAGGAAA TTTAGAATAT TTATTAAATC	279060
CATATTCAAA TAAATTTTTT GCAATCGAAG ATCTCATTTT CTCTCCAAAT CCATTAATTC	279120
CTTTTTCAAC CCCCAATACA ACTGCTATTA ATCTTCTCTC ACCCTTTTTTA GCAGTAGCAA	279180
CAAGATTTAA GCCTGATTCC TTAATATATC CCGTTTTAAT GCCATCTGAA TAAGGGTAAT	279240
CATATATTAA TAAATTAGCA TTTCTTTGTT TTAAGTTTAA AAATTTTGAT GACAAAGCAG	279300
TTCTTAAATT TCTACTCTTT GGATAAATAA AATACTTTAA AGAATGAATA TTAAGCATAA	279360
ATTTAAACTT TTCTATATAA GATTTACAA AAAAAGCCAT ATCTAGTGCT GTAATCTTAT	279420
TCTCGCTGCT ATATCCAGAA GGTTCACAA AATGCATATT AAAAAGCCCT AAATTTAAAA	279480
CATTAATATT CATTAAATTA ACAAAGCTAT TtAAATTGCC TACTACAAAC TCAGCAATTG	279540
CAATAGAAGA ATCATTACCC GAAGAACTG AAAGTCCTTT TAAAATCTCT TCAAAATTAA	279600
CAATTTGACC TTTTCTAAA AACATCAAAG AAGAATTGGG GGGTGCATTA TAATATGAAG	279660
CAGAATCGCT AATAGGAAGT ATGCTTTTTA ATTTTATATT TCGCTTTTCA GCTTCAATTA	279720
AAGCTGTATA AATTGTAACA ATCTTTGTAA GAGATGCTGG AGGAAAAACC AAATTGGGCT	279780
TCTTAGAATA AAGTATTCGC TTAGTATCAA AATCTATTAA AACTATTGAC TTTGCATACT	279840
CTGATAATTT ATTAATCTCA GCTAAATTAA CTGCAAAAAG ATTATAACAA AACGGGAAAA	279900
AAATTAAGAAA TAAAGTTAAT AACAATTTCC CAATAACATA GATACTATTC ATGTTGTAAT	279960
ATTAAATTA TATATTATTT ATTGATTGTT AATTACAATA CAATTAAAAA GGAGCCATTT	280020
TTATGAATTC TTATGATTTT ATAACAGCTT TGGTACCAAT AATCCTAATA ATTATTGGAC	280080
TTGGCATAAT AAAAAAGCCA GCTTACTATG TAATACCCAT ATCATTAATA GCCACCGTTG	280140
CTATAGTTAT ATTTTATAAA AACTTGGGAA TAGTAAACAC AAGTCTTGCA ATGCTTGAGG	280200
GCGCCTTAAT GGGGATATGG CCAATAGCAA CTGTAATTAT TGCTGCCATA TTTACATACA	280260
AAATGTCAGA AGATCAAAAA GATATAGAAA CTATTAAAAA TATTTTATCA AACGTATCTT	280320
CTGATAGAAG AATTATAGTA TTACTAGTTG CATGGGGATT TGGAAATTTT TTAGAAGGAG	280380
TTGCTGGATA TGGAACTGCT GTTGCAATTC CTGTATCAAT ATTAATAGCA ATGGGATTTG	280440
AACCATTTTT TGCCTGCTTA ATCTGTTTAA TAATGAACAC CTCATCAACC GCCTACGGAT	280500
CTGTGGGAAT CCCTATAACA TCTTTAGCTC AAGCAACTAA CTTGGATGTT AACATTGTTT	280560
CATCTGAGAT TGCATTCCAA CTAATACTTC CAACCTTAAC AATACCTTTT GTACTGGTAA	280620

TTCTTACAGG	AGGGGGCATT	AAAGGATTAA	AAGGAGTATT	CCTTCTTACC	TTACTCTCAG	280680
GAATGTCAAT	GGCAATATCT	CAAGTATTTA	TATCAAAAAC	TTTGGGTCCA	GAAC TTCCTG	280740
CAATCCTTGG	AAGCAT TCTT	TCTATGACAA	TAACAATAGT	TTATGCAAGG	TTTTTTGGAA	280800
ATAAAGAAAC	TACTGAGCGC	CAAAGCAAAA	ACACAATATC	CTTATCAAAA	GGAATTATTG	280860
CCTGCTCACC	CTACATTTTA	ATAGTAACTT	TTATAGTGCT	TGTATCTCCT	CTTTTAAACA	280920
AAATTCATGA	ATACCTAAAA	ACTTTTCAAA	GCACTATTAG	CATTTATCCA	GAAGCAAATC	280980
CCTTACACTT	TAAATGGATT	ATCTCTCCGG	GCTTCTTGAT	TATACTTGCA	ACAACAATAT	281040
CCTATTCAAT	ACGGGGAGTT	CCAATGT TAA	AACAGCTAAA	AATATTTACA	TTAACCTTGA	281100
AAAAAATGGC	ATTATCTTCC	TTTATAATCA	TATGCATTGT	TGCAATATCA	AGATTAATGA	281160
CACATAGTGG	AATGATAAGA	GATCTTGCTA	ATGGAATCTC	AATAATAACA	GGTAAATTTG	281220
GACCATTATT	TAGCCCACTA	ATTGGAGCTA	TTGGGACATT	TTTAACAGGA	AGTGATACGG	281280
TTTCAAATGT	TCTTTTTTGA	CCTTTACAAA	CACAAATGGC	AGAAAATATT	GGAGCAAATC	281340
CTTA CTGGCT	TGCAGCAGCA	AATACAACAG	GAGCAACTGG	AGGGAAAATG	ATTTCTCCCC	281400
AAAACATCAC	AATAGCAACA	ACA ACTGCTG	GATTAATTGG	ACAAGAAGGC	AAGCTTTTAT	281460
CAAAAACAAT	AATTTATGCT	TTATACTACA	TTTTAGCAAC	AGGATTGCTA	GTTTATTTAG	281520
TATAAATTAA	TCATTTAAAA	TAAATAAGAT	TAATTTATAC	TAAAATTAAT	CTTATTTATA	281580
GATTTGAATA	ATACAAAAAT	CACAAAAATA	TAATATGGCC	TTGAATTTTT	ACCTAATATT	281640
TTAATATTAT	ATACATGTTA	TATATATGTT	AATATATTAT	ACATAATAAC	ATATCTATAA	281700
TATATTTATT	AATACGTTTA	ATTAAAAACT	AAA ACTAATA	AAAGTTTATA	ATTACAACAG	281760
GAAGGTATAA	TTATGAAAAG	CCATATTTTA	TATAAATTAA	TCATATTTTT	AACCACATCT	281820
GCAGCAATAT	TTGCAGCAGA	CGCATTAAG	GAAAAAGATA	TATTTAAAAT	AAACCCATGG	281880
ATGCCAACAT	TTGGATTTGA	AAACACAAGT	GAATTCAGAT	TAGATATGGA	CGAGCTTGTT	281940
CCTGGGTTTG	AAAACAAAAG	CAAAATTACC	ATTAAGCTTA	AACCATTTGA	AGCTAATCCC	282000
GAATTAGGCA	AAGACGATCC	ATTCTCAGCT	TACATTAAGG	TAGAAGATCT	TGCACTAAAA	282060
GCGGAAGGCA	AAAAAGGCGA	TCAATTTAAA	ATTGACGTGG	GAGATATTAC	AGCCCAAATC	282120
AATATGTACG	ATTTTTTTAT	TAAAATAAGT	ACTATGACAG	ATTTTGACTT	TAATAAAGAG	282180
TCTTTATTTA	GTTTTGCACC	TATGACTGGA	TTTAAAAGCA	CTTACTATGG	ATTCCCAAGC	282240
AATGATAGGG	CAGTAAGAGG	GACAATTCTT	GCAAGAGGTA	CTTCTAAAAA	CATAGGAACA	282300
ATTCAGCTGG	GATACAAACT	CCCAAACTC	GACCTTACAT	TTGCAATAGG	GGGAACAGGC	282360

ACGGGTAACA	GAAATCAAGA	GAATGACAAA	GACACTCCAT	ACAATAAAAC	ATATCAAGGA	282420
ATCCTTTATG	GAATTCAAGC	AACATGGAAA	CCAATAAAAA	ATCTACTTGA	TCAAAACGAA	282480
GATACTAAAT	CTGTAATTGC	AGAAACACCT	TTTGAATTAA	ATTTTGGCTT	GTCAGGAGCC	282540
TATGGAAACG	AGACATTCAA	TAATTCATCA	ATAACATACT	CTTTAAAAGA	TAAATCCGTA	282600
GTTGGCAACG	ATTTATTGAG	CCCAACTTTA	TCAAATTCTG	CAATTTTAGC	ATCTTTTGGA	282660
GCTAAATATA	AGCTTGGATT	AACAAAAATA	AACGATAAAA	ATACCTATCT	TATTTTGCAA	282720
ATGGGAACTG	ATTTTGGAAT	AGATCCTTTT	GCAAGCGATT	TTTCTATATT	TGGACACATC	282780
TCAAAAGCAG	CGAATTTCAA	AAAAGAAACA	CCCTCAGATC	CTAACAAAAA	AGCTGAAATA	282840
TTTGATCCAA	ATGGCAATGC	TCTTAATTTT	AGCAAAAACA	CAGAATTGGG	CATTGCATTT	282900
TCAACAGGAG	CAAGTATAGG	TTTTGCTTGG	AATAAAGATA	CCGGTGAAAA	AGAATCCTGG	282960
GCGATTAAAG	GATCTGATTC	CTACAGTACA	AGACTCTTTG	GAGAACAAGA	CAAAAAATCT	283020
GGAGTTGCAT	TGGGAATAAG	CTATGGACAA	AACCTTTACA	GATCTAAAGA	TACAGAAAAA	283080
AGATTAAAAA	CCATATCTGA	AAATGCATTT	CAAAGCTTAA	ATGTTGAAAT	TTCAAGCTAT	283140
GAAGACAACA	AAAAAGGGAT	TATAAATGGA	TTAGGATGGA	TAACATCTAT	CGGTCTTTAC	283200
GATATTTTAA	GACAAAAATC	TGTAGAAAAC	TATCCTACAA	CAATTTCAAG	CACCACTGAA	283260
AACAATCAAA	CTGAACAAAG	TTCAACAAGC	ACAAAGACCA	CAACCCCTAA	TCTGACATTT	283320
GAAGATGCAA	TGAAACTCGG	CTTGGCCTTA	TATCTTGATT	ATGCAATTCC	AATAGCATCC	283380
ATTTCAACAG	AAGCATATGT	AGTACCTTAC	ATTGGAGCAT	ACATTTTAGG	ACCTTCTAAT	283440
AAACTCTCAA	GCGATGCTAC	AAAAATTTAT	TTAAAAACAG	GACTTAGCCT	TGAAAAACTA	283500
ATAAGATTTA	CAACAATTTT	TCTTGGATGG	GATTCAAATA	ACATTATAGA	ACTTGCTAAT	283560
AAAAACACAA	ATAATGCTGC	TATTGGAAGT	GCTTTCTTGC	AATTCAAAAT	AGCCTACAGC	283620
GGAAGCTAAC	AGCAAAAGAA	GGGCTTTGGC	CCTTCTTTTT	TATCTTTAAA	AACAATTGAG	283680
GATTACCTTA	TATTTCTTTC	CTTGCAAATT	TTTTCATAAG	CATCTTGAAT	TTTTATAAAT	283740
TTATCATTTG	CATCTTTTTG	TCTTACAGGA	TCATTTGCAA	ACTTATCAGG	ATGATATTTT	283800
ATAACAAGGC	TTTTATACGC	CTTTTTAACC	TCATCATCGC	TAGCACTATA	TGTTAACCCC	283860
AAAACACTAT	AAGGATTTAC	AATTTTAATA	TTAATATCTT	TATAAGCTTC	ATAACCATCA	283920
GATTCAAGTT	CTAAAAAAC	ACCAACATAA	GAAATAAATT	TTTCAGCTTC	TAAATTTTTA	283980
TACCTAGAAA	GCCTGTTAAT	TTCTTTAAGA	GTGGCAAAAA	GCCATATAAA	AAGATCTTTG	284040
TGCTGAAAAT	AACCAAGCTT	AAGGGTATAT	AAAATTTTAT	CAGCATTATT	ATTTTTAGTA	284100
ATAGCAGAAT	GAAAAATGGT	ATACAATTCT	GATTTACCAC	G TTCAGACAA	ATTCAAAGAA	284160

TTGATAATAA	AATTGACATA	ATTTAGCTGC	TCCCCAGTTA	CAGTTCCTAA	AATAGATAGC	284220
AATTTAGCCA	TTAATAAAAA	AGAAAGTTTA	TAAAATTCAA	ACTCTCTAGA	TCTAGAATAT	284280
GAGTAATCCC	TTGTAAAGTA	TATTCTAAAA	ACACCTAAAA	AACTAAATAA	TATCAAAATA	284340
AAAGGAAATA	AAATAAAAAAG	CATTGCTATT	AAAACGGGAT	TAAAAATAAA	AATAAACAAAC	284400
AACACTAAAA	AAAACACTCT	AATTGGGCTT	GGCATTATT	GATCATAACC	TCCAGCGTAA	284460
TCAAGGCATG	TCAAAATCTC	TAATAAATCT	TACAACTTCC	TTTTTTTATTT	GTTTTAATTC	284520
AATATCAGAC	TTTGCCTTTA	AAGCTCTAAC	AATAAATTTA	GCAACATTTA	AAGAATCGCT	284580
TTCATTTAGG	CCTCTAGAAG	TAATAGCAGC	GCCCCCAATT	CTAATACCAG	AAGCCAAAGA	284640
AGGGCTTTTT	TTATCAAAAG	GAATAGCATT	TTTATTTAAA	GTAATATTTA	CGCTCTCAAG	284700
TAATTTCTCA	GCATCAGCAC	CGGTGAGATC	CGAACTACTA	AGATCAACCA	AAAACAAATG	284760
ATTGTCTGTG	CCCCCACTAA	CAATACGAAA	TCCTTCCGAT	TTGAAATATT	CAGCCATAAC	284820
TTTAGTATTT	TTTATTACGT	TAGCAATGTA	TTCTTTAAAA	CTTTCTTGAA	GAGCTTCTTT	284880
GAATGCAATA	GCCTTACCCG	CAATAACATG	AACTAAAGGA	CCCCCTTGAG	TTCCAGGAAA	284940
AACTGTAGAA	TTTACAGCAT	TAAACAAAGG	CTTCTCTTTT	CCATTAAAGT	TTACTAATTT	285000
GTCAAAATCC	TTTCCAGAAA	GTATTATTCC	ACCTCTTGGC	CCTCTTAAAG	TTTTATGCGT	285060
AGTACTTGTA	GTAAGATGCG	CCACATCAAT	TGAGGAATTA	TGAAAACCGG	CAACAATAAG	285120
GCCTGCAATA	TGAGCAATAT	CACACAAAAG	ATAAGCAGAA	ACATCATCTG	CTATTTCTCT	285180
AAATTTTTTA	AAATCAATTT	CTCTTGAATA	AGAAGAAGCT	CCAGCTATTA	TTAAATTTGG	285240
CCTGCAATCT	TTAGCTATTT	TAAGAACTTC	ATCATAATCA	ATTAGCTCAG	AATCTCTAGA	285300
AACACCATAA	AAATAAGTGT	TAAAAAATAT	ACCAGAAAAA	TTTACCCTGC	TGCCGTGAGT	285360
TAAATGCCCT	CCATGAGATA	ATTGCATACC	AAGAATCCTG	TCACCCGGGC	TAATAAGAGC	285420
CATTATGGCA	GCCATATTGG	CCTGAGATCC	GCTATGAGGT	TGAACATTGG	CATACTTTGC	285480
GCCAAAAAGC	TCTTTTGCTC	TCGAAATTGC	CAGAGTTTCA	ATCTCATCAA	TAAAAGAACA	285540
ACCACCGTAG	TATCGATTCA	AAGGATATCC	TTCGGCATAAC	TTATTAGTTA	AAATACTACC	285600
AACAGCCTGC	CTTATCTCTA	AAGATGTAAA	ATTTTCAGAA	GCAATAAGTT	CAATATGCTC	285660
TCTTTCTCTT	AATTTTTCCT	TTTCAATTAA	ATTAAATATT	TGATCATCTC	TCATTAAAAA	285720
TTATCCTCCA	AAACAAACCT	ATGCATTAAA	GAATACGATC	CGTTTGTCAA	GCTTTTATAC	285780
TTTAAAAACC	CAGAATCTAA	ATATCCATCA	AAAAATTTCAT	TTTTATCATA	GTCCTCTTTG	285840
CATCCATATT	GAATATAGTT	ATCAGATATA	TTCAAAAAAT	ACTTAGAGCT	ATCCTTAAAT	285900

AATACTGCAT	TTATTATATC	AAAATATACA	AAACCAACCC	CAGCTAAAAA	AAACTCAAAC	285960
CAAAAATGCT	CTTTTAATTT	AAGAGAATTA	GAATCATAGT	AAAGCCCAAC	TATATTTCTC	286020
AGCGGAATAT	CATACTTTAA	AAATAATAAA	TTAGTAAGAA	CTATTAAATT	GCCAGATGAA	286080
ATTTTTTTTT	CTTCAATAGA	ATCCTTTAAA	CTTAAATTAT	TCTCAACAAT	TTTAAATTTT	286140
GAAGTCAAAA	CATCAATAAT	TGCTTTAGCT	AACTTATAAA	CTGAATTACT	GCCAGAGGTT	286200
TTAGATAAAA	TTAAAGAATC	TAAAGACATT	AAATCAACAT	AGCTGTAAGA	TAAATAATCT	286260
TTTTTTTTGT	CTTGAACATA	CTTTTTGTAC	TCTTGATTGT	TAATATCTCT	ATTAACTTCA	286320
ATACTTTCTA	AATATTTTCG	ATCTAAAAAT	TCCAAATTAA	GTTTATAAGT	TTTTACCCTA	286380
GTCTTAAAAA	TAAATTTATT	TGTCTTCAGG	TTTTCAAAAA	ATAAATTATC	AATATTAAAA	286440
TCAAGATGCT	CACTATTGCG	CTCTGTAATT	TTTTGACGCT	CATTCTCAAT	TGGTCTTAAA	286500
TAGAAGATAT	TAAAATTAAT	ATCTTGGGGG	TTTGAATCAA	AATTACTACT	AACATCTTGA	286560
CTAAAATAAA	TCTCTTCAAT	TATTACAAAC	TCTTTAAAAT	CGCTCAAAGT	CCACTTAAAA	286620
AAATCATTTT	TAACAGAAAA	CGGAACTTTA	TTGCTTTGAA	TATTGTCCAA	TAAAACATAA	286680
AGCTTCCCAC	TAGAATTTAA	AGTTTTAGGA	GAAACAAATT	CCACTCTATT	CTCAGAAACA	286740
TTTAAAATAT	TTTGAGGTAA	AATTGTATAA	AGCTTATCCT	TAGTTTCAAG	AAAAATTGTA	286800
ATAGTACTAA	AAGGTGAAAA	CAAATTCATA	CCCTGCAATA	AAGTTGAAGA	ATTTGCATTT	286860
AAAATTATTT	TATCCTCTGA	AAAAATAAAA	GGTATATTTT	TCCTATTAAG	CTTAACAGGA	286920
ACTTGCCTAC	TAATAACAAG	AAAAAGTTTC	TTGCTAGTGC	CCCTTTCGCC	TTTTACAAAA	286980
ATAAGTCCAG	AATTCACCTC	ATCTGTAATT	TTAAAACTA	TTCCCGTGTT	ATTCCAGCTA	287040
ATAATGCTAC	TTTTAACCAA	ATAATTATTG	TTGATATTAA	TCTCCCCTGT	ACTGTACCCC	287100
AAATTATTTT	CTTTAATAAC	AATAATATCC	TTGTGCGAAG	TGGGAATTGG	AGATATATCA	287160
TAAATAATTG	GCTTTGAATA	AAATAAAAAAT	CCAGAAAAAA	CAAATAAAAA	TAAAAAATAA	287220
ATAAAAATCA	GGCTTAAATA	AAAATATTTG	TTTTTTAAAA	AAATAGCCAA	ATGTTAGCCT	287280
CTTTTAACCT	TAGTTCCTTC	CTTAGTATCA	ACCAAAACAA	AACCTTTTTT	GGCAAAAAAA	287340
TCTCTGATTT	CATCAGCACG	CTTAAAAATTT	TTTTCACATT	TAGCTATTCT	TCTCTCTTCA	287400
ATCAAAGCTT	TCATATTCTC	ATCAATAACT	ACGTCATGGT	TTTGTAATTT	TTTTAAATTT	287460
TCTTCTCTCA	GATTAAGTGA	CATAATCTCA	TCAAAAATAA	AAGCTAATCT	AAGCTTTGAA	287520
ACAAAGCTTA	GATTGTCAGA	TTTAATTATC	TCCCAAAGCA	AAGCCAATCC	TTGAGCAACA	287580
TTTAAATCAA	AAGAAATTTT	TTCTACAAAA	GAGTCATAAT	ATCTTTTTTC	TACACTAAAA	287640
CCAAAATTTT	TTAAATCCTT	ATTAAGTGTA	TTTAAATCAA	CTGGATCTAA	AGATTCATAA	287700

AAATAACTTA GCTTGTTTAT CAAATTTTCT CTAGCAATCT TGCTTGCTTG AAGATTATCT 287760
AATGAAAATT TTAATTGGTT CCTGTAGTGC GATGTCAAAC ATAAATATCT AAAATCAAGA 287820
GGGGAAAAAT TTTGATCTTC TAAATCTTTA ACTGTAATAA AATTTCCACG TGACTTTGAC 287880
ATCTTATTAT AATCCATAAT CAAAAATTCT CCATGAACAA AGACATCACA CCATTTTTTA 287940
TTCAAAAAAC ACTCTGCTAT TGCTATTTCA TTTATGTGGT GAACTCCAAT ATGATCAACT 288000
CCTCCCAAAT GAATATCAAG AGCATCTTTG AAATACTCCA AATTCATCGC AGCGCACTCC 288060
AAATGCCAAC TTGGATAACC AAATCCCCAA GGAGAATCCC ATTTTCATCTC CTGATCTTTA 288120
AACTTAGAAT TAGTAAACCA CAAAACAAAA TCGGTTTTAT TCCTTTTAAA TTTATCAACA 288180
TCAACTCTGG GTAAAGTCAT ATCTTTATCA ATAAGATCAA TGCCGGCCAT CTCACCATAG 288240
CTTTTAAAAC AAGAAGTATC AAAATACACA TTACCATTAG AAAAATAAGT AATTTTTTTTT 288300
TCTTCAAGAA TTTTAACAAC CTCTATCATT ATGGGAATAT GTTTACTTGC AACAAGAACT 288360
TTGTCGGGAT ATACAATGTT TAATTTTCTA CAATCGTTAA AAAAAGCCTC TGTGAAAAAT 288420
TCACTAATCT CATAAACTGT AAGGCCCTTC TCTCTGCGG TCTTAGCAAC CTTATCTTCT 288480
CCATCATCAA GATCACCTGT TAAATGTCCA ATATCTGTAA TATTCATCGC ATAATTAACT 288540
TTATACCCCA AAAACCTTAA AGTTTTAATT AACAAATCTC CAAAATATA AGTTCTAAAA 288600
TTCCCGATGT GAGCATAATT ATAAACAGTA GGCCCGCAAG CATACACTTT AACATTTTCA 288660
AAATTTGTTA ATTCTGAAAA ATCCTTTGTT CTAGTATTAT ATAACTTTAA AATCATACAT 288720
TTCTCAAAAT TGAAAAAATA AAAAATCTAA TTTATTATTA AGTACGTATG CCTAAAAGCC 288780
TAAATAATTT TCTTAAAAAA ATCAATATTA AGCCTCAAAC AAAAATCTA GCTAACTATA 288840
CAACATATAA AATTGGAAAC ATTTGAAAT TATTTCTCAC CCCTAAAAAT ATTAAAGAGG 288900
CTGAAAATAT TTTTAAAGCA GCAATAGAAG AAAAAATTAA ACTATTTATT CTGGGGGAG 288960
GATCAAATAT TTTAGTCAAT GACGAGAGAG AGATTGATTT TCCAATAATA TACACCGGAT 289020
ATCTAAACAA AATAGAAATT CACGAAAATA AAATTGTCGG CGAATGTGGT GCAGATTTTG 289080
AAAGTTTATG TAAAATTGCA CTTGATAACA GCTTAAGTGG CCTAGAATTT ATCTATGGAC 289140
TACCCGGAAC ACTAGGGGGC GCTGTGTGGA TGAATGCTAG ATGTTTCGGG AATGAAATCT 289200
CTGAGATACT AAAAAAATT ACATTTATAG ATGATAAAGG AAAAATATT TGCAAAGAAT 289260
TTAAAAAGA AGACTTTAAG TATAAATAT CGCCTTTTCA AAATAAAAAAC TTTTTCATAT 289320
TAAAAATTGA ATTAAATTTA AAAAAGACA ATAAGAAAT TATTGAAGAA AAAATGAATA 289380
AAAATAACA AGCAAGAATA AATAGAGGTC ATTATTTATT TCCAAGTGGT GGAAGCACTT 289440

TTAAAAACAA	TAAAGCATTT	CTCAAGCCTA	GTGGACAAAT	AATTGAAGAG	TGCAAGCTCA	289500
AAGGATTAAG	CATTGGAGGC	GCCACAGTAT	CTAAATATCA	TGGAAACTTT	ATTATCAATA	289560
TTAACAATGC	CACTTCTAAA	GACATAAAAA	GCTTAATTGA	AAAAGTAAAA	GCTGAGGTCT	289620
ACTTGAAAAC	TGGACTTTTA	CTAGAAGAAG	AAGTTCTTTA	CATAGGATTC	AAATAATCAA	289680
AAAAACTAAA	AAAGAATATC	TTTAATCTCA	TCATTAATCT	TTTGAATCAA	TTCTTTTGTC	289740
TTTAATATCT	TATCCTTAGA	AGACTTTACT	AAAGATGAAT	ATTCTTGAAG	AGAACTTACC	289800
GCATCTAAAT	TCATCTTAGA	AACTTTAAAC	TCTTTTAAAT	CTTGACTAAA	GTTGTAAAC	289860
TTGCCACTAA	TAAAATAATG	ATTATTAAAT	ATTTCTTTAT	ACATATTCTT	AGCATCTCTG	289920
ATCTTAGTAT	CGTGAGACAA	ATACCTTTCT	TTAAACTCGC	CAATTTCTTT	AAAATGCTTA	289980
GCAAGAGTAA	GATCTACTTT	CTCGTGTCTT	GAAAAATTGT	TGTCCACATT	ATCTTGAATG	290040
TCTATGAAAT	TTTTATAAAT	TGTATCAATC	TCTGAATTAA	TTACTGCAAT	AATGCTGTCTG	290100
ACCGTTTTAA	GTTCATCTTT	AATGGTTTTA	GAATATTTTC	CAGAATTAAT	AGCAAGCTTT	290160
CTAATCTCCT	CAGCAACAAC	TGCAAAACTT	TTACCTGCAT	CACCTGCTTT	TGCTGCTTCA	290220
ATTGCTGCAT	TCATAGCAAG	CATATTGGTC	TGAGCTGAAA	TTGAAACTAA	AAGTTATTTT	290280
ACACTTTGCA	AACTATTTGT	TTGAGACAAA	AGATCTGCAA	AATTTTTATT	CACATTTTCA	290340
AAAACAATAT	TTAAATCAAA	AACCTTACTT	TTAATATTTT	CAATATCAGT	AGAATTTATA	290400
GTAGCAACCT	TATTAAAAAT	TTCTAAATTT	TTATCTATAC	TATAGAAAAA	ACTAACACTC	290460
TCTTCAAAAT	TTGAAGAGAT	TTCTGATATA	TATTTATTGT	GATCATTAAT	CGGATCAGCA	290520
ATAGATTCAA	AGCCTTTTAA	AATATCAACA	ATTGATTTTT	CAAATCTAGA	AAAAGTATCT	290580
CTTAGTTGTT	CGTAAACTAA	AATGCTAGAA	TCTATACTCT	CAGTATTTGA	TATAGCAGTT	290640
TCTATTTGTT	CCAAATATTC	ATTCAAATCT	TCAGAATAAA	ATTTTATCTT	CTCAAAAGAT	290700
TCATTACTCT	TAGAAGACAG	ATTATCTAGC	TTTGAACTAA	TATAAGAAAT	AATAGATGAA	290760
GAATACTTAA	CCTCTAAGGG	AGATTCAAGA	CTAAAAGGAT	CGCTTTTTGA	TTTTTGATAG	290820
TCAACAATTC	TGTTAAAATC	ATTAATTAAT	GAAAAAACAA	AAGTATTGCA	TAAATAAAAA	290880
ATAATTGCAA	AAGACAATAA	TAAAAATGCA	ACAAATATAA	CCCAATTTGA	TTTAAACATA	290940
ATAGGAATGG	AATTGACATT	TAAAAAAGC	CCCTGAGTCA	AAAAATCATC	GGTTTTTACA	291000
AAGTTTAAAG	AATAAAAAATC	TCTTTCATAA	TTAAAAGTGT	ACTGAGAGCT	AGAAGAATCT	291060
TTTTTAGCAT	AAGCTATAAC	TTTACTCAAA	AAATTCTCAC	TATAAGCTGT	AGAAAAAGAT	291120
TTGGCCTGAA	GATTATTAAG	GTTTGAAAAA	ATGGGCATGT	AATTTCTGTC	AAGCATAAAA	291180
AAATTATAAT	TTTTACTACC	AAATTTAAGA	GAAGAATACA	ACTGATTTTC	AATAATATCT	291240

AACGACTCAT	CAAAGCATAT	TAAAATCCCT	ATCACACCCA	ATGTTGAAAC	AGAATCTCTA	291300
ACTGGAAAAC	TTATTATAGA	ATAAATTTTC	CCATCTATTT	GCATATATCT	TGAATAATAC	291360
TTAGAATTTT	TTTCTACAGG	AACAGAATAA	ATTGGATCCA	ATCTAACATC	TTTTAAGCCT	291420
AAAGATGAAA	AATTTGAATT	TGATATTAAA	ACATTTTTC	CTATAGGAAT	ATAAAATATA	291480
CCTTCAAGTG	AATCTTCTGC	TAAAGGAATA	GTTTTAAAA	TTTTATCTAT	AGAGTTAAAT	291540
TCCCTTGACC	TTAAAAACAA	ATCACTATTT	TCATCCAAAC	TATCACCTAA	TTTTAAACTT	291600
GAAGACAAA	GAAAGCTTTT	TGAAGAATTC	ACCAATATCC	CAAACCTATA	GCTATCTCTT	291660
ATAAGCTCCT	CAAGAAACCT	AGAGGATTCC	GAATATTTGG	CTTTAATAAC	AGCAGACACA	291720
CTGTTTAAAA	ACAACTTAGA	ATCAAATTTA	AAGCGATCCA	AATATTCATT	TTTATGATTC	291780
ATATAAGCAT	AGCCTATGAA	TAAAAAATTT	AAAAAAAGGA	ATCCAAATAA	AACTAGATAA	291840
AGAAATCGTT	TAGTATTTTT	CAGATTAACA	TCAATTAAAT	TCTCATCTGT	CATAAAAGCT	291900
CTCCAAACAT	AAATATTAGT	ATGATTAAAA	TCTTAAACA	AACTTTCAC	CTTCATAAAT	291960
CATATATAAA	TAATTACTAA	TAACAATTGG	CAAATTAGAC	TTTTCTTTCT	AAATCTTAAA	292020
GATTAAATCC	TTCAAATATT	TGCAAATAAT	TATTTTATTA	TTTAGCTACA	TGCATATATA	292080
ATTATATAAT	AAAACATGTA	GAATACTAAA	AATTTAATGT	TTTAAAAATT	TTATGAAAAA	292140
ACAAAATTTT	GAGGAGACTT	AGTGAAAAGA	AAGAACTTA	ACTCCAACCT	TTTTTATAAA	292200
TTCAATTTTA	TAATTCTGGC	ATATACAATA	ATAATTATTG	CAACAACCTT	TTTGCTACTA	292260
GATCAAGGCT	ATAAAAAAAT	CATAACAAAA	GAACCTCAAG	ACTTTACAAA	ATTCATTAAC	292320
CAGGCAATGA	TTAAAAGCTT	TTCTGATGAA	TCTAAAGAAA	TAATAAAAGC	TTTAAGCATA	292380
TTAACGACTA	GGTACGACTA	TCGGTCTGCA	ATCCTAAATA	ATAAAAATGA	AGAACACTTA	292440
GTATCTGATA	AGATTTTAAT	TACACTCCCC	TCCTTTATTA	AAATAATAGA	GTATACAAAC	292500
AAAGATGGAT	ACATAATCGC	ATCAAGCGAA	AAAAAAAGAA	CCAGTCAGTA	CATAAGTTTA	292560
AAAGAATTGC	TATTGGGCAA	AGCTTTAACT	GCATTTCAAA	TTTCAATTCT	TCACAACAGT	292620
CTAGCAAAGA	TAAATAACAA	TTTTTACATT	CCAATAGCAT	ATAAAATAAC	AGATTCAAAA	292680
AAATCTAATG	TTGGATATAT	TATTTTATAT	GCTGACATTT	CAGAAAAAAT	CGCTGAGCTA	292740
AAAGAATATC	TTTTACTACT	TTTGAAAAAC	TCATTGCTAG	AACAAAATGC	AAGCACCGAA	292800
AACTCATCAA	AATACTTTAA	TGTATACATA	ATAAACAGTA	GTGGTGATGC	ATTTGGAGGA	292860
AAAGATGAAA	TTTTAAAGAA	CATAAAGCAT	ATATTTGGAT	TTAACCCAAA	AACATTAACT	292920
GAAATACTAA	ATACATTATC	TCAAGGAAAA	GCAAATTACA	ATACAAGCAA	TTCAAATGAA	292980

ATAATCTCCT	TAGCAAGGAT	CACAACATCC	AATTGGTACT	TAGGAATAAA	AATAGATTAT	293040
AACAACATAT	TTTCAAAAGA	ATTTAAAAAT	ATGAGATTGG	TTTCGCTTTC	CATTATATTT	293100
ATCTTAGTAA	TAATTTTTAT	ATTAATAATG	ATATCAACCA	TAAAACTTT	AATAATATCA	293160
AAAATAGATA	AACTCAATGT	TGTCATTCCA	AAAGTTAAAA	ACGGTGACTT	AACATTTAAA	293220
ATCGAATCAA	AAGGCAAAGA	TTCAATAAGC	TCAACAATAA	ATCTTTTTGG	TCATTTTATT	293280
GAAAATCTAA	AAAATGTAAT	TAATTCACTG	CAAGAACGAG	TAAAGCTGCT	TAAAGAAAAT	293340
GGAGACCATT	TATTCAGCGA	GATAAATAAA	ACACATAATA	CAATAAAAAA	TTCAAATCAA	293400
TACATAGAAA	AAACACAAGA	AGAAGTAGAA	AAGCAGGTAG	AATTCATCTC	TAATACAACA	293460
AATATAATTG	AAAGCCTATC	AAAAAATATT	TCATCTCTTG	ACAATTCAAT	TGAAACTCAA	293520
GCCGCAAGCG	TTGAACAGTC	CTCATCGGCT	ATAGAAGAAA	TGATAGGAGG	AATACAATCA	293580
ATAACAGAAA	TAACTCAAAA	AGCTGCAAAA	AGCACAGAAG	AACTAAAAAG	GTTCTCTGAT	293640
GATGGGCGAA	AAAAACAAGA	AGAAGTTATT	ACTCAAATTA	AAGAGATTTT	TAAAACTCA	293700
ACAAGATTAC	AAGAAGCAAA	CTCTTTAATT	TCATCTATAG	CAAGTCAAAC	CAACCTACTC	293760
TCAATGAACG	CTGCAATTGA	AGCATCTCAT	GCTGGTGAAG	CCGAAAAGG	ATTTGCAATT	293820
GTTGCAGAAG	AAATAAAAGA	CCTAGCAGAA	CAAGTAACAT	CACAATCAGA	ATCTGTTGCT	293880
TCATCAATTA	ACGAAATAAT	GGATTCAATA	ACCAAACCG	TAAACACCTC	TGAATTAACA	293940
AATAAAGCTT	TCAATCAAAT	ATTCGATTCA	ATCAATTTAG	TTGTTCAAGT	AATAGAAGAA	294000
ATAAATCATA	CAATGCAAGA	GCAATCAATA	GGTAGCCAAG	AAATTTTAAA	GGCTTTAAAT	294060
ACAATGCGGG	AAATAACATA	TGAAGTAAAA	ATTGGTTCAA	ATGATATGTT	TAGAGGCAAT	294120
AAAGAAATCA	TTAGCACTAT	CAAAGTGTTA	GGAGAAATTA	ATATTACGGT	CTCAAAGTCA	294180
ATGAAAGGTT	TAAAAGAAGA	GATTAATACG	CTAGTAGAAG	CAATTGAGCG	TATTAAAGTT	294240
TTAGGAACTA	CAAAGTCAAG	CCATATTTCT	GGGATTAGCG	AAAGTATAAA	TCAATTTAAA	294300
ACCAAATAAA	CTAGATTAAA	AGGAAATAAT	ATGCAAAAAA	AGACATTTTA	TAATACTGAA	294360
AAATATCTTA	AAAGCCATTT	AATGTTATTT	CCTATTTTTG	CTTATACAAA	AACTTTTTTA	294420
GATGCTAGTA	TCGCATCTGT	TTGGATTTC	ATATGCATTA	TACTTCCTGC	CCTAATAATC	294480
AATCAAATAG	AATTGAAAAA	GCAAAAAAGC	CATATATTAG	GGATATATCT	ATTAATAATA	294540
GGAATTTTTA	CCAGCCTAAC	TTACTTAGTT	ATGCTCTACT	TAACACCAAC	TTTATATAAA	294600
GAATTTAAAT	TTTCAATACC	CATTTTAATA	GCCATAATAA	TATCATTTCA	TAAAAACGAA	294660
CCCTTTAAAA	TTCTAAAAAA	CCCATCAATG	ATAATTAAAT	ATTCTAAAAT	TCCAATTTTA	294720
ATTTTCATTA	CCCTAAGCTC	AACAACCTCA	CTTATTAGAG	AAATATTAAA	CACGGGCAAT	294780

TTAAACTTTT	TTAACAACGA	AATACCTATA	ATAAAGGGAC	TTATAAATAT	AAAAATGTCTG	294840
GCCCATAGCT	CAAACATTTT	TATTGTAGCG	TCTTTATTTT	TACTATTAAT	CAATATGCTA	294900
ACAAAAATTA	AAGAGAAAAA	AATGAATAAA	AGTGT'TAAAG	AGGAAAAAAA	TGAATAAAAG	294960
TGTTAAAAAA	AAGATTAAAG	ACGAAATTAA	TGTTATAGTT	ACTAATCTAG	CATTATCAAA	295020
TAACATAAAG	CTAGATAATA	TCAATATAAA	TATTCAAAAA	CCTCCAAAAA	GTGATCTGGG	295080
AGATATTTCC	ATATTAATGT	TTGAAATTGG	TAAAACCTTA	AAACTCCCTA	TTGAAATCAT	295140
CTCCGAAGAA	ATAATAAAAA	ATCTTAAAC	TAAATATGAA	ATTAAAGCTG	TGGGGCCTTA	295200
CTTAAACATC	AAAATTTCTA	GAAAAGAATA	TATAAATAAT	ACAATACAAA	TGGTAAATAC	295260
TCAAAAAGAT	ACCTATGGAA	CAAGTAAATA	TCTAGACAAT	AAAAAAATAA	TATTAGAATT	295320
TTCATCACCA	AATACAAACA	AACCACTGCA	TGTAGGACAT	CTTAGAAATG	ACGTAATAGG	295380
AGAAAGTCTG	TCAAGAATAT	TAAAGGCTGT	GGGTGCAAAA	ATTACAAAAA	TAACTTAAT	295440
AAATGACCGA	GGGGTTCATA	TCTGCAAATC	AATGCTTGCA	TACAAAAAAT	TTGGAAATGG	295500
CATTACCCCT	GAAAAAGCTT	TTAAAAAAGG	AGATCATTTA	ATTGGCGATT	TTTATGTTAA	295560
ATACAACAAA	TACTCACAAAG	AAAATGAAAA	TGCTGAAAAA	GAAATTCAAG	ATCTACTTTT	295620
ACTCTGGGAG	CAAAAAGATG	TAAGCACAAAT	TGAACTTTGG	AAAAAGTTAA	ATAAATGGGC	295680
AATTGAAGGA	ATAAAAGAAA	CATACGAAAT	TACAAACACC	TCATTTGATA	AAATTTACCT	295740
TGAAAGTGAA	ATTTTTTAAAA	TTGGAAAAAA	TGTCGTATTA	GAAGGGCTTG	AAAAAGGATT	295800
TTGTTACAAA	CGAGAAGATG	GCGCAATATG	CATTGACTTA	CCTTCAGACT	CAGATGAAAA	295860
AGCAGACACC	AAGGTAAAAC	AAAAAGTACT	CATAAGATCA	AACGGAACAT	CTATCTATCT	295920
TACCCAAGAT	TTAGGAAATA	TAGCAGTTAG	AACAAAAGAA	TTTAATTTTG	AAGAAATGAT	295980
TTATGTGGTT	GGAAGCGAAC	AAATTCAGCA	CTTCAAAAGC	TTGTTTTTTG	TAGCAGAAAA	296040
ATTAGGCCTT	TCTAAAAACA	AGAAACTTAT	TCATTTGTCA	CACGGAATGG	TTAATCTTGT	296100
TGATGGAAAA	ATGAAATCAA	GAGAAGGCAA	TGTAATTGAT	GCGGATAACC	TAATCTCAAA	296160
CTTAATAGAA	TTAATAATAC	CTGAAATGAC	ACAAAAAATT	GAAAATAAAG	AGAGCGCTAA	296220
AAAAAATGCT	TTAAATATTG	CATTGGGAGC	AATTCACTAT	TATCTGCTAA	AATCAGCTAT	296280
ACATAAAGAT	ATTGTATTTA	ATAAAAAAGA	AAGCCTGTCT	TTTACGGGAA	ATTCTGGACC	296340
ATATATCCAA	TATGTTGGAG	CAAGAATTAA	TAGCATTCTT	GAAAAATATA	AAGCACTTTC	296400
TATTCCTGTA	ATGGAAAAAA	TTGACTTTGA	ACTTTTAAAA	CATGAAAAAG	AGTGGGAAAT	296460
TATTAAATTT	ATATCGGAAT	TAGAAGAAAA	TATAATCAAT	GCGGCAAAAG	ATTTAAACCC	296520

TTCAATACTT	ACCAGCTATT	CATACTCGCT	TGCAAAGCAT	TTTAGCACGT	ACTATCAAGA	296580
AGTTAAAGTA	ATAGATACAA	ACAATATCAA	TTTAACAGCC	GCAAGAATCG	AATTTTTTAAA	296640
AGCCATATTA	CAAACAATAA	AAAATTGCAT	GTACCTGCTC	AATATTCCCT	ATATGTTAAA	296700
AATGTAGGCA	AGAAAATTTT	ACAAAATTTT	CTTGCCTAAT	ATCCGTTTAA	ATCTAAGTCA	296760
CTTTTGCTAA	AAATTAATTT	TATTTTATCT	TCATACTTTT	TGGATATATA	ATATCTTTTT	296820
AACTTAAGAG	TATTGGTAAG	CTCTTCTCCA	ATTGTAAAAG	GATCCTGAAG	CAAAACAAAG	296880
CCTACTATTT	TTTCAAAATT	TTTAAAACCT	AATTTAGTAT	TAATAGTGTC	TGAAATATGC	296940
TTAGAATAAA	GTTTATTGAC	GTCTCATTTG	GCTAACAAAT	CACTTCTGGA	AGAAAAAGAA	297000
ACTCCACTAG	AATTTGCCCA	TTTTTCAAGA	TTATCAAAAT	TAGGCACAAT	AACAGCCCCC	297060
AAAAATTTTT	GATCCTGACC	AACGATCATA	ATATTTTCAA	TAAACAAAGA	TTTACCCAAA	297120
ACTCTCTCAA	GGGGCTCAGG	CTCAATATTT	TCCCCGCCCC	TCAGAACAAT	TGTATCCTTG	297180
CTTCTACCAA	CAATTGAAAT	TTCATTATTA	ATTGTTAATC	TAACCAAGTC	CCCAGTGTTA	297240
AACCAACCAT	CTTCTGTTAA	AACTTCACTT	GTCTTAGCCT	TATCCTTAAA	GTAGCCACTC	297300
ATTATTTGTG	GCGACCTGAC	CCAAAGCTCG	CCTTTTTCTC	CATAAGGCAA	AACTCTCCCA	297360
TCAATTCCAA	CTACTTTGTA	TTCAACATCT	GGCAAAATAG	GGCCGACAGT	TTTTTGCTACA	297420
GGGCCTTTAA	GACGCCTAAC	GCTCAAAATA	GGGCCCCGTTT	CAGTAAGACC	GTAACCTTCA	297480
AGCACTTTAA	TTCTTACGGC	CTTAAAAAAA	TAATCAACAT	AATCAACCAA	TGCCCCACCA	297540
CCAGAAACTC	CAAATTCAAA	ATTTTGCCCA	AGAGCATTTT	TTATTTTTTTT	AAATACTAAA	297600
ATATCGCCCA	ATAATTTAAT	AGGAAAAATT	AAAACAATCC	CAATAAATAA	AAATAATTTT	297660
GAAAAAGCG	AAATAAGAAA	ATTAGTTTTT	TTATAAATAG	GAGAAAGCCC	TAAAAATCTC	297720
TCCTTAAGCT	TTGCATAAAT	AATCCCAACT	TTTAAAAACC	CTCCAAACAC	AAACTTCTTA	297780
ATAAAAGATT	CTGATACCTT	TTTAATAATA	CCTATTCTTA	TACCTTCCCA	AATTCCTGGT	297840
ACAGAAACAA	TCATTTGAGG	ATTTAAAAGT	AAAAAGTCTT	TTAACAAAAC	AGGACCTATG	297900
GGCTTTGAAT	ATGCAATTGC	TATGCCTTTT	AAAGCAACTA	TATATTCACA	AGCCCGCTCA	297960
AAAGAATGCC	AAAGAGGAAG	AATAGAAATC	ATTATCTTGC	CGGGTTTAAG	TGTTGGAAGA	298020
TAATCATAAA	GTCTATCTAA	TTGAAAAATA	AAAGATTCAT	GCCTCAACAT	TACTCCCTTT	298080
GGCATACCTG	TTGTACCAGA	AGTATATATT	ATAGTTGCAA	TGTCTTTTGA	AGAACCTTTT	298140
TCAATCTCCA	TATCAAATGA	TTTTGGATTA	GCTCTTAAAT	ACTCAGTTCC	AAGTTCTAGT	298200
AATTTTTTAT	AAGAAAATAC	AGTAATATTT	CCTATTTTTT	CTTCATAAGA	TTTATCATCA	298260
TCAATAACAA	CAATACATCT	TACCAATCTA	AGATCATGCT	TTTTGGATAA	AACCTTGTGA	298320

AGTTGCTTAT	TGTTTTCAAC	AAAAATAAAA	GTAGATTCAG	AATGGTTAAT	AATATAAGCT	298380
AATTCATCCT	CAGAAGAATC	ATTTCCCCTG	GGAACATCAA	CGCAGCCTAA	CCCCAAAGTA	298440
GCAACGTCGA	TTATTATCCA	TTCTCTTCTA	GAATCAGAAA	TAATTACAAC	CTTTTCTCCC	298500
CTTTTAATGC	CACAATGCAA	AAGCCCAGAA	GCCACTCTTT	TTGTCTCATT	CCAAAAATCA	298560
GCGTATATTT	GCTTCTTAAA	ACTTTTTGAT	TCCCCCTCCT	TATACATAAA	AATATCAAGC	298620
TCACTATAAA	GAGCTACCAC	ATCTTTAAAA	CGCTTAGGCA	CAGTATCACT	CATAAATCCC	298680
CCTCAAAACA	ATTTAAAATT	AATTCAAAAA	AAGCAACAAG	CTGCTAACAA	TAATATTATA	298740
AAAACATATGT	ATAAAAATCA	CATAATATAC	ATTTTTATAC	CTTAAATAAG	TAAAAGCAAA	298800
AAATATCCCT	AATATAAATG	TAACCAAAAA	TCCTAAAATT	CCATAATATA	AATGCCCATA	298860
AGCAAAAAAC	ATACTACTAA	GAATGGCGGT	AGCTACAACA	GGAAATCCCA	TTTGTGTAAA	298920
CTTAGTAATA	ACAAAAGCCC	TGTAAAAAAG	TTCTTCAAAA	GCTCCTGTAA	AAAAAGAGGT	298980
AAAAGTCATT	AAAAAAAATG	CTTTTTTACT	GCTAATCTTC	CAATTAAATC	CAGCATTTGTT	299040
TTGAAAATAA	TAGACAAGTA	CCGATTCTGG	CAACAAATAT	TCAAGCAAAA	AAGCTATTAA	299100
AAAAATGACT	ATCATTGCAA	TCAATATTGT	TTTAATAAAA	ATTAAACAG	AATCCCAAAG	299160
AAAAATAAAT	TTAAATTTAG	GAATAAAAAA	CTCTACTCTA	AAATCATCAT	AAGAACTGGT	299220
AAGTTTAAAA	AAATAAATTA	TAAAAATAAT	TAAAAAAGAT	CTTGAAATCC	AAAAATAAAA	299280
ATGATTTTCA	TCAACATTCC	AAAATTCTGA	ATTAACATTT	ACAAAAGGAG	ATGCCAAATA	299340
AACAATAGCA	TAGACCAAAA	AAAGATCAAG	CAAAGCCCGC	TTGAATGGAT	ATTTATTTTT	299400
TAACAATTGC	ATAAAGTATT	GTAATTAAAT	AATTATTAAT	TGTCAACGAA	TGATTATTGA	299460
TTGATTAAATC	AAAACAAATT	AAAATTCAAA	ATATAATTAT	TTATAAATAA	AAATAAGAAT	299520
ATTATAAATG	ATTTTAATAT	TTGTCCTTAT	TTCAC'TTAAT	TTATTAATTC	AATATTATTT	299580
AAAAC'TCAAT	TTAATTTATT	TTAACACAAT	GCTAGCATTA	TTTTTTATTA	TAAAAAACAA	299640
CAAACACTTA	GCACTTAGTT	TTATTTTTTG	CACAATATTG	CTATTAAGTT	TTCAAGCGAG	299700
ATTAAATTTT	AAAACATTAA	AAAAAAATAT	TTATCAAATA	ACAAACATTA	AAAATTTTAA	299760
AAAAGATTCA	AAAACCATTG	TAGAAGTAAT	TGACAATAAA	TCAAATATGT	ACAAATATAG	299820
CTTCAAAAAT	ATTGAAAATA	TTTACAAAAT	AGGAGATATC	ATTAAAATTG	AAAATCAAAA	299880
AATAAACTT	ATTAAAAGGC	CCTTTTTTGC	CAAGCTTAGA	GAAAAATATA	CAAACGCCTT	299940
AAACAATTTT	TTCCTACAC	TAAATCCCAG	CTATTCCCAT	TTTTCAAAAG	CAATAATTTT	300000
GAATATCAAA	TCAGAAATAA	CAAAATATGA	AAAAACATTA	TTTCAAAATG	CGGGGATTGC	300060

CCACATTTTG GTAGTATCTG GACTGCATTT TTATCTAATA AGTTTAATAA GTTACTATTT	300120
CCTTTTAATA ATCACTAATG AAAAATTAAA ATACTTAATA TTAAGCATAA TTTTATTAAA	300180
TTATCTAATA TTAAGTGGAT TTGCACCTTC AACGGTAAGA GCATTCTCTAA TAACAGAATC	300240
TCTTATAATA TACAACTAA TTTACGGCAA AATTAATTTA ATAAGCTGCA CATCTATTAG	300300
TTTTATAATA AATGCTCTTG CATTCCCCGA AACGCTAAAT TCAATAGGAT TTCAGCTCTC	300360
CTATCTTGCA ACAATAGGAA TATCAGCATC GGTTCATCTA AAAAATAGAT ACGGTCTTAA	300420
CAGGCTAGAA TCATCAATGC TTACAACATT TTTTATTCAA ATATTCACCT CGCCAGTAAT	300480
TTATATCAAT AATTTTGATC TAGCACCAAT CTCAATACTG TCAAATTTAA TAGCTATTCC	300540
ATTAATATCA ATTTTCTTAG CAATAACAAT ATTAAGCTTA ATAAGTTACT TTTCAAGTTT	300600
AAATTTATTT TTTCCCCTTG ACCTTATAAA TGCCTACATA TTTCAAGCAA TAAAAATTAC	300660
AGCAGCATTT TTTAGCAAAT TCTTTATAGT CAAGCACCAT CAAATACCTA TATTTTAAAT	300720
ATTAAGTATT TTTCTTATAA CTTACATTAT TTATAATAAC GAAACTAAAA AAAATTAAAA	300780
TAATTTTAAA ATATCTGTCA TTATTAAGAA TAATATGATA CTATCTCTTT TATCTATGAA	300840
TATCAACTAT AACAGTATAA CTAGCATAAA ACAAACATTA AAAGAAAGAA AAATCGCTCC	300900
AAGAAAATTA TGGGGACAAA ACTATTTAAT CAACGAAAGC ATAAGGCAAA AAATAATAGA	300960
AAGCTTAGAT ATAAAAGAAA ATGAAAAAAT CTGGGAAATT GGCCAGGCC TTGGCGCAAT	301020
GACTGAGATT TTATTAAAAA AAATAATCT TTTAACCAGCA TTTGAAATTG ACTTAAATA	301080
TTAGAAATA TTAAATGAAA AATTTGAAA ATTAATAAAC TTAAATTGA TAAAAGGGGA	301140
TTTTTTAAA AAATACAAA ACGAAAATCA AAACATTGAT AAAATATTTT CAAATTTGCC	301200
ATACAATATT GCATCAAAAG TAATATCTAA ATTAATTGAA GAAACTTTT TAAAAGAAAT	301260
GGTATTCACA GTGCAAAAAG AATTGGCCGA CAGAATAACT GCAAAAATAA ACAGCAAAA	301320
CTATCTTCA TTTACGGTCT TAGTACAATC ACACTTCAAG GTAATTAAAA TATTAGACAT	301380
AGGAGAAAAC AATTTTTATC CTGCACCTAA GGTAAAGTCC ACAACACTAA AATTAATTCC	301440
TAAAAAAAC AACATAAAA ACTTCAAAGA ATTCAATAAA TTGGTTAGAA CTGTATTTTC	301500
AAACAGAAGA AAGAAATTAA AAAACACTAT TATTAATTTT ATTACCAATA AAGCTACTCT	301560
GAGAGAAAAT TTTTTAAAG AATATTTAGA CAAAAGACCT GAAAACATTT CTGTTGAAGA	301620
ATTTATACAA ATTTCCAACA CTTTAAATGC TTATCATTA AGCACTTGCA AATACAATTT	301680
CATCAACAGA ACAGCCCCTT GAAAGATCGC TAATGGGCTT GGAAAAACCT TGTAATAAGG	301740
GACCGTAGGC CTTGGCAAAA GCAAATCTCT CTACTAATTT ATAACCAATA TTCCCCGCAT	301800
CTAAATTGGG AAATATTAAA ACATTAGCAG AACCTGCTAC TAAAGATTCT CTACATTTTT	301860

TCTCTGCAAC ATCTTTTATT ATGGCTGAAT CAAGCTGCAG CTCACCATCA ATAAGTAAAT	301920
CACTCTCTTT ATTCCTAACA ATATTTAAG CATTCTTTAC TTTTTCAGTT TCTTTAGCAC	301980
TAGAAGACCC TTTTGTGAA AAACTCAAAA GAGCAACCTT GGGCTTTGCA TTTAAAATAT	302040
CTTTAAAAGA TTTAGCACTT TGCAATGCAA TTTCTGCAAG CTCTAAAGAA TTGGGATTGA	302100
CCACTACAGA ACAATCTGCA AAAAATAAGA TTCCATTATG TCCAAAACAA AAATCAACAT	302160
TACGAGCAGT GCATAAAGTA TCCATAATCA TAAAAGATGA TATAATCTTA ACACCTTCCA	302220
ACTTAGGGAT TATTCTTAAA GCATTAGACA AAACCTTAGC AGAAGTTGAG ACAGCCCCAC	302280
AAACACAAGA TTTAGCATAA CCAAATCTTA CCATAAGCAT AGCAAAAGTA ATTTTCATCTA	302340
AAACTTGAGT CTTTAACTT TGCTTCGTAA CTCCCTTTAA CTTTTGTAAA CTCCAATATT	302400
CATCCAAATA CATTTCAATA TCTGGGAAAG AATTAGGATC AACAACTTCT ATTCTTCCTA	302460
AAATATCAT T GCAATTAGAA AATTCTTTTA AAGAATTAAT AACAGTATCT TTTTGCCTA	302520
TCAAAATAAT CGAATCTGCA AGATTTTTTT GCAAAATAAC AATAGCTGCC TTTAAACTC	302580
TAGAATCACT ACTTTCGGGA AAAACTATAT TGGCCTTAAG CTTATTCTCT TTTACAAATA	302640
TTCTTGCCTT CTTAAAAACA TAATCTTTTA AACAAAACAC CTTATAAAAA GAATACAACA	302700
CAATTGATAA TGCATAAAAA AAGACATTTT AAAATAAAAA ATCTTTTTTC ATACATGATT	302760
TTCAATTATA AAAATTAAAT ATTTCTTAA GTTTTCTTAA AATTTCTTGT ACAACTTTGG	302820
CTGAATTGAA AGCAGCTATT TTAGAAAATT TACTATATTC AACCTCATTC CCTTCTTTAT	302880
TTACAATGTC AGATATTGAC CTAATAACTA TAAAAGGTAT ATTAAACATA TGAGAAACAT	302940
GCCCTATTGC TGCACCTTCC ATCTCAACAG CTATTACATC TTAAAGTTT CCTATAATTT	303000
TGTTAATATA AGTTGGATCA ATAACTGAT CTCTGAAAC TATTAATCCT GAATATGCAT	303060
TAGAACCTCC AACCTTTGAT TTAATGGCCT CTATGGCATT CTTAATTAAA TTTTATTGG	303120
CATTAAATTT TTGAGGCAAT CCTCCTGTAA GCTGTCCTAC CTTGTATCCA AATTTAGTCA	303180
AATCAACATC ATGATATGCA ACCTCTGAAG ACACCACCAC ATCTCCCACT TTAATATCTT	303240
TGTATTTAGC ACTAACAACG CCACCAGCAA CGCCAGAATT AATGACATGA CTTATGTTGT	303300
ATTTTGACAA AATGTAGCTA GTCCACACAC CAGCATTAAC CTTACCAACC CCACAAATAA	303360
TAACCATAAC ATTGCGATTA GACAACTTCC CCTTTAAAAT CTTTTTATTA AGACCATACT	303420
CCTTAAGAAC TATTTCTTCC TTATTAGACA TAAGCTTATT TATCTGATCA AACTCAGAGT	303480
CCATAGCAGT TACTATTAAA ACATTGACAT TTTTAGAAAA AGCAACATAA CTGTTTGAAA	303540
AAACTAATAA AAAAATAAAA AACTTTATTA AACAAATTATT CATAAAATCA CACTCCTTAT	303600

AATAAAAGAA	TATTTATATC	ATTTTTTACA	AAAAAGCCAA	AATTGAATTG	CTTTTGAAAG	303660
AATTTTTGTA	AAAGATATTG	AAAAAAAATA	TCCTATCCAT	ATTACAATAT	TAATAGCATA	303720
AAAAAAGGGA	AAACTGAATG	AAAAAATGA	ATCTAGTTAC	AGCTGCTCTA	CCCTATGTTA	303780
ATAACATACC	TCATCTTGGG	AATTTAGTTC	AAGTGCTATC	AGCTGATGCT	TTTGCAAGAT	303840
ATTTCGAAAAT	GTCAGGAATT	GAAACTCTTT	ACGTCTGCGG	AACAGATGAA	TATGGAACAG	303900
CTACAGAAAC	CAAAGCCTTA	ATTGAAAATA	CTACCCCTTT	AGAACTTTGC	AATAAATATT	303960
ATGAAATACA	TAAATCAATT	TACAAATGGT	TCAATATTGA	ATTTGACATC	TTTGGTCGCA	304020
CAACCAACAA	GAACCATCAA	GACATTGTAC	AAAATTTTTT	CCTACAATTA	GAAAAAACG	304080
GCTATATAAA	AGAGAGAGAA	ACTGAACAGT	TTTATTGCAA	TAAAGATTCA	ATGTTCTTGG	304140
CTGATAGATA	TGTAATAGGA	GAATGCCCAG	AATGCCAAAG	CATGGCTAAA	GGAGATCAGT	304200
GCGACAAC TG	TTCTAAACTT	CTAAATCCAA	CAGACCTAAT	AAATCCAAAA	TGCATAATTT	304260
GTAAAAACAA	GCCTATTTTA	AAAAAAACCA	ATCATCTTTA	TTTAGATCTT	CCCAAAATAA	304320
AAACAAAAC T	TGAAAAATGG	ATAAAAAATC	CAGATACTAG	CAAGAATTGG	AATACCAATG	304380
CCCTTAAAAAT	GACAAAGGCT	TTTTTAAGAG	ATGGCCTTAA	AGAAAGGGCA	ATTACAAGAG	304440
ACCTGAAATG	GGGAATTCCT	GTGCCTAAAA	AAGGTTTTGA	AAATAAAGTA	TTTTATGTGT	304500
GGTTTGATGC	TCCAATAGGA	TACATTTCAA	TTACCAAAAA	CATTATCAAA	AATTGGGAAT	304560
CTTGGTGGA	AAACAATGAT	CAAGTAAATC	TTGTACAATT	TATTGGGAAA	GACAATATAT	304620
TGTTTCATAC	AATTATATTC	CCTTGCATAG	AAATTGGAAG	TGAAGAAAAT	TGGACAATAT	304680
TAAATCAACT	CTCATCAAGC	GAATACTTAA	ATTACGAAAA	TCTTAAATTT	TCAAAATCAG	304740
AAGGAACAGG	AATTTTTTGA	AACGATGCTA	TTACTACAGG	AATCCCCCTCT	GATATTTGGC	304800
GATTTTATAT	TTATTATAAC	AGGCCTGAAA	AATCTGATTT	TCAATTTATG	TGGCAAGATC	304860
TCATGGAAAAG	AGTAAATACA	GAAC TTATTG	ATAATTTTTC	AAACCTTGTA	AACAGAGTAT	304920
TAACATTTCA	AAGAAAATTC	TTTGGAGATG	TAATAGAAAC	AATAGAAATT	CAAAATAAGT	304980
TTTGGAACA	AATAACACCA	AAATATAATA	AAATACTAAA	TCTTTT TAAA	AAGACAGAAC	305040
TAAAATCTGC	TCTCAAAGAA	ATACTTAAAA	TTTCTTCCCT	TGGAAATAAA	ATATTTCAAG	305100
ATAACGAACC	CTGGAAAAGA	AAAAACAAC T	CTCCACAAGA	AACAAAAGAA	CTAATCTCAA	305160
ACTTAATATA	CCTAATCAGA	GACTTATCTA	TTTTAATGAT	GCCATTCATT	CCCGAAACAA	305220
GCAAAAAGAT	ACAACAATTC	TTTGGCAACA	GTTATCAATT	TTCAACCAAA	ATTCTTGGAA	305280
CTAAATCGGG	AATTAAAAAA	ATTGAATTCA	CAGAAATATT	ATTCAATAAA	CTAGAGCAAA	305340
AAAAAATTAA	TAATTTAAAG	CTAAAATATT	CAGGAGATAA	AAACATGAAA	GAAAACGAAC	305400

AAGCAGAAAA	CTTGCCTATA	GCAAAAAGAGC	AACCGGAAAA	CTTGTTTAGA	GAAAAAGTGC	305460
TCTTAAGAGT	TGTA AAAAATA	AATAAAATAG	AAAGAAATCC	CGAGGCTAAA	AACTTATTTA	305520
TATTAAAACT	AGATGACGGA	ACTAACAAGG	ATAAACAAAT	AGTAAGCGGC	CTTGAAGGAT	305580
ATTACACAGA	AGAAGAACTT	TTAGGAAAAC	ATATAATAAT	AGTAGACAAT	TTAAAGCCTG	305640
CAAAGTTTAG	GGGAATAAAA	TCTGAAGGAA	TGCTAATAGC	TGCTGAGGAC	AAAAATAAAA	305700
ATTTTAAAGT	TATAATTGTA	GAAGATTCAA	TTCAAAATCC	TATTGCTGGA	GAGAGAATAA	305760
TACTTGAAAA	CGATCAGAAT	AAAGATCTTG	CCTGCCCACC	TAAAATTGAC	ATAAATAAGT	305820
TTTTTAAAGC	CAATATAGTA	GCAGAAAACG	GAGAGCTTAA	AATAAACGGA	ATAAATTTAA	305880
TATTAGAAAA	TTCTAAGAAC	AAAATTTTAT	CTAAAGATAT	TCCAAACGGA	ACAGTTTGCT	305940
AAGAGCTATT	AATGACTATT	AAAAAAATAA	AAACAAAAGA	AATGGAAGAA	AATTATCTTC	306000
AAAGCGAACT	GTGGGCATTA	ATAAAAACAA	CAAAAACAG	TTATTGGAAA	GCCATAGCAT	306060
TTGAGAGCGA	TGTTCTTGGC	AAAATTGTTG	TAATGCAAAG	AAGACTATTT	AAAAATTTTT	306120
ACTTAGCATA	TATTCCGCAT	CCAGAATTCT	CAAACAAAAC	TCTTGAAAAC	ATTAATATTG	306180
ATAAAATCAG	TAAAAGTATT	AAAGAATTTA	GCATAAAAAT	AAAACCCTAC	TTACATAAAA	306240
ATACAATCTT	TTTAAGATTC	GATTTAATGT	ATTACTACCA	AAGAACACTG	AATGACAAAT	306300
ACTCTCCATT	AAAAACTAAA	ATCAAAATATC	TAAAAAAATC	CTTTGATGAC	ATACAACCCG	306360
CAAACACAAC	AATATTAAAC	TTAAATAATT	CTCTTGAAGA	GATTTTGCTT	AACATGAAAA	306420
AAAAAACAAG	ATATAACATA	AAGCTCAGCA	CAAAAAAATA	TCTAAATATA	ATAATAGATG	306480
ATAAATTTAA	ACATTTAAGT	GAATTTTACA	AGCTATACAA	AGAACTAGC	AAAAGAGATA	306540
AATTTACTAT	TCACTCAGAA	GAATATATAC	AAAACCTAAT	TCAAATATTC	AAACAAGACA	306600
AAAATGCTCA	AATAAAATTG	ATAATTGCAT	TTTACAATAA	CATAATTATT	TCTGGCATAA	306660
TAGTGGGAAT	TTACAAAGAA	AAAGCAGTCT	ATCTTTATGG	GGCTTCAAGC	AAGGAATATA	306720
GAAATTTAAT	GCCCAATTAC	GCTGTACAAT	TTAAAGCAAT	AGAAATGTTA	AAAAAATTAG	306780
AAATAAAAGA	ATATGATTTA	TTAGGAATTC	CCCCAATTGC	AAATAAAAAC	CACCCCTTAT	306840
ATGGTCTTTT	TAGTTTTAAA	ACAGGATTTG	GAGGCAATAT	TATTCATAGA	ATTGGTTGTT	306900
ATGATTTTAC	TTACAAAAAT	TTTATTTATA	AGATTTATGC	AAATCTTGAA	AACTTAGAT	306960
ACTTCTATTA	CAAAGTAATA	AGGAAAAAAA	TTTAACCAAG	ATTATTAACT	AAATTTTTAA	307020
ATTGCAAACC	TCTATCAAAC	TCATTATTAA	AAAGCTCAAA	AGAAGCACTA	GCAGGAGAAA	307080
ATAACACAAT	GTCACCCGGA	CTTGAAATCT	TGAAAGCATA	ATTTACTGCA	TCTCTTAAAG	307140

AATCAAATAG	AAAATATTGT	ATGCTACTTT	TTTCTAAAT	CTTAATAATT	TTTACAGTTG	307200
CACTACCTCT	TATTAAAATC	CAAGTTCTCA	CAATATCTGC	AATCTTGCTA	AAACTTAAAA	307260
AATCAAGCTC	TTTATCGGTT	CCCCCAACAA	TTAAGTTGAT	ACGGTTATCT	TTTGTTTTCA	307320
AACTTTTAAC	AGATAAAACA	GTAGACTCAG	GAATAGTTGA	AGCTGTATCA	TTATAAAACA	307380
TTACATTTTG	AACTGATTTA	ACAAACTCTA	ATCTGTGCTC	AATACCTTTA	AAATTACTTA	307440
AAATCTGACC	CGTGCGATTA	AGGTCTATGT	TTAAATAATA	CGAAACAAAA	AAAGTAATAA	307500
CTTTAGGAAT	TATAAAAACA	GCTCGTGAAT	TAGAAAAACT	TCCAATCAAG	CTGTCATTAA	307560
AATATACTTT	GCCTTCATTG	CAATAAAAAA	TATCTTGATC	AAAATCACAA	GGATTAAATT	307620
CGGAAAATAA	AATAACTCTG	ACTTTTGATT	TAAATTTTGA	AAAATATTTG	CAATAAGCCT	307680
GATCCTGAAT	AATCACAATT	CCTGAAGTTT	GATTTACAAA	AATTTTGTAC	TTATCAATAA	307740
TATAATCATC	AAAATTTAAA	TAATAGTTTT	GATGATCGTT	GTAAACATTT	GTAATAATAC	307800
TAATAATAGG	ATTAAAATTC	TCTAAAGATT	GCAACTGCCA	AGAAGAGAGC	TCTAAAATCA	307860
AAGGAGATTT	TCCATCAAGT	TGATCAAAAA	AACTTAAAGG	AGATACACCA	ATATTGCCTC	307920
CAAGCTTTAC	CCCCGGATAT	TTTCTTTTCA	AAGCTTGATA	CAAAAGAGAT	ACAAGAGTAG	307980
ATTTTCCTTT	AGTGCCTGTT	ACTGCAACTA	TAGGGTTCTT	GTAAACATT	AAAAATAAGC	308040
TAATATCTGT	CTCAATTTCGT	TTTGCAAAC	TTAAATATTT	ATTATTGGGT	TTCACACCGG	308100
GATTTTTTAC	AACAATGTCA	GCATTTTTTA	AATCGTTTAC	ATCGTGTTTG	CCTAAAACAT	308160
ACCTAATTTG	ATCCTCAAAA	TCTCTTAAAG	CATCAATACT	TAAAGCTAAT	TCCGTCTCGC	308220
TTTTAAGATC	AGTAATTACT	AATTTTGCCC	CACGCTTTAA	TAAAAATCTA	GAAAGAGCTA	308280
CTCCTCCTCC	ATTAAGGCCT	AAACCCATGA	TTAAAAAATT	TAAATTTTTA	ATTTCTGCTA	308340
AAAGCACAAT	AAAATTATAT	CAAACCTGCC	AACTGTTTAA	ACGGATTTAA	TCCACCTTTC	308400
ACTATAAAAA	TAAGGAAGTG	AAACAACAAG	TTTGATTGCG	TCCTCAAGAG	ATGGAATAAA	308460
AACAATAATT	TCAAAAGGCA	AATTTGTATA	ATTTGCTAAA	ACAAAAGCAA	TAGGAATGGT	308520
ATAAACAAAA	GTCACAGAGC	CTTCCATAAT	AGCGCCAAAA	CTTGGAGATG	CTCCTGCACG	308580
AAAAAATCCA	AAAAGATACT	GAAAAGCAAG	AGCCATGAAA	AAGGCAGAAA	CAGAAGAATA	308640
TCTTAAAATA	ATTCCTATAA	GGTGCGAATA	CTTTAATGTA	TAAAAAATAT	AAGGAGCAAA	308700
AAATGAAAAT	ATAACAATA	CAAAAAGATGT	TAAAAAAGCA	AGCTTAAGGC	CAATTTTACT	308760
CAAATATATT	GCAACTTTCA	TGATTTCTTT	TTTACTATTA	TGCATTTTCAT	AGCCCATCAT	308820
AATATTTAAA	GAAATACAAA	AGGAATGAAT	TATATTAAAG	ATAATAAAAT	AAATAGAAAA	308880
AGATATGCTG	TAAGCAGCAT	ATTTATGAGT	ATCAATTCCT	ATAAAAATCG	ATGTCAATAC	308940

AAGATAGCCA	AAAAACCAAG	CAAACCTCAT	TAAAAGAATT	GGAATAAAAA	ATTTAATTAG	309000
CTGAGCAAAC	GGCTTAATAT	TAATATTCAA	ATCATCTAAC	TTAAAGTGCA	AAATTGAATT	309060
TTTGTTAAAA	GCTGTACAAA	CAAGATAAAC	AATAAGCTCT	AAAGTACGAA	TAACTGTTGT	309120
TGCAATAGCA	GCTCCTAATA	CTCCCATATG	AAAAACAAAA	ATAAAAATAT	AATTAAATAC	309180
AAAATTCAAA	AGCACTGAAA	AAACAGAAAT	GTAAACTTGA	AATTTAACAA	TTTCAACAAC	309240
CTTAAGAGCA	TTAGCAATAA	GTCTTTTAT	GATTGCAAAT	ACGAAAGAAA	AAATAGCTAT	309300
ATTTAAGTAA	GCTGCTCCAT	AGTAAACCGC	CCGCTCATCA	TTAGAAATCA	ATCTAAGTAA	309360
AAAAAAAGGA	TTCACTATGG	AAATCAAAAAT	AAACGGAAAA	GAAAATAAAA	TAATAGTTAA	309420
TATACTAATA	AAAAACGTAT	TTCTAAAAGCT	CTTAAAATCA	CCCTGATTGT	ATTGTCTTGT	309480
AGCAATTATA	TTATAAGCTC	CTGCCATGGA	AAACCCAATA	GTAACAAACA	GTTCAAAAAA	309540
TTTATTTGCA	AGAGAAACTC	CTGCAACAGG	ATAGTCACCA	AGATATGCAA	CCATAGCATT	309600
ATCTGTAAGG	GAAATAAAAT	TAAATAAAAA	AACTCAATA	GCAGTTGGAA	TCGCAATTTT	309660
TAAAAGATCT	TTATAAATTT	TATCCTTTTT	CGATACACCC	AATGAATACA	TAAATTTCTC	309720
CAAATAAAAA	AATTAAGATT	TTTGTAAGA	CAAATACCGG	AACCTACAAT	AAAGCAAAAG	309780
GAATTGCTTT	CAAATTAGTA	TAATCAGAAT	GAATTCTAGA	TCCACCAAGA	TTATTAAAAT	309840
CTTTATTAAC	ACTAAATATA	TCACGCTATC	CCATACTCAA	GCAAGTTCTT	CATACTCAAT	309900
CTCTCGTATC	CAATCATCGT	GAAAAAATTC	AATTATAATA	AATATATTTT	TAATAATCTC	309960
TTCCAGATTT	ACAATAAAAA	CAACTATTGG	TAAACTTAAA	TTTGTATAAA	ACACCAATAA	310020
ATAAGCAACT	GGAAGGGTAT	AAAAAACAAAT	TACTCCCGAT	TCAATAAAAA	AACAAACATT	310080
TGGTATACCG	CTAGCCCTAA	AAACCCCAAC	AAGAACTTGT	GCCGTAAAAG	CTTTAAAAAT	310140
TACAATACTT	GCAAAAACAT	AAATAAACAC	GCTAACAAAGT	TCGGGAGAAT	CTAATTTACT	310200
AAAAATATAA	GGTGCAAAGC	TCGATATTCC	AATAAGCAAA	ATAACTACAA	AAATGCCCAA	310260
AAGAAATCCT	AAAAAAGATA	AAAAAAATCC	AACTGATCTA	ACATGTTTCT	TATCGTAAAT	310320
CATTAAATGG	CCAATAACAA	CCCCTGTTGC	AAGTCCCATA	CCATGAAGCA	ATACAAAACA	310380
AATATCAAAA	AGATTTGATG	CAACAGCAAA	TGAAGCGTAT	TCAATGCTCC	CAACACGAGC	310440
ATAAAATGCA	TGCAAAATAG	TTATACTTAA	AACCCAAAAA	ATCTCGTGAG	ACAAAACAGG	310500
TATAATTAGT	TTCAAATTAG	CCCTAGTAAC	TACCTTTGGA	GCAAAAAAAT	CGCCAACTT	310560
AATCCGATAA	TATGAATTAC	TGCTTATCAA	ACTATATAAA	AAATAGAAAA	CAAACCTAAC	310620
AATTCTAGCA	AGCACAGTAG	CATATGCGGC	ACCTTTTATT	CCCATGCTAA	AGCCAAAAAT	310680

AAGAATATAA TTAAAAACAA TATTTATTAA AACAAACAATA GAAGTAACAT ATAAGGGTAT	310740
TTTTACTTCT TTAGCACTCT TAAATCCCAT AGCAGATAAA AAAGAATATG CCATTAGCAC	310800
ATAAGACAAT GAAATAATTT TTAAATACTC TGATCCAAAA TTAAAGAAT CCTGATTAGC	310860
TGTAAATAGC TTTATAATGT TTCTTGAAA AAGAAATGAA AATATAAAAA AAATTATTCC	310920
TATTGTAGTT CCAATTAATA ATATATAAGC AAAAGATTGT CTTACTTGAA GAACTTCTT	310980
TTTTGCAATT GCTTGGGAAA CGTAAGCGCT TAAAGCCGTA CCAAGTCCAA ACACAATAAT	311040
AAAAAAAAGA AAAGTTACTC TATTTGCCAA AGAACTCCC GTAACATGAA AAGAGCCCAA	311100
ATAGGAGATC ATAAAATTAT CAAAAAAGT TACCATTGTA AATAAAGCG ATTCAAAAGC	311160
TGTAGGAATA GCTATAACAA ATAGCTCTTT TATTATCTGG TCATAATTTT TAACTTTTT	311220
GATCATATTC CTTATATACA GTCTCCTTTA TTTATTACTT TTAATAAAT TTAATCCAAT	311280
CTAGAATATA CATATATTTA GAATTAACATA TTAATTATAC TAAATATAT TATAATTAAA	311340
TAATATGAAA TCAATTTATG CTTTATTATT TCTATTTATT AATTTATCTT TGTTGGCTAA	311400
CAACATTTCA AAAAAGATT TAGAAGTACT GCTAAAGATT GCCCAAGCAA TGAATAAGGA	311460
ATGCAAAAAT TTTATTGAAA AAAATCCTAT TCAGTCTTA AAAGAAATAA AACCTTAGT	311520
AGATGCAGAA AAAAATAACC TCTTAACCT AATAAATAAA AAAATACCAA TTCCTGAAAA	311580
TTATAAAATA CCTGATCTGG TAAATATTGA TGATTTTGAA GATCTTAAAA ATCTTGGAGC	311640
AAAGACTATT AAAGTAAGAA AAATATTAAT CGAAGATTTA ATTCGACTAA TAAAAGATGC	311700
AAAAAAATTT GGGATTGAAA TTAAAATCAA ATCTGCTTAC AGAACGCAAG AATATCAAAA	311760
ATTTTTATTT GATTACAATG TCAAACTTA TGGCAGAAAA GTTGCAGAAA CCAATCAGC	311820
AATTCAGGC CATTCTCAAC ATCATATGGG AACAGCAATA GATTTTATAA ATATAGATGA	311880
TAATTTACTA AACACAAAAG AAGGAAAATG GCTTTATGAA AACTCTCTAA AATACGGATT	311940
TTCCGTTTCA TACCCAAAAG GATATGAAAC GGACACTGGA TATAAAGCAG AGCCTTGGCA	312000
CTACTTATAC ATAGGACCTA AGCCATGCTT TATTCAGAAA AAATATTTTA ATAATTTACA	312060
ACATAAGCTT CTTGAATTTT GGAACCAGAA CAAAACAAAT CTTATTAACC TAATTGAAAA	312120
ATATGCAAAC TAAATACTTC TTCCGGCATT CAAATAAGAA CAAAAAGAT TGTCTAGTAA	312180
ATCAATATCA AGCTTATCGT AAGCAGAATT ATCATAAAAA AATAAATCAA GCTCTTCTCG	312240
AACTAAGACT ATGATTTCTC TATCATCAAC AAAATTAGCT ATTTTAAATT TCAAATATCC	312300
TGCTTGTTCA AGTCCAAATA AATTACCAGG CCCCTTAGC CTTAAATCTT CTTCTGCTAT	312360
TTTAAATCCA TCCAAATTTT CTTTATAGT TTTTAATCGA AATTGCCCAG CACTTGTCOA	312420
AGGCTCTTTA TATAGCAAAA AGAAAAAGA TTGTAAATTG CTCTACCAA CACGACCTCT	312480

AATTTGATGC	AAAGTAGAAA	GTCCAAAACG	CTCAGCATGC	TCTACTACCA	TACAAGTTGC	312540
ATTTGGACAA	TCAATTCCAA	CCTCAATAAC	ACTAGTCGCC	ACCAAAATAT	CTACTTTTTT	312600
CGAATAAAAA	TTTTTCATAA	TTTCTTCTTT	CAAATCAGAT	GGCAACTTAG	AATGAAGCAT	312660
GTCCACAACA	TATTCGCCAA	AAACTTCTTT	TAATTTCAAA	CACATATTAT	TAACATCTTT	312720
TAATTCAAAT	TTTTCTGAAG	ATGAAATTAA	TGGATAAACA	AAATAAACCT	GATGACCCTT	312780
TAAGAGCTCT	TTTCTTAAAA	ACTCATAAAC	TTTATCTTCA	TTTCCATGCC	TTGCTAAATA	312840
AGTAGTAATA	GGCAAACGAC	CCTTAGGCAA	GGTTTTAATA	AACGAAACTT	CAAGATCACC	312900
AAAAAGTGTT	AATGCAAAAC	TTCTAGGAAT	AGGTGTTGCA	GACATTAAAA	GCATATCCAC	312960
CCCTTCTCCT	TTGTTTTTAA	GCTCTTCTCT	TTGAACAAC	CCAAATTTGT	GCTGTTGTC	313020
AATGATAACA	TACGCCAATC	TTTTAAATTC	TGTACTTTCG	TAAAAATAG	CATGTGTTCC	313080
AACTATTAAA	CCAGAAGTAC	CATTTCTAAT	GCTTCTTAGA	GCTTGTTCCCT	TATCCTTCTT	313140
TCTTAAACTA	CCAGTCAAAA	GAGTCATTGA	AATGTTAAAA	GGTGCTAATA	TGTTAGATAA	313200
ATTATCATAA	TGTTGACGAG	CCAAAAGATC	TGTAGGGGCC	ATAAATGCTA	CCTGATATCC	313260
AGCTTCAATT	AAAGGAAGTC	CTGAAAGCAA	GGCAACAAGG	GTTTTACCAC	TTCCAACATC	313320
ACCTTGAAGC	AATCTATTCA	TTGGCTTAGA	AGAGTTAAGA	TCAAAGAATA	TCTCATCAAT	313380
AGAAATTTTT	TGATCTTCTG	TAAGCTCAAA	GGGCAAGCTC	GAGACAACCT	TTTCAAGCAA	313440
ATCTTTTGAT	AAATCTTTTT	TTTCTCGAAA	AAGAATCTTA	GAAGATCTAT	ACCTGAAAAA	313500
AACTGAAGCA	AAAAAATTTT	TCTGTAAATT	AATGTCTTTT	TTGCCTTTTC	AAGCATTTCT	313560
AATGAACTTG	GAAAGTGAAT	CTCTTTTAAA	GCATCACTTA	ACGATAATAA	AGAATACTTT	313620
TCTATTAAAA	ATCTAGGAAT	GTCTGTTTGC	CCAAACTTAA	AAAAATATTC	AAGAGCTTCT	313680
TTTACATATA	ATGAAATTTT	CTTGACGTT	AATCCCTCTG	TCAAAGAATA	AACCGGAAGA	313740
ATTTTTTTTAA	ACCTTTCAGG	CTTGTCGCTG	TAAACTTCGC	TGTCAAATTT	AGAACAACCT	313800
CATAAACCAC	TATAATCGTT	ATAGGTAAAT	TTAGAATAAA	TATAAAATTT	TTTATCTATT	313860
TTAAAAACAT	TCTCTAAAAA	AGCCCTATTG	AAAAGCAGAA	TTTCGAAAGG	TTCTCATTTT	313920
ATACTTTTAA	CTGTAACTT	TAAATTTTTT	TTAGAACTAT	CCCCAAATTT	TTTATGCCCA	313980
AGAACTGTGA	ACACCGTCAT	CATATCACAA	CTTTTACCT	TAGAAAAATC	TGGAAAAGTT	314040
TGTATATTTT	GACGATCTTC	ATATTTTACA	GGAAAAAAT	CAATAAGATC	TTTAACATTA	314100
AAAATTTGCA	GATTATTTAA	CCTTTCAACC	CCTTTCTCAC	CAAGACCACC	TATACCTTTA	314160
AGCTCATATT	CAAACTCATG	TAAAAACATT	TTAATCTCCT	AAAAAGGCAA	ATATGTTCCCT	314220

AAAGCTCTAA	TAGCAAATAC	AACTTGTTCA	ATAATAATTA	TAAATGCTAC	CATTAAAGCA	314280
CTCCCAACAA	TCAAACGTAA	AGTATAAGAC	ATGTGTTTGT	CAGTAATCAC	ACCACTTATC	314340
TTAGTGGACA	AAGGAAGTAA	AAATGAATCG	ACTGTTTTAA	AAAAGTCTGA	GCCTTGGAAC	314400
AAATTCAAAA	GCAATAATAA	TAATCTCAAC	AATAAAAAGA	AACTATAGC	AATAAAAATG	314460
CTTCTAAATA	TCTCCCAAAC	TTCAACAATG	AATAAAATAA	TAAATGTAGA	AAGCTTATAA	314520
TTCCCATAG	CCAACATTCT	TTCAAAAATA	GTAAAGTTA	TTAAAGCTGC	AATTGGAGAA	314580
AAATCAAACA	TACCAAATGT	AAAAAGAGGA	ATTTTTCTAA	AAAAAGATAA	AAATGGTTCT	314640
GTGACAACAT	GTATAAATCT	GAAAAATACA	TTGGTATTAA	TCCCTGAAGA	CACAAGCCAG	314700
CTAAGAAGAA	TCCTAATTAA	AATTAAAATC	CTATAAATCT	GCAAAAATAC	CATTAAAATT	314760
TGTATTAAAA	CAACCAAAAC	AGCACCTCCT	AATCAACCCA	AACATCTTCA	ACTATCACAC	314820
ACTTTCTCAA	CTTATCAAGC	TTATCTTCAT	CTGGCACAAA	ATTTAAAATT	GAATTCATTT	314880
TTAATTTCAA	ATCTTTACCA	TTTTCCCTTA	AATAAAAATA	AACATTTGAA	AATCCAGAAT	314940
TGTCCTCAAA	ATTACTTATA	CTTTCCTTTA	AAGAATTAAG	TAATTGTAGG	TCATTTAATT	315000
TATTATTTAA	AACTTAATA	TGAATATTAT	TTATTTTATA	TTCGGAAAGT	CTCTCAATAT	315060
TTACAACTTT	TTCAACCACA	ATTGAAAATT	TATCTCTGTT	AAACGTAAGC	CTACCTACAA	315120
CCCCAATAAC	ATTGCCTTCA	AGTAAAAAAT	TTCTATATCT	TTCATAGCTT	TCTGTAAAAA	315180
CTACAATATC	TATTGCGCCT	TTAAAATCTT	CTATAACGCC	GAAAGCCATT	TTTGCATTAT	315240
TTCTTTTAGT	TTGAATAACT	TTTACTGAAT	TTAAAATTCC	AGAAAATTGA	ACAATGCTAT	315300
CTTTTTTGGC	AGCAAGATCT	GTAAAACAT	TTAACTGGA	AAACTGTCA	ATTGCCTTTT	315360
TATAAGGATC	AAGAGGATGA	CCCGACACAT	AAAATCCTAA	AAGCTCTTTT	TCAAATCCTA	315420
AAAGCTCAGA	ATAAGAATAC	TCTTTAAAAG	TTTGATAATT	AAACTTTGC	TGAATTGGAT	315480
CTTGACTTTC	AAGAGCACCA	AATAAGCTGT	TTTGACCAAG	TTTTTTATTA	TTTTTATCTT	315540
CTGAAACAAC	TTCAATCAAA	TGATCAAGAT	TTTCAAATAA	AGTTTTTCTA	TTTTGATCCA	315600
AACTATCAAA	AAGTCCAGAT	TTTATTGCAG	ATTCTAAAAA	TTTCTTATTA	ATTACTTTAT	315660
CATCTACACG	TCTTATAAAA	TCTTCAAAAG	AACTATATTT	GCCGTTTTTT	TCTCTCTCAT	315720
CAATTATTAA	ATCAACAACA	ATTCCCTCAA	GATTTTAAAT	CCCATTAAGC	CCATAAGAAA	315780
TCCCAGAATC	AGTTACACGA	AATCCCTTAA	ATGATCGATT	TATATCGGGC	TTGAGAACGT	315840
TTATGCCTAT	AGCTTTTGAC	TCTTCGATGT	AATAAGAAAG	CTTATCATTA	TTATTAATTT	315900
CATTGGTCAA	ATTGGCAGCC	ATAAAATATT	CAGGATAATT	AGCCTTAAGA	TAAGCGGTTT	315960
GATATGCTAT	TAAAGAATAC	GCCGCTGCAT	GCGATTTGTT	AAATCCATAC	CCAGAAAAGG	316020

GCTTTAAAAG TTCAAAAATT TCACTAGCAA TTTCTTTGTC ATATCCTTTC TCAATAGCGC 316080
CTCTTAAGAA GTCGACTTTC ATTTCAATTCA TCTCGTCTTC TTTCTTTTTTA CCCATAGCAC 316140
GTCTTAAAT ATCGGCCTTG CCAAGAGAAA AGCCTCCAAT TATTTTGTGA ACTTCCATTA 316200
CTTGTTCTTG ATAAACAATA ACCCCATAAG TTGGTCTTAA AACTTCCTTT AAATCGGGAT 316260
GAGGATATTT AATTCTCTTA ACACCTTTTT TAGCAGCAAT AAATTGAGGA ATAAATTGCA 316320
TAGGACCTGG CCTATAAAGA GCATTTAAAG CTATTAAATC TTCAATGCTA TCGGGCTTTG 316380
CGTCTTTTAG AATTTGCTGC ATTCCTTCAG ATTCAAATG AAAACAGAC GCACTTCTTC 316440
CTTCTCCTAG CATATTAAAA GTCTTAACAT CATTATCTGG AATATTTTTT ATTTTAAAAAT 316500
CTGGATTTAC ACTTCTAATA AGATTTTCTG CATTTTTTAT TAACGTCAAT GTTTTCAAAC 316560
CAAGAAAATC CATCTTAACA AGCCACATT CTTCAGCAA ATCCATTGTG TATTGAGTAG 316620
AAACAGAACC TTGCTTATAA TCCTTATAAA GAGGCACATA GTCGGTTAAA GGGGTTTTAG 316680
AAATCACAAT TCCTGCAGCA TGAGTTGAAG CATGTCTATT CATTCCCTCA AGAACCAATG 316740
CGGCATTCAT TAATTCTTTA TAAACAGGCT TGCTAGTAAA ACACTCTTTC AAAGAATTGT 316800
CATCTAAAAC CTCTTTTAAA GAAACTTTAG GACCATCAGG AATAAACTTA GTAAGTTCAT 316860
TTGATTCAGC AAATGGAATA TCTAAAACCC TAGCCACATC CTTAACTACA GCCTTAGGCT 316920
TTAAGGTTCC AAAAGTAATT ATTTGAGCTA CCTTATCTTC TCCATATTTG TTGGTAACAT 316980
ATTTTATAAT CTCATCTCTG CCTTCAAAAC AAAAATCAAT ATCAAAATCA GGCATAGAAA 317040
TACGCTCAGG ATTTAAAAAT CTCTCAAAAA GCAAATTATA CTTTAAAGGA TCAATATCAG 317100
TAATCCTAAG AGCATAAGCC ACAATTGAAC CAGCACCAGA ACCACGCCCA GCTCCAACAG 317160
GAATATCGTT ATCATGAGCA AATTTAATAA AATCCCAAAC AATCAAAAAA TAGCCTTCAA 317220
AGCCCATTC AATTATTACG CTCAATTCAT AAAAAGCTCT ATCTTTTATT TTGCTTGTC 317280
AATTTTTATA TCTAAATTTT AACCCCTCAA GTGTGAGATG TTCCAAATAT TCACCAAGAG 317340
TATTAAATTC AACAGGAATT TGATAATCAG GCAAAATAGG ACCTGGAAAA GTTATTTTAA 317400
AGTCATCACA CTTTTCTGCA ATCCTTACAG TATTTTCTAA AGCTTCGGGC AAATCATTA 317460
AAAGTTCACA CATTCCTCT TGAGATTTAA TATAAAATTC ATTGGTTTCC ATTTTAAATC 317520
TATTCTCATC GCTTTTCTTA GCACCAGTAC CAATACAAAC AATGATGTCT TGAGCAGTTG 317580
CATCTTCTCT GTTAACATAA TGAGAATCAT TAGCTGCTGT TAAAGGAACT CCAAGTTCTC 317640
TAGAATACTT AACCAGCCTT TCATTTACAA TGTCTTGATC TTTAATACCA TGCCTTTGAA 317700
GCTCAAGATA AAAATCATTG CCAAAAACCT TTTTAAACCA AAGAATTTCA TTCTTGGCAT 317760

CTTCAAATCT ATTGGCCAAA ATAAGTCTTG GAATGAGCCC CCCAATGCAA GCTGAAGTAC	317820
AAATCAAACC TTCTGAATAT TTTTCAAGGT CATCTTTATC TATCCTTGGA CGATAATAAA	317880
ACCCTTCAAG ATAAGAAATA CTTGTAACT TTAATAGGTT TTTATAACCC AACTCATCTCT	317940
TGGCAAGCAA AATTAAATGG TAAGACATTT TTCCAAGATC ATCCTGTTTT TTTAAAAACT	318000
TAGAAGTTTT TGCCATATAG GCTTCAATGC CAATTATTGG CTTAATTCCT GCTTTTTTAG	318060
CTTCTTTGTA AAATTTAATA GCTCCAAAAA GATTGCCATG ATCTGTAAAT GCAATATGCG	318120
ACATATTGCA TTTTTTTGCT TTTGATATAA TATCTGATAT TTTTGCAGCT CCATCCAAAA	318180
GAGAATAATC TGAATGAACA TGAAGATGAA TAAACCTAGA CCTAAAACTC ATACCTAAAA	318240
TTATTTTATC AAAATAAAAC TTGATTTTTA ACAAACCTTA ATCAAATAAA TAAAAATTAA	318300
AAAAGTCATA ATAATTTTTA AATCTCTAAT TTAAATTATT GCAACAAATC TTATCAAAAT	318360
AATCAAGAAA AAATACTAAT TCCTTGATTA TCCAATTCAA TTACCATCTT TTTAATGTGC	318420
TCAAGTTTTC TAACAATTC TTCAGATAAA CTCTCAGCTT GAGACAAAAA ATCTTTGGCT	318480
TGCCTTAAAC CGCTATCACT ACGATTCTCT ACCCTAAATA TAATCAAAAT TTCAGCTGCA	318540
AACTTATTAA TATTTAAATA AGGAATGTAT ACTTCTTCCC ACAACTGCCT GATAGCATCA	318600
TTCTTGGGAG ACAATCCTTT ATAAAACAAT CCAAACCCAT GCTTGGAAGC ATCTGTCTGA	318660
ATGAATATTG TCCTTTGCCC CTCAACAAGT AGTCTCAAAT TATTAATCCA AGAAAATTGG	318720
TCTGAGATAA TAAATTCTAG CTCTTTTAAA AATTCATCAT TAGACAGCAT AAAAGTATCA	318780
GAGCCAATCA AAGAATCACA GTTTCTTGAA TAATAAGCCA TATTAGCATC TATACTCTCA	318840
AGACTTTCAA TCAAAGAAGA AAATTCCTCT TGACTTCTTG AAAAGCGCTT AAATATGCTC	318900
TCAAGATAAT TAAGCTGTTT AAGAATCTCG GCAAAGAACT TATCAATATC AATCTGCAAA	318960
TCCTTAAGGT TATGAGAAAT CAAATCTTTA GAAACCTCCT CAATTCCTT TACAGAAATC	319020
ATATTCATAA CACCTTTTGC CTGATCAGAA AGTCGCTTGA TCTCATCTGC AACACAGAA	319080
AATCCTTTAC CATATTCTTT AGCTCTTGCA GCCTCAAGCT TTGCATTAAG AGAAATCATA	319140
TTGGTAGCAC CTAAAAAATT ACTTATTGTT TCTAAGCTGC CTTGAATTCC AACAAATAACA	319200
GAAGATATTT GATTTAATTT TTCCTTATTA TTTTACCAA GATCACTAAA AATAACGCTT	319260
ATCTGATTAC GAGCATTATT TGTCATCTCA ACAAAGTAG AAAATATCTG ATCAAAATCT	319320
TCTATTTTCAG AAAACAAAAAT CCTTTGTAAT GACTCAAATC CTACTTTTAA AGTAGAAATG	319380
GAAGCTTTGG TATGATAAAA TCCCTTTAGC ATTTCCTTAA CAGGAGCCTT ATATTCGTAA	319440
GTAATCAAAT CTTTTTTGTC ATTACCAACA ACATTTAAAA GATTTAATC AACAGCTTTT	319500
TTCTTTTTTT TAAAAACGA AAATTTTTTC ATAAAGGGAT TCTATCATAA AACTTTTTTT	319560

TTGAATAGGG	TCACCAGTAC	TTAATTTGAC	ACATTATTTTC	AACTTTTAAAT	ATCAAATCAA	319620
ATACATCAAT	AAACAAAAAA	TATTTTACACA	TTTAAATGGT	AAAAATTAAT	TACTTTGAAA	319680
TAAATTTAAG	CTTTCATCTT	AAACCATAAA	ACCATCTAAA	GATACAAATC	ATTCTCCTCA	319740
TTTAATTTAA	TTTAATTTAA	TTTAAAACTA	ATTTTAAATT	AAATTTACTT	TCTTTTACC	319800
CAAGAGTAAC	GCCCACTAAC	TTCAATTATAC	TCAAAAAGAA	CATCTCTGTA	AGAAAAAAA	319860
CATAAAAAAA	TATCAATAAA	CTCTTCTAAT	TTAGCTTTAA	CTTTTGCAA	GTAAAAATCG	319920
TTGTCAAAT	TAAAAATATC	GTCTGATTCT	ACTGTAAATA	ATTTATCATC	TTGCTTGAGG	319980
ATAACTTTTT	TGGGTTGCCA	AAAAAGAACG	TTGATTTTTT	TGTCCTGAAG	AAAAAATCTA	320040
TTAAATTCAT	AATCAAGATC	AACTTGATCC	GTTTTTGCCT	CAACAATCCC	AACAATAACA	320100
CATCGTTCAT	GATCAATTCT	TTTAATCAAA	ACAGCATCTG	TAAGCACAAC	TCTCTCGCCA	320160
ACTTCAAGAG	CAAAGTCTC	TTCTATTTCA	TATTGCTTAT	TAAAAGGAAG	ATTTGCAATT	320220
TTCTTAAAAA	GATTGAGAAG	TATGTACTTA	GTGCTCACCT	CTTTATTGCT	TATTCTAAGA	320280
CAACGAATCT	TCATTCTATA	CTTAAGCTCA	TCAAAAAAAT	ATTTAACTAG	CCTTTTCATT	320340
AAAATTGTTT	TTCTAATGTC	TTCTTCCTTC	ATTCAATCCT	CCTGATAAAA	ATTGCCAAAA	320400
ATTAAAGCTA	TTATATAAAT	ATAATAAAAT	ACAAATTTTA	TTAAAGAAAT	CAAAATATTT	320460
TATTATATAC	TAATTATAAT	TAAATCATTG	CCGAAAATGA	AAGGGAAAT	TATGTTAATC	320520
AAATTCATGT	TCTCAAATAT	TAATTTAATA	TTAATAGTCA	GCATGACTTT	ATTTAAAAATA	320580
TTATTAGAAA	TAATATACCG	AAAAATATTA	TTAAAAAAA	TAATTACCAG	TACCGAAACA	320640
TTAAATGCTG	AAAAAAAACA	ATATAAAATA	ATTGTTATCT	TTGTTTTAGC	TTTAAATCAT	320700
TTATTACAAA	GTTTTTTAAT	AAATGCTCTT	ATCAATTTAT	TCAACAATCT	AATAACTCTT	320760
ACTAACAAC	CTCTTGGAAG	CTTAATAGAC	TTAAATTATA	ATATATTATC	TGCAATACTA	320820
ATATCTAGCA	TAAGTTGGCT	TGCCTTTAGC	TTACCCAAAG	TAATAAACGA	TATAATCTAT	320880
GAAAAAAGAC	CGTTTAATTT	AACAATAGCT	AATGCTTTTT	TTGACCTTTT	AACAATAATA	320940
TTACTAACCA	TATTCTCTAA	ATTATTTTTA	AGCTATAAAA	TATTGCAATT	TGAGAACACT	321000
ACAAACATTA	ATTTTGGAAG	CCTGCCTACT	CACTAAAAAA	CCAAATAGAC	ACTCAAATAC	321060
AAGCTTTAAT	TAATCCTAGA	AAAAGCTTGG	CTGGATTTTC	TATTCTTGTA	ATAAGTTCTG	321120
GATGAACTG	GCAAGCTACG	AAAAATTTAT	TTTCAGGAAT	TTCTATTAAT	TTTGCCATTT	321180
TAAAATCACT	TGAAAATCCA	GATACTATAA	GCCCATTTTT	TGCAAATAAA	TCTATATAAT	321240
CATTATTGAC	TTCATACCTA	TGTCTAAATC	TTTCAATTAT	CCGATCTTGG	CCATAAAGTT	321300

TAAAAGCTAT	TGTATTCTTT	TTAAGAATCA	CAGGATATCC	ACCAAGCCTC	ATTGTAGCGC	321360
CCTTATCTTT	AATTCCTTT	TGCTCAGGAA	GTAAATGGAT	AACAGGACTT	TTTAAGGGCT	321420
TGTCTCTTGC	TAAATTTTCC	TCCGTATCAG	CATCAAGTAT	TCCACAAACA	TTACGAGCAA	321480
ATTCTATTAC	AGCAAGCTGC	AAACCAAGAC	AAATTCCAAG	AAAGGGAATA	TTATTCTCAC	321540
GAGCATATTT	AATAGCCATA	ATTTTACCTT	CATATCCTTT	GCCTCCAAAG	CCGCCAGGAA	321600
CAATAATGCC	GTCAAACCTC	TTTAAACAGC	TCTCATTTAA	ATCATTAGAA	TCAATTAAAG	321660
TGCTTTTAAT	AAGCAAATCC	AAATGGGCTG	CAACATGAAC	CAAAGACTCT	CTAATTGATG	321720
CATAAGAATC	ATCAAGTTCA	GCATATTTAC	CACAAATAGC	AATATTAATA	ATTTTTTTAG	321780
GCACAAAAAA	ATTAGATTTT	ATAACTCCTA	CAAGCTTTGA	AAGCTCTTCT	ATTTTTGGAT	321840
CAACCTTAAT	ATTTAACTTA	GAGCTTAAAA	TCTCATGTAC	ACCCTGCTTA	TAAAAAGATA	321900
TAGGAATTTT	ATAAATAGTA	GAAACATCAA	CATTGTCAAT	AATAGAAGTG	CTCTCAACAT	321960
TGCAAAACAT	TGCCACTTTT	TTTCTGATTT	GGTCTGTCAA	TACTTGTGAA	CTTCTAGCAA	322020
TAATTAAATC	GGGGAAAATA	CCTGCTTTAT	TTAAGGTTTT	AACACTTTGT	TGAGTAGGTT	322080
TAGATTTTTG	CTCATTAATT	CCAGCTGGAC	TTGGCACATA	TGTTAAATGA	ATAAAAGAAA	322140
TATTACCACT	CCCAATCTCC	TGTCTTATTT	GTCTTACTGT	CTCAATAAAT	AAAATATTTT	322200
CCATATCTCC	TACGGTTCCA	CCAATTTCAA	TTATCAACAT	ATCACTATTC	TCAGAACTTG	322260
CAATCTGAAA	AATTGTAGAT	TTGATCTCAT	CAGTAACATG	GGGAATAAGC	TGAACTGTTC	322320
TTCCCAAATA	TTTACCCTTT	CGCTCATTTT	CAAGTATCTT	TTTGTATATT	TTGCCCATTG	322380
TAATGTTCCA	ACTAGACTTG	GCATTAAGAT	TTAAAAACCT	CTCGTAATGA	CCAAAGTCCA	322440
TATCAACCTC	TCCTCCATCA	TCAAGCACAA	AACTTCTCTC	GTGCTCAACA	GGATTAATAG	322500
TACCAGGATC	AGTATTTAAA	TACCCATCAC	ATTTAATTGG	AGTAACTCTA	AAATCATATC	322560
TAAACAACCT	TGCAATACTT	GCCGATGTAA	CTCCTTTACC	AATTCCAGAG	ATCACGCCTC	322620
CTGTTATTAC	TAAAATCTTT	AAGTTTTTTT	TCATGTATAC	CCCAAAATTA	AAACTTTAAA	322680
TTTCAATCCA	ATTAAGCTTA	TGCTTAAAAA	GAATTCACAA	ATCATAATAA	AATATACTTG	322740
CATTAAAACA	AACAAAAACA	TTAAATTAAA	ATAAAAATTA	TTAATGCTTA	GCTAAAAAGC	322800
TATTTCTAAG	CCATTGTTTT	AAATCTTTTA	AAC TATTTTA	ATTATAATTA	ACAAAACAAT	322860
ATAATGAACC	TTTGGTTAAA	TAGTAATAAT	TAAACATTGC	CAAAAAAACT	AAAAACCCAA	322920
GAATAGCAAA	CAAATTGCTT	TTTTTTCTAA	TACTTCCAAA	GTCTACTATC	TTAAAAATATG	322980
AAGCCAAATA	TAAAAAAAAT	CCCAAACAT	AACTATTTT	AAAAAATAGG	TCGCCTAAAA	323040
ATCTGTCAAA	AGAAAAAATT	AAATCCGAAG	AACATGGCAC	ATATTTAAAA	CCCAAATAAA	323100

GAAAAGACGT AGAAAAAAC AATAACACAA TGGTCCCCTAA AAAGAATATC AAAACCTTAA 323160
CAAAAGGATG CGTTTTAAAA GTTATTCTAA AAAACATAAA GATTGGAAAA ATAGATAAAA 323220
AATTAAAATA ACGAACAAAT AAAAAATCAT AAAAAATATCT TAATTCTAAG AATGGAGTAC 323280
CCTCGCCTCT TAAAAAGAAT GCATTATCTA GGAATAAAAA AATATTAACC CCTAAATAAT 323340
AAATAAATAT TAAAATTAAA GGTAGTGCAA ATAAATATTT AATTAAATTG AAAAAATAAT 323400
GCTCAAAAGT TGAAACAGGC AAAGATAAAT AAAGAATATT TCTGAACGGA TCGTGAATTA 323460
CTTTGTAATA ATCACACATG GTAAAAATCG ATATAATCAA GGTAAAATA AAAATTTTAG 323520
GAGCAAAAAA TTTTAAAAAA TCAGTTGCTG AAAAATTAAA ATAAAACTA ACAAGCAAAT 323580
AAGATATAAA TATCATTCCT AAAACTTGAA TTATTAATAA AGTATAGAAT TTTTATTGT 323640
AAATAAAATC AAAATAAAT AAATTCAAAA ATCTTTTTAA GCTAAACATC TTTTATTACC 323700
TCTTCTTTTT ATTTTCAGTA ACATATAAAA AGAAAACTC AATATCAACA ACTTCAGCGC 323760
CATTGCTACT CTCAAATAA AGCGCCTTAA ATCCATCCTT ATTTTTTTCA TAATATAATT 323820
CATTTCCATT CAGCTCGCTG ATAATTTTAA TCTTATAATT TTTATTAATA TAAGATACTG 323880
AATTGGAAAA AAGAATTGAC TTTTCCCCAA CAATGATTAA ATAATCCACA ACCCCTGCCA 323940
AATCTCTTAC ATTGTGGCCT GTAATAAAAA TGATTCTATC CTTTAAATTA GAAAGCATGT 324000
TTCTAAAAAC ATTTTTTGAA ACAATATCAA GACTATTTGT TGGCTCGTCA AACAATAAAC 324060
AAGAAACATT TGCAGCTAGA GAGAATGCAA TAATACTTTT TTTCTTCTGT CCAAAGAAG 324120
CTGAAGATAA GTCAAGAGAA ATATCAAGAT CAAAATCCGA TAAATATTTT TTAAATCTG 324180
CCTCATTGAA ATTTGGATAA AATATAGATA AAGCCTTGCT GTATTCGGCT AAAGACAATC 324240
TGGAAGTGA AAATTCTTCA GGAATAAAAA ACAAATTCAC TAAATTCAAG GGATTTCTTG 324300
GAAAAGsTGC TAAAGAGTTA AACAAAATTT TCCCTTTTAA GGGCTCCAAA AGTCCACTTA 324360
CAAGTTTAAG TAAAGTTGTT TTTCCAACCTC CATTTTTGCC AAGAAGCAA TAGGCTTGAG 324420
GGGTCTCAAT GTTTAAATTT AAATCCGAAT AGACTTCTTT TCTCTTATAG GAAAATTTTA 324480
CATTAACAGC CTCAATAGCC ATAAACACTC CTTAATATAT TAAAAGTTAA AACATAAAAA 324540
ATAATTAAAT CAAAAATATA AATTCAATTT TTTATGAAAA ACTTATAAAT AAATATAGAA 324600
AAATTTACAT AAAGTCTTGA GCTAAAATTC CAAATTTTAA GCATAATTCT AGGTAAAATT 324660
TGAATTTTCA TAAATCCAAA ACTTTTTGCA TATTCATAAC AATCTTGAAA TTCAGATAAT 324720
CCTTTAATCT CATCAAGAAC AGAAATAAGC TTTTCTTTAT AAGCCCTATA AACAAAGCTTA 324780
TCAGAGATAT TCCAACATAAT AATATAAATT TGCTTAAAG AAATAAAATA ATAAAATTGC 324840

AAGAAAAATT TTTTATACAA ATTTTGACAT TCGTTAAAAA TACCTTCTCT TTTTAATAAA 324900
GTTTCCATTG TATTAAGAGA TAATTTAGAT TTATGTAAAA CACTAATAGA AGAACTCATG 324960
CTTCCCATTG TTTGGAAATT AGTATAAAAA TAATTATTTA CAAAAGAAAC TTTAGAAGCT 325020
TTTAAAAAAA TTTGCATAAC AAAAAGTATA TCTTCAAATA CTACATTTTG CTGACGAATA 325080
TTATTCTTTA AAATTAATTC CCGTCTAATC AATTTATCCC ATAACGTTCC AACACAAAA 325140
TTTTTCCTTC CAAAAGTCGC ATAAACAGTA AAAAGCAAAT TTTTAAACGC CTCCTTGCCCT 325200
GTTAATGGAT AATTAGGAAA AGGAAGTAGA GATTTTCTTT TTACATTTAT TGCAAGAAAA 325260
TAAATATAAA ATTGAGAACA AACAAATATCA GAATTATCTG CTTTGTGCTCT GTTATATAGA 325320
ACTTCAAGCA TGGTGCTCTC TACAGAATCA TCACCATCCC AATAAATAAC ATATTCCCCT 325380
TGAGCCTCAG AAAGTCCCTT GTCTCTAGAA GCAGAAAGAC CCATATTTTT TTGACTAAAA 325440
ATCTTAATAA AGCTATACTT ATTGGCATAT TTTTCTGCTA TCTCTAAACT ACCATCATAA 325500
GAACCATCAT CAATTAATAT AATTTCTTTA TCTTTTAATG TTTGATTAAC AGCATCCTTT 325560
ATCATTGCAT CAAGAGTTTC AGCCGAATTA AAAAAACAAA TAATAACAGA AACTTTATAC 325620
TTATGCACAA TATCCTCCAA AATAAAAACT GCTAAGCAAA ATCAACGCTA AAACACTTCA 325680
CAACAAATTC TTTTAATTTT TTGCATAACA ATTAAATTGT AATATATAAT TAACAAGTTT 325740
GTATTGTTTC AAACCTATTT TAATGAAAAG TTTAGCAGAA ATTGCTATAT TATTAAGT 325800
AAAAAATTTA AAAAACATCA ACCCAAATAA GGAGCTTGAA TGCTTGAAAT AATAAGTCTT 325860
GGAGGAGGAG TAATAAATTC AAACCAAATC AACATAGAAT TCATTAAAAA CTTTAAAAAC 325920
TTTGTTTTTA AATGGCTACT AGAAAATGAA AAAAGAAAAA TCATTTTAAT AGTTGGTGGA 325980
GGAAGAGTTG CAAGAGAATA CCAAGATGCT TATAAAAAA TCAATCCTGA TTTTAAAGTT 326040
CATGAACTTG ATGAGATTGG AATAATATCA ACAAGACTAA ACGCAGAATT TCTGAGTAAA 326100
GTAATGAATC CCTTTTGTA AGACAAAATT GTCACATAAT CCTTAAAAA TTTTCTTTT 326160
AAAGGAAAAA TATTAATTGC TTCCGGATGG AAATCAGGAT TCTCAACAGA TTACATTGCC 326220
GTAAATTTG CAGAAAAATT TAATAAAAAA GATATCATAA ATATAACAAA CGTAAATCAA 326280
GTTTATGATA AAGACCCAAA AAAATTTAAA AACGCAACAG CTTTAAAAA ATTAAATTGG 326340
AAACAATTAC AAAACATTGT GGGCCAAAAG TGAATCCAG GCTTAAATTT ACCTTTTGAC 326400
CCAATAGCAA CAAAAGTCTC TTCAAACTT GGAATACCC TTTACATAGT AAATGGAAAT 326460
AATATTGAAA ACTTAGAAAA AGTTTTTAAC AAAAATAATG ATTTTTTTGG CACTATTATA 326520
GTAAATAAAA AGTTAATGCC GGTATGGCGG AATTGGTAGA CGCGCCAGAC TCAAAATCTG 326580
GTGAGGGCAA CTTTATGTCG GTTCGACTCC GACTACCGGT ATTTTGATTG CTTTTTTAGA 326640

AGCTTCAAAA TTATCAAGCA TTACTAATAA AATAATTGCT TCTTTTAAGA AAAATTTTCT	326700
TTCATAAATT ACTTGTTTAT ACTAATAAAA ATTTAATATA AACCTTATGA TTAATAAAAT	326760
TTAATACTAT TAAAATAAGG ATAAAGCACC TCTTCAATA GGTTGTCCTT ATTCTAAAAT	326820
AACATATTGA AAATCATTTT AATTATAATA AAACTTTAAA GTCTACAAAT TAATTGCAAA	326880
TATAAACTTA AAATATCTTT GAGATTGTCT TCATTAAAGC TTCAGGATTA AAAGGTTTAA	326940
CAAGCCAACC AGTAGCGCCC GCTTTACGAC CCTCATCAAC CTTAGATTGC TCAGATTCAG	327000
TGGTAAGAAC AAGTATAGGA ACAAAGCTGC CAAATTCTCT TATCTGCTTA ATAACCCCAA	327060
TGCCGTCTAA ATTAGGCATG TTGATATCTG TAATAACAAG GTCAAAATCT TTATCTCCTT	327120
GCCCAACTGC TTCTTTAAAC CTTAAAACCC CTTCTAAACC ATCTTTTGCT TCTGAGACTC	327180
CAAAACCGTT TTGTTCTAAA ATATAAGCAA CGCTTTGCCT TATTGCCCTA TTGTCATCAA	327240
TAACCAAAAT TCTTTTTTTC ATCTAATTTT CTCCTAAAAC CCTCCTAAAA AGTATATAAA	327300
AATTAAAACA AAATTACACT ACCCTCATCA AAGGAATGAA CATCCTCGGC TTCCTCTATC	327360
AAAGATAATA AGTGTTTTTT ATGAACAAAT AAAGTAAATC GATTAGCAAT TCTATTAACA	327420
AATCTTTTAT CTTCAATCTC AACAGATTGA ATTCCAACCT TAGATAATTC TAAATTAAGA	327480
TTGAAATTTA TTTTGCTTTC CATATTGCTT AAAAAGTTAT CTATATCTAA AAGAGAATTT	327540
TTTAAATTTT TAACATTGTA GACTTCTAAT TTAATCTCTT CAAATATTTT CATAAATTCA	327600
ATTGAAAAAA CTTCATAAGA CAAAATATTA TCAATAGCTA TATTCTTAAT GTCAAGAATA	327660
TCATTTTTTA TTTCTATGAA TAATTTTTTA AATTTATTAA AATAATTCTT TTCAAGATAA	327720
AATCTATTGT CATAATCCTT AACAACTTTT TCAAGAAAAA AGATTATTTG ATCCAAAAAT	327780
TCTATTCCCT TGGTAATGTT AGAATCAATT TCTTTGATAA TCTTAGACAT TTCTGAAATA	327840
TTGCCCTCCA TGGCTTTAAG TTCAGATCTT TTGACAACTT CTATCTTTGA GGCTATATTA	327900
ATATTTTGAA ACCTAGCAGA AATAGCTGAA ATATTTGAAA ACATTAATTC TAATGATTTT	327960
ATAAGCTTGA CCTGTTTATA ATATAAATTC AAAAAATTAG AATTATTCTT CTCAACATCA	328020
TCAATTCTTC TAAGCAGATC AGACAAAATA CTAGAAAATT GTTCTATTAT TTTAGGAATA	328080
TCTATGTATA AAGAATTATC AGACCTTAAA TCGTTAATGG TTTGAATAGA ACTAAGAGAG	328140
GAATCAATAA ATTTCTCAAA AACAGPATAA TTTTTTTCAG GCTTTTCAAG AACATCTTTT	328200
ACTATACTT TTGATGTATC CGTAAAAACT GATAAAATTT TTAATTTTGT GATCTCACTT	328260
ATATCTCTAA ATTTAAAAAC ATCAATATTA GAATACATAA TATTTAAATG TTGCAAAGAT	328320
TGAGTTAGCC TGTCTTGAAA CTGAAGATAA GAAATAGAAT TTACAAGTTT AAACTTAAAT	328380

TCAGATAAAA CTTTAAAT ATCATCATAA AGAGCAATGA CACTTCCTAT TCCATCTGAA	328440
AAAGCATCTA TTTTTCAT TAAATTATCT CTAAATTCCT CAAGAATTTT ATTTTCAGCT	328500
GTATTGCTTT CATATACTTG ATTTTAGCT CTATCCAGAC CAATTTTAAC CTCGCGACCC	328560
TTGCTTGTA GTTGATCTGC CTGTTTGATC ATAGATTGGG TTAAACCTT AATTTCACTC	328620
GTAATATAAG AAAAGGCTCC ACCAGCCTTA CCCGCTCTCA TAGCAACTGT TAACGTATTA	328680
ATAGACATTA TTTCCATATC AAGAGAGCTT TTTTTCATTC TTTCAATAAC ATCTTCAAGT	328740
ATTTCTATAT CTTTAACCTT ACTCCGTATT ATGCTAAAT GAGATTCAAG AGAAGTTGTT	328800
GAAGAATTAA AGTAAGCAAC AAAATCATCT AATGCTCCTA TAATTTTGGC TATAAAATTA	328860
TTCAAAGAAG AATCATTATC AAGATCAAGA TTGGAAATCA AATCAATACT AAAAGATAAA	328920
TCCTTAGAAT CTTTAGAAAT TTTTCTATT AATTTAGGAA TTGATTTGCT TAAATTTGAA	328980
TAAATATGCC TTGTGCTTTC ATCAAAAGCT TCAAGTTTGT GAAATAAGGT TGCCAAACAA	329040
TCGTTGGCAT CAAAACCAT ATTGTCATTA TCCATTTTAA GATCTCCTTA GAACATGATC	329100
TGCTATTTTC CTTAAAGGAA GGATTTTGTC TACAGCCCCT ATTTTATAG CTTCCATTGG	329160
CATACCAAAA ACAACAGAGG TTTCTTGATC TTGGGCAATA GTATAAGCGC CATTTTTTTT	329220
CATTTCAAGC ATACAAACAG CACCATCATC TCCCATACCT GTAAGGATAA CTCCAATAGC	329280
ATTAGAGCCT GCATACATTG CAGCAGACCT AAAAAGTACA TTCACAGAAG GCTTATGTCT	329340
ACTAACAAGA GGTCCATCTA ATAGGTTTAC AAAATAATTT CCGCTACTAT ATTTTACAAT	329400
CAAATGATAA CTTCCATTAG CAATTATTAC AAGACCTGGA CGAAGAATGT CTCCATCCTC	329460
AGCTTCTTTA ATATCAATAT TAAACTCATT GTTTAGGTTT TTTGCAAAAG ATTTTGTA	329520
TCCTCCAGGC ATATGCTGAA CAATAATAAT TGGGGGAGAA TCTTTTTTAA AAGACCTTAA	329580
AAAAATTCTT AAAGCCTCTG TACCGCCCGT TGAAGAGCCT ACAACAATAA TTTTACCAGT	329640
TTTGTGCTTA TTGATAAGGC CTTGATATTT AATAATAACA TCCGGATCAT TTTTGGGAGC	329700
AAAATTAATA ACATCAGAAA CTCTATAACT TTTTCTTATA CTTGAATCAT TTAAATTATT	329760
TTCCCTCAGC TCTACTTTAG AATTACTAGA AAAATCGGGT GCTTGAATCC TTTTAACTTC	329820
AAAAGAAGAT ATTAATTTAT TTTTGCCTAG ATTTTCAAC TCCAGCTTTA TTAAAGCTAA	329880
ATACTTACTG CGAAATAAAT CAACTGTAAG CTTAAATTA AGCTTATTTA TTATTAATTT	329940
AACCTTTTCC TTGCTTTGCT CAAGACATCC AAAATTTGGT AACATTTTCAT TTTGAGCAAT	330000
AAATACAACC GGAAGAGATA TATTATTAAG GACATTGTTT AAAGAATTCC CAAAATTAGA	330060
TCTTGCTGTA TTCTCATCAA TAATACTAA ATCTGGAAAC TTTTGTAATA ATACATTAAT	330120
AAGATTTTAA GAATTAAAC CAGCATTTAA TATCTCAACA TCATTATCTT TAGAAAAAGC	330180

TCTAACAAAA ACCTGCTTTA TAAGACCTTG AATATCAATT ACTAATATCT TCATTATTAT 330240
ATTTTAATAT TTTTAACCTT TAAAACCAAA AAGCTGCATT TTCTATTTTC TATTTTCTTT 330300
ATTTTATAAG TTTAGTTATT GCATCTATGT CAACAACCAA AGCCAAACTT CCATCACCAA 330360
GTATAGTAGC TCCAGAAACC CCTTCTACTC GAGAATAAAT TTTACCCAAA GCCTTTATGA 330420
CAGTTTGATG TTGACCCAAA ACTTCGTCAA CCACAATGCC CATTTTCCCA CTATTTGTAT 330480
TTACAACAAC AACTTGCTCA CTTAAACTCT TCTCGCTAGA AACCTGAAAA AACTCTCTAA 330540
GCCTAATATA ACTAATCATG CTGCCCCTAT AATTCATTAC ATTGCTTTTA GTCTCAATTC 330600
CATCTATTTG AGAAATTAAC TTATTAGATT CTAAACAAGA TTCAACATTA GAAAGAGGAA 330660
CAATAAAATG CTCATCTTTT ACTCTAACAA GCCAACCCCTC AATAATAGCC AAAGTCAATG 330720
GAAAAATTAA CTTGATTCTA GTATATTTAC CAAATTCACT TTCAAGTACA ACATGCCCCC 330780
TTAAAGATTC AACCTGTTTT TTGACAACAT CCATGCCAAC TCCACGACCT GATATATCAG 330840
TAACAGAACT TGCAGTTGAA AATCCAGGCT CAAAAATCAA ATTATAAACA TCAATCTCTG 330900
ATAAGGTTTT GGCAACTGAA TCAGAAATTA TATTGCGCTC TATAGCTTTT TTAAGTATTT 330960
TATTCTTATC AAGCCCTCTT CCGTCATCCT CAATAATAAC AATAACAGAA TCCCCAGATT 331020
GACACGCTGA AAGCTTAATA ATACCTTTGG GATCTTTACC TAAACTTTCT CTCTCTTGAG 331080
CCGATTCAAT TCCATGATCT ATTGAGTTGC GAATTAAATG AACTAAAGGT TCATTTAGCT 331140
TTTCAATAAT ACTTTTGTCA AGAACAGTGT CGCCTCCAGA AGCATGATAA AGAATTGACT 331200
TACCAAGGCT AGTAGATAGA TCTTTTACTA TCCTTTGAAA TTTTACAAAC AAAATCTCAA 331260
TAGGAACTGT TCTAAGCCCT GTTGATATAAT CCCTAAGCTC ATTAATAAGC AAAGAAAATT 331320
CTGCTGATAT TGAATTTAAA ATATTACTAT TCCTATTTTC AGCTTCTTTT GAAAGTTTTG 331380
ATTGTATTGT AACAAGTTCT CCAACAAGAT TTACCAAATG ATCAAGCTTT TTAGAATCCA 331440
CCTTAATACT AGCAATATTA ACCTTGCTTC TAGCAGTATC ATCTTGAATA TTAGATCTAT 331500
TTTTATCTCC ATTGAAAAAG GATTTCCCAA CAAATGCCGA TTTTCAAAT GAAGAATTAG 331560
TCAAGTCTTT GCTGTTTCTG TCCAAGTGCA ACAAATTAAA ATTTTGTAGAC TCTACATTAT 331620
CACCTTCATT TGCCTCTAAA CATTTATCCA ATTCTTGAAT ATCAATTTTT GATTGAGAAAT 331680
CTAAAAATGT AAAAATATCT TCAATGCTCT CTCTACTCTC TTCTGTATCT AACCTTATCT 331740
CCCAATCAAC ATAAACATTA TCAGGAGAGA TAAGCTCTAA ATCAGGAATG TTATCTACTT 331800
TGGCCCTAAC ATAACCACTA CCCAAATTAA TCAACTTGCT CAATAAATTT ATAGGCTTGT 331860
GCCCATGAAA CAAAATACCC TTAGCCGGAG AAAAAAGAAT TTTGTAATC TTAAATTCAG 331920

ACTGCAAAGC CTCATCATCA AATTTATTCT CTGAATTAC TTAAACAGAC TCTTCCAAAA 331980
CCGAAGTGT ATCAGACTTT GAAAAATCAT TTTCTAAAGC TTCTTGAAAA GCTCCCTTAA 332040
CATCATTAGA AATATCAAGA ACCTTTCTAA TTTCATTTAC CAAAAACTGT TTACGCTTAT 332100
CAAAGTCGAT CTCAGAAATT ACTTCATCGC CTTCAATAAG CTCTCTAATA AAATCAACAG 332160
ACATTAAGGT AGCATCAATA GCCGCCTGAT TAAAAGCAGC CTTACCATTT TTTACAACAT 332220
CAAGAACTGT TTCTATTTTCG TGGACAAGCG ATGCTGTAAA ATTAAAGCCA AACATACCAG 332280
AACTTCCCTT TATGGTATGT AAATTTCTAA AAATAGAATT AACAATATCT TGATCTGAGC 332340
TTACCTCAAG ATTAAGAAGC GCTTGCTCAA TATCTGAAAT ATTTTCTATT GATTCTTCCT 332400
TAAAGGAATT CTAAATTTA TCAATAACAT CACTACTATC CATAAGCTTT CCTTAAATCT 332460
AAAATCCAAC TAAATTAAGT CCTAAATCAA AGCTATCAAC ATCTTCAATA TCTACTAAAA 332520
ACCCGCCATA TATTAATGAA CTAAAAACCT CATCGGATGG AACTCAATT TTTACAAACA 332580
AATTTCTATT CTTAGCATAT TTATTAGATG CATACAAAAT TTGTATAAAA GTAATATCTA 332640
TTTTTTCAAC ATTTGAAAGG TCAATAATAA GAGTATCCCC TTCTTTCATT TTCTTAAAAA 332700
TATGCAACAA ATCTTCTTTT ACCTTAAAAA TACTATTTAT TACAAGCTCT CCTTCAGGCC 332760
TATAAATCAT GACTAAAAAC TCCTATTGCT GCTGATATTC AGGATCATAT ATTGTTGTAT 332820
TTCTAAATTT AGAAAGCTCT CTAACGTCAA ACAAATTTTC TACATTTAAA ATAATAATAA 332880
ACTTATCATT ACTCTTGCCA ATTCCTGAAA TAAATTTTGA ATTAAACCTT GATCCAATCT 332940
TAGGAGCATC ATCAATACTA AATGGATCTA ATTCAAGAAC TTCATTGACA TAATCTACTA 333000
AAATTCCAAG ATTAAATTCA TCCCCCTCGT AAACCAAATT CAATATAATA ATATTTGAAA 333060
TGTTAACTCC CTATTCCCTC TTTTATCAT CCTCATCAAC AGCACGATCG CTCATTCCAA 333120
ATTGTTTTTCG AATATCAATT ATTGGAACGA TTTTGCCCCCT ATTATTTATT ATTCCTGCCA 333180
TGTAATTGGG AGTCCTTGGG ATTTTGTATA TCTTAGTATA TTCTAAAACC TCAACAACAT 333240
ATTTAATCTC AATAGCATAA AGTTCGTCCA AACTAAATAA AAGATACTGA CTAAAGAAT 333300
CTTGACATC TGAATCTGTG CTCATAAACG CCCCTTTGAA TGTAATTTAA ATCGCAAATA 333360
GAATGCTAAT ATCAAGATTA ATATTACCTC ATATATTGAT AAATACAAAT TAGAAGTTAA 333420
TAAAATTTAA TTTACCAAAA ACAATAAAAA ACATAATTTT AACAGAATTC TATCTTATAA 333480
TTTAAGGTAG AAAGTTGTAG GTTAAATTAA ATTTAATATA AAAAAGTTAA CAATGCAAAG 333540
TAAAAACAAA CTAATCAGAT TATTAATAAT TATTATCACA TTATTTTTC AATGTTGAAAA 333600
TATTTTTTACA AACGAAAAAT CTAAAAACAA TATAACTGGA CAAAACAGTA CAACTGATCC 333660
AAAAATAGAA AGCTTAAAAG CAAAAACTAA AATAAAATTT GGTTTTATTC TACCTTACCC 333720

TACTGCAATA GAATTCAGCA TTAATAACTT TGATATTGGA GTAGGGGTAA CAATATTGAG 333780
TGTCTCGGAA TTTTTCCTAA AATCACC AAT AGCATTGTTA TTTAAAATAT ATTGTGACTA 333840
TATATTTTTA AATTTAAAT TTAAAGATTC AAATTTTATC TTTTCTTGG GATCTAGCCT 333900
ATTTTTTGAA ATAGGCAAAA TTACAAGCTC AGATTTAACA AATGTTTCTT CTGGGATTAC 333960
CTATAAATC GGAGTGGGT TTGCCCTTGGG AATAATATAT GAAGCTTATT ATGACATTAT 334020
TGAAATTATA ATAAAAACAA CACCATCAAT TTTTATTGGC CAAATGCCTA ACGGAAATTT 334080
AATATTTCCA ATAAAAGGTA ACTTTTCTAT TGGAATAAAA GGCTCTCTTA AGATATAGTT 334140
TTCACTTTT AGATAAAAAA AATTATTGGA CTAAAATTCT TTTAAAGGCT AGAATGCTAT 334200
ACTTAGGAGA TAATAAGCA ATGAGAACAA AAATAATTAT TATGACAATT ATTATTTTAT 334260
TAGCCCCAAT CTCAGGATTT TCTAATTCAA AAGAATCTGC AAGGGGTAAA TTTGGAGCAG 334320
GAATTATACT TCCATTACCA ATTGCTCTAC AGATTAATAT AGGAACTTT GATCTTGACA 334380
TTGGTCTTTA CAGCGGAGTA AATAATTTGT TTTCAGACTG GAAAACATTA TTTATAGCAT 334440
TAGACTATAT TTTCTACATA TACACATTCC CGGGAGCTGC TAATATTTTG GATTTTTCAG 334500
TTGGCGCAGG GGGATATGGA ACAATATGGT TTTCAAGATT TGGAGGCAGT AAGTCAGGCT 334560
CAGGACCAAT GAGCATTGGA GCAAGATTGC CTTTGGCCTT AAATATTGCA GTATTTAGGA 334620
AGAAATTCGA CATATTTTTA CGAATAGCAC CCGGACTTGG AATGAATGTT TGGAGTAATG 334680
GCGTTGGATT TAGATGGGAA GTATTCGCAG GATTGGGACT AAGATTCTGG TTTACTTAAT 334740
AATAAAATTC TTTTAAATA AGTTTAAATA AAGAACAATT GTTGAAAAAT CAAACCGAGC 334800
TCCCAAAAAC TTAAACATAA GATTTTAAGG GCAAGGTCTT GTTTTATTG TTTTAAATTT 334860
CAAAAATAAA ATATAATAAT AAGACAAAAT TTGGGAGACA ACCGTGAAAA AAATTTTAT 334920
ATTGTTTATC ATGATTGCAA ACATATCTAC AAATGGTTTT ACAAAGATT CATATTTAAA 334980
TAGAGGAATT GGCTTTGGAG CAAGCATTGG AAATCCAATT ATTA ACTTAA TAATGTCATT 335040
TCCTTTCATT GATTTTGAAA TTGGCTATGG TGGTAGTAAT GGAATAAATC TATCAGGCCC 335100
CAAACCTGAA TCAAAATTTT ATGATTTTAA TTTATTAGCA ATAGCAGCAC TTGATTTTAT 335160
TTTTACAATA TCTTTGATAA AAAATTTAAA TTTAGGAATT GGAATAGGAG GAAATATAAG 335220
CATATCGTCT CACACATCTA AATTAATAAA TGTAGAATTA GGATTTGGAA TGAGAATTCC 335280
ATTGGTTATT TTTTACGACA TTACAGAAAA TTTAGAAATA GGTATGAAAA TAGCACCTTC 335340
AATAGAATTC ATCTCAAATA CAAGGTCTCT TGCTCAACAT AGAACCTATT CGGGCATAAA 335400
ATCAAACCTT GCTGGGGGAA TATTTGCTAA GTACTATATC TTTTAACACC AATTCATTCT 335460

AATTTATTAA ATTTATTGCC AAGCGCTATG AAAAAATTCA CCTCGTTTTG AGTCTAATCT 335520
TTCAAAAGAA TGAGCACCAA AAAAATCTCT TTGTGCTTGA ATTAGATTAG AAGGCAGATA 335580
ATTAGTAGAA TAAGAATCTA AAAACGAAAG GCTGGCATAA AATGCTGGCA AAGGAATCCC 335640
AATTTCACTA GCCTTTGAAA TTATTCTTCT TAAAGATTTG TGATTATTTT TTAGTAAATC 335700
TAAAAAATAA TCATCAAAAA GCAAATTAAT AAGATGAGGA TTTTATCAT AAGCCAATTT 335760
AATTTTATCT AAAAAACTGC TACGAATAAT ACAGCCTTCT CTCCAAACCA AAGAAATTTT 335820
ACCTAAATTC AAATCCCAAC CATAATTCAC AGACGCGGTC TTAAGCATCA TAAACCTTG 335880
AGCATAAGCT ACTATTTTGT AACTAAAAG AGCATAATAA AGATCTAAAA TCCAATCACT 335940
AAGCTCAAAC TCAAAAGAAG AAGTATCCAT CTTAAGTAAA TCGCTAGCAA TAATCCTTTC 336000
GTGTTTTAAC CCCGACATAA ATCTTGAAAA AACAGATTCA ACAATTAAAT TTACAGGCAC 336060
ACCAGATTCA AGAGCATCAA TAGCTGTCCA AACACCAGTG CCTTTTGTAT TTGCAATATC 336120
TAAAATCTTA TCAACTAAAT ATTCATTATT TTCTTTATAT TTAAGAATCT TAGAAGTTAT 336180
TTCTAGTAAA TACCCTGAAA GATCGCCTTC ATTCCATTTT TCAAAAACCTT CAGAAATTTT 336240
CAAATTATCT AAATTGAAAG CTTTTTTCaT GAAAAAATAA ACCTCGCTGA TAAGCTGCaT 336300
ATCAGCGTAT TCCACTCCAT TATGTATCAT TTTAACATAG TGCCCAGAAC CGTTCTCCCC 336360
AATATAAGTC GAACAAATAT CATTATTTTT AGTTTTAGCT GCAATTTTAT TTAACATGGG 336420
CTCAAGAATT TCATAGGCTG ATTTACTTCC TCCATACATT AGCGCAGGAC CAAATCTTGC 336480
TCCTCTCTCC CCTCCAGAAA TTCCAAGTCC TACAAAATAA ATGTCTTTAG CAAACAATTC 336540
TTTTTCCAAT CTCATTGTGC TCTTATAATG AGAATTCCA CCATCAATAA TTATGTCTGA 336600
TTTATTCATA AAGGGTAAAA TTTGCTCAAT AACCTTTTCT ATAGCAGAGC TTGTCACCAT 336660
TAAGATGATT TTTTTTGGAG TTTTAAAGCT TTTAACAAAA GATTCAATAT CTTTAAACC 336720
ATTTATCTTT TTATGAGAAT TTTGTTTAAAC AAAAAATTCA GTTTTTTCAT TATCTCTATT 336780
GTAAACAGAA ACATTAAAAAC CGTTATCAGC AATATTTAGA GCTAAATTAC TACCCATAAC 336840
ACCAAGTCCA TAAATTCCTA CATCCATTGC ATTCTCCTTG ATTCTAATTT TCTATTTTAA 336900
ACAAATTGCT TTATTTATTA TTTTGTAGATT ATGTTATATT ATAAAAAAG TAAAGATTAA 336960
ATTGAAAAGG AAAAGTTGCA TGAAAAACA ATTTGATACA GAAGTAAATG ATTTGCTTTA 337020
TTTAATCATC CACTCTCTTT ACTCCCATAA AGAAATATTT TTAAGAGAAT TGATATCAAA 337080
TGCGTCTGAC GCCATTGATA AACTCAAGTT TTTAAGCTTG ACAAACGAAA AATTCAAAAA 337140
CATTGCTCTA GAACCAAAAA TAGAAATATC GTTTGATGAT AAAAGCATCC TAATTAAAGA 337200
TAATGGAATC GGAATGGATG AACAAGATTT AACTAATCAT CTTGGCGTAA TTGCAAAATC 337260

AGGAACTAAA	GAATTTATTA	ACAATTTAAA	ACAAGATGAA	AAAAAATCTG	CAAGCCTAAT	337320
TGGCCAGTTT	GGAGTTGGAT	TTTACAGCGC	ATTCATAGTA	TCAGAAAAAG	TAGAAGTTAC	337380
ATCAAAAAAA	GCATTAGAAA	GCGACGCATA	TATTTGGTCT	AGCGACGGCA	AAACAGGATA	337440
TGAAATAGAA	AAAGCAAAAA	AAGAAGAGTC	AGGTACAGAA	ATAAAGTTAT	ATCTTAATAA	337500
AGAAGGCCTT	GAATATGCTA	ATAAATGGAA	AATTCAAGAA	ATTATCAAAA	AATATTCAAA	337560
TCACATAAAT	TATCCCATT	ATATTAAATA	CAGCGAACCT	ATAATGAAGG	ACGGGAAACA	337620
AGAGGGAATA	GAAGAAAAAG	AAGAAAAATT	AAATGAAACT	ACTGCTCTTT	GGACAAAAAA	337680
TAAAAGCGAA	ATTAAAGCAG	AAGAATACAA	TGAATTTTAT	AAAAATACAA	CCTTTGATTA	337740
TGAAATCCA	TTAATGCATA	TTCATACAAA	AGCCGAAGGA	AATTTGGAAT	ATACTAATTT	337800
ATTTTACGTC	CCAAGCAAAG	CTCCCTATGA	TTTATATTAC	CCAAACACTA	AGCCTGGGGT	337860
AAAGCTATTT	ATAAATAGAA	TCTTTATTAC	AGATTCTGAA	GGCAGCTTGC	TTCCAAACTA	337920
TCTAAGATTT	ATAAAAGGAA	TTATAGACTG	CCAAGATTTG	CCACTCAATG	TAAGTAGAGA	337980
AATTTTACAG	CAAAATAAAA	TTTTGTCTAA	AATAAAATCA	TCTTCTGTAA	AAAAAATACT	338040
AAGCGAGCTT	GAAAAGCTAA	GTAAAAAAA	TCCTGAAAA	TTTTTCAGAGT	TTTCTAAAGA	338100
ATTTGGGAGA	TGCATTAAAG	AAGGTGTTTA	TTCTGACTTT	GAAAACAGAG	AAAAGCTTAT	338160
ATCATTAAATA	AGGTTTAAAT	CCTCAAGTGT	AGATGGGTTT	GTGTCTTTTA	AAGAGTATAA	338220
AGAAAGAATG	AATGAGAGTC	AAAAAAGCAT	TTACTACATA	ACAGGCGGTA	AAGAAAATAT	338280
ATTAAAAGAA	AACCCAATAG	TAGCTGCTTA	TAAAGAAAA	GGATTTGAAA	TCTTAATCAT	338340
GGACGATGAA	CTCGATGAAG	CTATTTTAAA	TCTAATTCCA	GAATACGAAG	GATTAAAACT	338400
AAAGGCAATA	AATAAAAACG	AAACCAGCAA	TGAATTAAAA	GATGAAAATT	TCAAAAAAAT	338460
TGAAGAAGAA	TTCAAAGATA	CCCTTACAAA	AGTAAAAGAA	ATCCTCAAGG	ATCATATAAA	338520
AGAAGTCAAT	CTATCAGCAA	CATTGATAAA	AGAGCCTTCA	GCAATAATAA	TTGATAGCAA	338580
TGATCCAACT	TACCAAATGC	AAAAAATCAT	GCTGTCAATG	GGACAAGAAG	TAAAAGAAAT	338640
AAAACCAATA	CTTGAATTAA	ACCCTAATAA	TAAAATAGTC	CAAAATTTAA	AAAATCTAGA	338700
GCCTGAAAA	TTAGAAAAAA	TAAGCATTCT	CCTTTTTGAA	GAAGCTATGT	TAACCTCAGG	338760
AATGCCCAGC	AAAAATCCAG	GAAAATTTAT	AAATATAATA	AACGAATTTA	TAGAAAAAGA	338820
CTTCTTATAA	TTAAAAGTAA	AAAGAGAGAG	TTTTAAGCTC	TCTCTTTTAA	CTTTTAACT	338880
CGCAACACCA	AATCTTTGCC	CGCTATAACA	GGCTTTGTTT	GAGATATTTT	ATGCCTAATT	338940
TCTTCTGTCA	AGACAGTTGA	AGATGATAAA	ATATATTCAG	AATCATTTTC	AAGCCTTCCA	339000

AAAGAATATT	CTATACTTGA	AACTTCATCA	GAATTTGCAA	TAACAACCGG	AGTAATAACG	339060
GATTCTGAAT	GCTCTTTTAA	ATATTCAAGA	TCAAGCCTAA	TAATAACTTC	ACCTTGTTTA	339120
ACATTAATGC	CCTCTTCAGC	AACTCTTGTA	AAACCCTTAC	CATTTAAATT	AAGAGTATTA	339180
ATTCCAAAAT	GGACAAAAT	TTCAACGCCC	TCTTTAGTTT	CAAGGCTAAA	GGCATGATTG	339240
GTTTTAAAAA	TTTTACCTAT	TTTCCCATCA	CAAGGCGCCA	ACAACTCATT	GCTTGTTGGA	339300
AGAATTGCAA	TTCCATCGCC	AACTATTTTT	TCAGCAAAAG	CTTCATCGGG	AACCTTATCA	339360
ATTGACATAA	CTTTTCCACT	AATCGGAGCA	ATCAAATCCA	ATGTAGCGGT	TTTTTTAAAA	339420
AAATCTAAAA	ACCCCATAAC	TAATCTCCTA	TAAATTTATC	AAAATAACTT	AAAGTTTCTT	339480
GCTTGGAATC	ACTATTTAAA	ACCTTATTTG	CCAATTCTTC	TAATTCCATT	ATTGTATACT	339540
TTTTAAGCAA	ATATTTAATT	CTAAGCGTAG	CACTAGGAAT	CATGCTTAAA	GACCTAAACC	339600
CAAGGCCTAC	AAGAAGCAGT	GCTCCAGCAT	CATCTCCTCC	AAGCTCACCA	CAAACAGACA	339660
CATCAATTCC	AGAACTAACC	CCATCATCAA	GAACCTTTTT	GATTAATTTT	AACACAGCAG	339720
GATTATACTT	GTCATATAAA	TTTGATATCT	TTTGATTACC	ACGATCAACA	GCTAAAACAT	339780
ATTGGGTAA	ATCGTTAGTC	CCTATGCTAA	AAAATTTCAA	TTTATTGGCA	AGTTTAGAGG	339840
AAATTAAAGC	TGCAGAAGGG	ACTTCTATCA	TGCAACCCAC	TTCCAAATTT	TCATCAAAAG	339900
GCAAGCCTCT	AGACTTTAAG	TTGATTTTTG	CATTATTAAC	AAAATATTCT	ATCGTTTCGA	339960
TCTCTTCATA	TATGGTAAGC	ATAGGAACCA	TTACCCCTTAT	CTTACCATAA	TGACTGGCCC	340020
TAAAAATAGC	ATTAAACTGC	GCCTGGATTA	ATTCCTCATA	TTCTTTATAC	ATCCTAAGTG	340080
CCCGAAAGCC	CAAAAAGGGA	TTTCCCTCTT	TCTTAAATT	AAGATAAGGA	ATTTCTTTAT	340140
CACCACCAAC	ATCAAGAGTA	CGAATCGTAA	CAACCCCTTT	CTTTTCCATT	GTTTCTATAA	340200
CTCTCTTATA	AGTTTCAAAC	TGCTCATCTT	CTGTTGGAGG	TTGTAAAGAT	CTCATATATA	340260
AGAACTCTGT	TCTAAAAAGA	CCTATTCCCT	CAACACCATA	TTTATTAACA	TAGGTAATAT	340320
CAACAGGTGT	TCCAATATTT	GCCTTTAAAA	ACACCTTTGT	GCCATCTTTT	GTTTCAGCAT	340380
CTTTATCTTT	TAAAGAAAAA	AGCTCTTTTT	CTAACTCTAC	TTGTCGCAA	ATCTTACCTT	340440
CATAAGATT	AATCTCATCA	GAAGAAGGAT	TTTTAATAAC	AATAGAAGAC	ATTGCATCAA	340500
TTACTATTTT	ATCACCATCC	TTTAACGCAT	CAATATCTGA	CAAAGTCATA	ACAAGCGCTG	340560
GAAGCCCCAT	TGTTCTTGCT	AAAATAGCAG	CATGAGAGGT	TTCTCCTCCA	ACAGCAGTTA	340620
AAAACCCTTT	AACATAATTT	AAGTCAAATT	GCATGGTATC	AGATGGGGTT	AATTCTCTCGG	340680
TAACAAGAAT	AATATCTTTA	TTAATCTCAG	AAAAATCGGA	TACTTGGCCT	AAAATGATAG	340740
AAATTAATCT	ATTTCTAATG	TCCTTATAAT	CAGACGCTCT	TTCTTTTAAA	TAAGGATCTT	340800

TATAATCTTC	TACACTTTTA	ACCAAATTTT	CAAACGCTAA	ATAAATAGAA	TAAGCAGCGC	340860
TATAATTTTC	CTTTACAATA	AGCTCAATAA	CAAGCTCATC	AAGTTCATCG	TCTTCAACGA	340920
TCAACACCTG	ACCTTCAAAA	ATACCTTTTT	TATCATCTCC	AAATTGAAGC	ATAGCTTTTC	340980
TCTCAAGATC	CCTAAGCGCT	TCAATTGCTT	TTGACTTCGC	TTTATTGAAT	TTTGATATCT	341040
CGCTATCAAC	CTGAGAAAAG	TCTATTTTTT	CTCTACTTAT	AATTTTATCA	AAATTTTTCC	341100
TAATACAAAG	AACTTCCCCA	ATGCCTATCC	CTTTGGATAT	TCTTTTGCCC	GATAAAGTCA	341160
TAACTTAAAT	CCTTCTAAAA	TTCATTCCCT	AAAAGATTCTG	ATAAGCTCTG	CAAGCTCTGA	341220
AGCAGCAATC	TCTTCATCCT	CACCTCAGC	ACATATCAAA	AGCTTTTTTAC	CTGATGATAA	341280
TTCCAAAGTT	TGAAGCCTGA	ACAAACTTTT	TCCGCTAACA	GACTTTCCAT	CAGATTCTAT	341340
TGTTATCTCG	CTAGAATACT	CTTTAGCTTT	TTTACAAAA	GTTGATGCAG	GCCTAACATG	341400
CAAACCGTTT	ACAGCCTTAA	TAATTGCTTC	TTTTTTTACC	ATAAGTACAG	AAACCCCTCA	341460
TTATGAATAT	TGTTTTTTTT	GATTAACCTT	TTACATTATA	ATACATAAAA	ATAAATTATA	341520
TATTCCCTTT	ACATAAGAAA	TATAGCATAA	TAAAGATAGT	AATTAACTT	ATTCTAACAA	341580
TTAAAAATTA	AAACTCATTA	ATATGTCTAA	ATAAAAATTC	TTTATTAGCT	TTAAATTTCT	341640
CTCTCCTATG	TTGAAATTTT	TAGAATCTCT	TATATTTTTA	TCCAACATTT	TAAGAGAATT	341700
TTCTATCTCA	GAAAATGAAA	GCGGCAAAGA	TTTGTTTAAA	AGTAAAATCT	GGAAATCCTT	341760
TATGACTATC	ACCTTGTCAT	CATAAAATAT	CTTTAACAAA	AAATCATTTA	TAATGTCTCT	341820
TTTTATGTTT	AAAAGAATAC	ATATAAAAAT	AATGTCCGAT	TCTTCTAAAA	TGTCAAAAGA	341880
CAAAGTATTG	AAAAATATTT	TATGATAAAA	GCTTCTGTTC	CATAAATTCA	TCATTGGAAA	341940
TTTAAATTTA	GTAATAAGAA	CAGTGTTTCG	ATTTGCAATA	TATTCAGCTC	TATTTAAATT	342000
ATAAGCACTA	AAAACATAAG	TTTTTTTGGT	TAAAACATTT	TTAAACTCAA	TTTGAGCATC	342060
AAGACTTATC	AACAAAGGAT	AAATATCAAA	AACGGTGTTT	TTATAATAAA	ACCCATTTGC	342120
AAGGTTAATA	CTATTTAAAT	ATATTTTATC	ATTAAATTTT	GAAATAAATT	CATAAAACAA	342180
ACTTGGAATA	TTTTTCTTAC	CAATCCGAAG	TATCTCGTTG	TAAGTCACAC	AAGGCCCCAT	342240
CTCAAGAAAA	TTACCCCTTA	AAGATACCTT	ATTAAATTTT	TCAAAATTAC	CAACAATAAA	342300
AAAATTATCA	ATGGGTGTTT	CTCTATTAAA	CAAATCAGGA	TTTTTTTTTAA	AATCCAGCTC	342360
ATTATAAATG	ATATAATTAT	TTAAATTTTT	GTAAATAAAA	TTAGATAGTA	TATTAAAACT	342420
TTCAGGATAA	TAAACCTTAA	CATTAGCCAT	TTTTTCTATA	CAATTCTTCA	GCTTTCAAAT	342480
AAAGAGATAA	AAAAGTATTA	ACATCCATAC	AATTACATTT	TAATGACTTT	CTATAGCCTA	342540

AAATATCTGA TTTGCTTACA ATCTCGTTTT CCAAAAAGTA ATAAAACAGC AAAATATTAG	342600
ATTCAAAACA ATTGCTACAA AAATTAAAAAT CGTCTTCTAA TAAAATCTTT TGCATGTGCT	342660
TATAAAAAC TTTTTTCTTA AGTCCTTCAA GGGTAACTAC ATTCCGACCA TTTAAAATAA	342720
AAGCGGGAAT TAAATCAGAA TAAACAAGTT TGAAATCCAA TAAAATTAAA AAAAATCTGT	342780
TATTAACAAT GTACTCCAAA CTATTGCTCT TAGCAAAAAA AATAGAATCC AAAAGATTTT	342840
TGGTCCCCAA AGAAAGACTA ATCTTTTTTG AAATACTCTC TCCATTTAAG TTGAAATTAA	342900
TTAATGTCAA TTTTATACT CCAACTATTT AAAATTTCTT CAAAATCAAG GGGCGTTTTG	342960
CTTGCAATTAA AATCAAATAC CTGAATCAAA GCAGTTCGAA TTGCAGAAAC AGAAACAATA	343020
AAAACACTTC TAAAAGAAAA AATAAACTCG CCATCTTCAA TAAACTCTAA GCTTAAACAA	343080
TCTTTAATAT CGCAACTTAC ATTAGCACGA CAAAATACAT AATCAACCGC TAATCCAAAT	343140
ATTGTGCGAA TTCTCTTGTT ATTTAACTTA AGCTTAGTAA ATTTGCCTTG TTCTACAAAA	343200
AAGCTCACAT TGCTAAAAAC AGCGCTAAGA GAATAAAATT CAAATTTAAG CTCAACAGAA	343260
CACCCAAGCA CACAATCATT AACATCGCTA ATAGCTATTT TTTCTTAAA AACTACAGGA	343320
TATTCATTTA TAAAATCTGA ATCTATCAAA GAAGAAAAAT TGTCCTTAAT ACTTAAATTT	343380
GCTTTTTCAA TTAAATAAGG ATCTTTAAAA AGAAGGTTAT AAAAATTACC AAAATCTAAT	343440
ACACTCTCGC CTATCAAAAA ATTTACACTG CTATAAGGCA AGCCCAGTGT TTTAGCCAAA	343500
CTATTTTTCA AATAATTGCT TAAATTGTTG TCAATAATAC TGTAGGGCAA AAATACATTT	343560
AATCCATCCT TGTATAAGAA AGCAACAACA TATTGCTCTT CGCTTAAAA ATAAGCACTT	343620
GAATTCAAAT AAGCAAAACC AACTCCCCTT CGACTAGTAT CAAAATGTC ATAATCCTTA	343680
TTAACACTTA AAACGGCAGA TTTCTTTATT AAAGAATTTT TTAAATCTAG TTTTTTAAAA	343740
ATTTTTAAAA AACTAGCATA ATCACCTTTA ATCTGTGTAA GCAAATAACC TATTGGCTCA	343800
CAAGACATCG ACAAAGCAAG ATTATAAAAA TTGGAATAAA TAAAATTATA AACAGAAGTC	343860
TCAAATGCCA AAAGATTGTC ATAAAAAAG ATAAAATCGC TTTTATTCTC AACAAAAAAA	343920
ATTTCTAAAA ACCCATCAAA AAACAAATTT TTGAAAATAT TATTAATAAA TTTAAAATAA	343980
AACTTATATA AAAAATTTAA AGGTCTATTT ATTATAATTT CTAAAAAAT TTTTGAGAGC	344040
TTATTATCCG CCACTAAACA ATTAGAACT GAAAAAGTTA AATTAAATT ATCTAAAATT	344100
CCAAAATGTC TTTTGTAGTA AACAATATTA ACCCTTTTAT TAATCTTTTT TGAAATTACA	344160
ATGCCTTGTA AAATTGCATT AAAAGAAATA GGGAAAATAG AGCTAGACCA GTAATTATCA	344220
AGAGAATTTA TTTTATTTT GTCTTTACTT ACACCAAAAT TTTCACTAAT AAAAAATTTT	344280
AAAAAAGAAA TATTGTCTAC ATTAGCATCA ATAATTAAAT TTTCAGAATC AAAAAATATT	344340

TTAACTAAAA	TAAAATCATC	TGAAAAACTA	TTGTAATCGC	TAAATTCATA	ACAAGCATT	344400
AAAACATTGC	AAGTTCAG	CTCTTTCTTT	GTAAATCCAG	AAGAATAACT	ACTATTCGCA	344460
TCACCAACTC	TTAGATTAAA	AAGAACACTT	TTTTCTGCTT	TTAGTAAATA	ATCCAAATTG	344520
TCTGAATACA	AAACCAAAGG	AATTTGACCT	TCAAAGCTTA	TTTTATTGTC	AAAAAGCTTC	344580
AAGTTAAATT	CATTAGAATC	AACAAAATCT	CTAAACTTTA	AAGTTATATT	ATCTTTATAA	344640
CTGATGCTAA	AAATTGAATT	TACATGTTCA	TCTACAAAAC	TAAAATCTTC	AATAAAAGAA	344700
TCTTTAACAT	TGCAGCAAAC	TGGCAAAGCC	CAAAATTCAT	GCGCATCCAC	ATTTGTTAAA	344760
CTCAAAAACT	CCACCAAACA	AAAAAATTAA	ATTAGTAAAA	ACCTAACATT	GCATAAATAA	344820
AAAGGATTAA	AAAATAAAAC	CTCAAAAACA	TCCGACCCTA	CCCAATACAT	GCAACAATCT	344880
TAAAATAAAT	TAATAAAAAA	TTCACTTAAA	ACTAATTTGA	AAACAGCACT	ATTTGTCAAT	344940
AAAAATAGCC	CCCGGCTATT	TTTATCTCTT	TTGATAAATG	GACAAATTAT	GCTAACATTA	345000
TAAATTATAG	ATGTTTTCTG	AATAAAAACA	AGGACCTTAT	GAATAAAACA	AAAAATCGAA	345060
GCCTTACGTA	TTTTATAATA	CTTTCATGTA	TATCATTATT	TGGGGCTAAT	AATAATACAA	345120
TAAGCTACTC	TAGCATTGAA	ATTCCTCTAG	AAGACTTAAG	TGAAGAATTT	AAAAGTTCTG	345180
GGAATAAAAG	CGATCAAATA	AATACCTCAA	AACATTTAAA	CAAAAACATA	GTTTCTTATG	345240
AAGACCCAAA	AAAGGGTAAA	GATCTAAAAT	TGCCAGAAAA	TATAAGAGAC	AAAAAACTAC	345300
CCCAAAAAAG	AATGGACGAA	AATGATCTAA	AATCTGTAAT	TGAAAATTAT	GAAAATAAAA	345360
TTAAAAACAT	AGAAAAAGCTT	TTAAAAACCA	AAAATCAAAA	AACATCGGAA	AATGAAAATA	345420
AAAAAATAGA	ATCAATCGAA	AAAAAAGCAA	AAAAATATGA	AATTTTAACC	AATAAATTAA	345480
AAAACGAAAT	AGTAGAAATA	AAAAAGCTCC	TTAACAAAAA	AATCAAGCCT	AAAGAAGATG	345540
AAAATTACGA	AAAAATAAAT	ATTGAAAACA	TTGAAGAAGA	AACTGATGAT	GATTTTGAAG	345600
ACAATTATGA	ATATAATGAT	GAAATTGAAG	mAACAAATGA	GGACAATTAC	CCTTCTAATG	345660
AAGGAATAAT	AAACAATCTA	AAAGAAAATC	TTAATGAAAA	CGAAAAATAT	TATGCTATTA	345720
ATGAAAAAAA	AATCGATGAA	CTTGAAGACA	GAATCAACGA	GAATGAAAAC	ACTATTTTAG	345780
ACTTGCAAAG	AGAATTAAGG	AATTTTAAAA	AAAAAGATAA	CTCAGATAAA	AACTTAGAAG	345840
AAATTGAGGA	AAATTTATCT	TCAATAGGAA	GAATAATTAA	TGATCTAAAA	AGAAAAATCA	345900
GCGCAAATGA	AGCAATAAAC	AAAGAAAATC	AAAAAAAAT	AAGAACTGAT	AAACACAAAC	345960
TCAAAGAATT	AGAAGATAAA	ATAAAGGAAA	ATGAAGAGAC	TATTTTAAAA	CTTCAAAAAG	346020
AATTAAACAA	TTTTAAAAAA	AAAGAAATTT	ATCAAAAACC	CTTAAATGAA	GAAACTTTCA	346080

CTCCAAGCAT	TACAAGTAAA	AATGACGACT	TAGAAGAAAA	TAAGAAATTA	AAAAAGGAAT	346140
ATTTAAAGCC	CATAGAAAAA	AAAGAAAGCC	GAGATCTAGA	AGAAAATACT	AAAAGCACCC	346200
CAAAAACAAC	TATGATAAAA	ACAGCAGATT	TTCAAATCTA	CCCTGACATA	TATCTTAATA	346260
ATTATAAATT	TAAAGAAAAG	GGAGATCAAT	TTGCATTTAA	AAAAGAAAAC	ACATACTATA	346320
TTGAAATAGA	TCCCACTAAC	AATTTAAATG	AGGCTTTAAA	AAATCATGAA	ATAATCTCAA	346380
AATATAAATT	TGAAAAATAT	TTCATTAACC	CTATTCTAAA	AAATAAGAA	GAATTTTTTTA	346440
GAACTTAAT	AGAAGTCAAA	AATATCCACG	AACTAGGAAT	TATGTATAAA	AATCTAAAGC	346500
CTGAATTTAA	GCAAAATAAA	ATAATTAAAT	AAAAATAAAC	ACTTTTATCC	AACTAATCTA	346560
AGTAACTTTT	TATGTCTTCA	AAAGACATAA	TTTTTATATT	TAAACTCAAA	GCTTTTTTTAA	346620
GCTTTGATCC	AGCTTTTTCT	CCTACAATAA	GAAAATCTAA	ACTCCCAGTC	ACACAAGTAT	346680
TAAAAATTGC	TCCTTTATTT	TTTAGCTTAT	CAATAATAAT	AGACCTGGAA	TAACCATTAA	346740
AAGTTCAGT	AATGCAAAAC	TTTTTACCGG	CCAATAACTT	ATTCTCACCA	TCAATCGCAA	346800
CAACCTCTTC	CATTTTAAAT	TCCAAATTTT	CAAAAAATTT	AAACTTATTA	AGCATTA CTG	346860
AATCATTA AA	AGCTTCAATA	ATATTTAAAG	CAATTTTTTC	TCCTATGCCT	TTAATTTTCA	346920
ACAATGTTGA	AAATGCAAAA	TATCTGTCTT	GACAAAGCTT	AAAAAGCTTT	GAAAATGAAT	346980
TTAAATTATT	AAGAAACAAC	AACCTTATTG	TATTTTCCCC	TAAATCTTTA	ATTCCCATAC	347040
TAAGAAGTAA	TTTACTAAAT	GGTTTTTTTT	TGCTAGCTTC	AATTGAATTT	ATCAAATTAT	347100
TTATCTTTCT	ATCTTTAAAC	CCTTTAAATT	CAAGAAGCTT	ATAAAAATCA	AAAGTATAAA	347160
GATCAATTTT	TGAAAAAATA	AATTTTTTTT	CAAAAAGAAA	AGAAATTATC	TTGTCTGGAAA	347220
ACCCTTCAAT	ATCCATACAA	TTTTTACTAC	AAAAATATTT	TATTCTCTCA	ACTGCTACTG	347280
AAGGACAATT	ATTATTTGGA	CAAAAAAAT	GTGCCCCCTC	TTTTACTACA	GCCGTTTTAC	347340
AAGCTGGGCA	ATTATCAGGA	ACTTTGAAAA	ATCCTGTTGA	AAATTTATTT	ATCACCATTT	347400
CAACAGCAGG	AATTACATCT	CCTCTTCTTG	AAACTTTAAC	AACATCACCA	ACATTCAACC	347460
CAATAGACCT	TATATAATCT	TGATTGTGTA	ACGTTGCACT	AGTAATAAAA	GCTCCTGAAA	347520
CAAAAAC TTT	ATCAATATTA	GCAACCGGAG	TAATTTTACC	ACTACGTCCA	ACCTGAACAA	347580
CAATGCTATT	TACCCTACTA	AAACCCGAAA	GCGCTTCAAA	TTTGTAAGCC	ATTGCCCATT	347640
TGGGATGATG	TGCAGTATAC	CCCAATCTTT	CTCTTAAAGC	AAAATCACTA	ACCTTAAGAA	347700
CAACACCATC	TATTT CATAT	TCAAAAGAAT	CTCTTTTTTT	TGTTATATCT	GCTATGTAAT	347760
TTAAAAC TTT	TCCAATTGAA	TTTTTTAGAT	CAAAAAACCT	AATCAAGGGA	TTGACTTTAA	347820
AACCCAATTT	CTTAAGTCTT	GCAGTAGCTA	AATCATTTGGT	TTTAAATTCT	AATCCAGCAT	347880

TCAAAAAATC	ATAAATGAAA	ATATTTTAAAG	GAAAATTAGC	GACTTCTCTA	CTATCAACCC	347940
TTCTAAGTAT	TCCCGAAGCC	AAATTTCTAG	AATTCGTATA	AGGCTTTTCC	AAAAATTTAT	348000
TTATTTTCAA	AAAATTTTCT	TTAGTAATAT	AAACCTCACC	CCTTAATACT	AAATCAACCT	348060
TTTCATCAAG	AAATAAAGGT	ATATATCTAA	TGGTTCCTAAC	GTTTATAGTA	ACATCATTAC	348120
CAAATTTTCC	ATTACCTCTA	GTAAGAGCTT	TTTCAAGAAC	GCCATCTTTA	TAATAAAGAA	348180
CGATAGAACA	TCCATCAATC	TTTGGCTCAA	CAGAAATGTT	AAAAGAATTA	TTAAAAATCAA	348240
TCTTATCTAT	CCATGATTTT	AGCAAAATCAA	GATCATAAAC	CTTATCAAGA	CTTAATATAG	348300
GTGCAGAATG	TTCAACCTCT	TTAAAAATCAT	TTAAAAGATC	GCTGCCAAAT	TTAAGAGTAG	348360
GAGAATCTAA	GGTCTTATAT	TCAGGGTACT	TACTTTCTAG	CTCTTGAAGC	CTTAAAAATAT	348420
GCTTATCATA	TACAAAATCT	TCAACACTAG	GCAAAGAATC	GACATAATAT	TCTTTATCCC	348480
ACTTTCTAAT	CAACTTCTTC	AAGTCTGCAA	TTTCTTGCTG	TACTTTGCTG	CTCATAGGGT	348540
AAAATTTAAC	ATATTCTTTA	TTATTTTATC	AAACAATTCT	AACAAGCAAA	AACCGACTTT	348600
ACTATACAAA	CTGTAAAATA	CCACCAAAAA	TACATGCTAT	TTTATTTATG	TTCAAATTAA	348660
AATAATCTTT	AAAGAAAAAT	ATCAATCAAA	AAGACAATAT	TATAAAAAATG	TGAATTATAT	348720
TTTAATTGTC	GTTAAAGATA	TTTTAATATG	CTAGAATGGA	TAAAAGGAGT	GCTAGTTTGG	348780
AAGAAAGCAA	AAAAGCTTTA	ATAGCTGATG	ACTCACTTTT	TATGAGAAAA	AACCTAATAA	348840
AAATCTTAAG	TCAATTGGGA	TTTAAAGAAT	TTTTAGAAGC	CGAAGATGGC	ATTCAGGCTG	348900
TTAAAGAATT	TGAAAAACAA	AATAATATTG	ATTTAATAAC	ACTCGATATA	ACAATGATGG	348960
GAATGGATGG	AATCACAGCT	CTTGAGAGAA	TGTATGAAAT	TAATAAAAAA	TTGCTTAAAA	349020
AAGTTAATAT	ATTAATGGTT	ACAGCTATTG	GAAAACAAGA	ATTAATACAA	AAAGCTTTAT	349080
CTCTTGAGAC	TAGAGGATAT	ATTACAAAAC	CTTTTAAAAA	AGAACAAATA	ATAGAGCAAA	349140
TTAAACTTTT	GGATTAGAGG	AAATTTTGAT	AGCAAAAAGAA	AAAATATACA	AACAAACACA	349200
AGTAAACACA	TCAAATCCCC	TATCAATATT	GATAATGCTT	TATGAGAAAG	CAATACAGGA	349260
TTTAAAAGTT	GCAAAAGAGC	TTATAAAAGA	TGAAAATTGG	CAAAATGCAG	TTAAAGCTAA	349320
TGAAAAAATC	TTTCATGCAC	AAGAAATCAT	TACTGAATTA	ATGTCAACCT	TAAATTTTGA	349380
GCAAGGCGGA	AACATTTCTA	CAAATTTACT	CTCAATATAC	TTGTTTCTAA	ATAAAGAGCT	349440
AGAAAATGTT	CTTTTGAAAA	AAGAAATACA	CAAAATTGAC	AATGTCATAA	AACAACTGCA	349500
AATATTAAGC	TTTGCCTGGA	AAAAATTAAG	CAAAAAAGAA	AATAATATTA	CTCAAAGTAA	349560
TAATGTTACT	CAAAGTAAAT	TAGGAATCAA	TATTGTCGGC	TAATGAAATT	TTAAAAAAAC	349620

ATTTTAGAAA	TTTATTATTA	GAATTAAAAG	AATTGAAATT	AATATTAACA	ATAGAAAGTA	349680
ATGAATTGCA	AAGAGAAGAA	ATAGAAATAT	TAAGTATAAC	CAATCCTAAG	AAAGATTTAA	349740
TATTAGAATC	AATCAAAAAC	TATTATAAAA	CAATAAATGC	ATGGTTAAAA	TTTAAAAACC	349800
AAAAATTGGA	TAATTTTGAT	TACTTAATTA	AAGAAATTAA	TCTACTAAAA	GAAGAAATAT	349860
ACATTAAATA	TCAAATTTGT	TGTGAAATCT	TACAACAAAT	TGCAAATGCA	AAAAGAAAAA	349920
TTCCAAAAAT	TAAAAAGCTC	CAAAACCTTG	CAGTAAACAA	TTACCCATA	ATGTTAGATA	349980
TTAAATATG	AAAGAACTTT	ACCTAATTGA	TGCACTAAAC	ATAATATTTA	GAAATTATCA	350040
CGTAATGAAA	AATTATCCAC	TTTTAAACAC	ACAAGGAGAA	AATGTAAACG	CATTTATTGG	350100
CTTTTTCAAA	ACATTATTTT	TCATAATAAA	AGAAAAAAT	CCTGAACATT	TGATTATCAC	350160
CTTTGACTCA	GAGGTACCAA	CTTTTAGAAA	ACAAAAATAT	CCAAGCTACA	AGGCAACAAG	350220
AGATTTACCT	CCGGACGATT	TAATACCTCA	AATAGGATGG	ATAAAAGAAG	GCCTTTTAAA	350280
GGCAAAAATA	CCAATCTTTG	AGATGGAAGG	CTACGAAGCT	GACGATCTTT	TAGCTAGTTT	350340
TGCCAAAAG	GCTGCAAAGA	ATAACTATTT	AACTTACATT	ATTTCTCCAG	ATAAAGACTT	350400
GCTGCAAACA	ATGTCAGAGT	ACGTAAAAAT	ACTTAAATTT	GAAAACAACA	GCTTTATTGA	350460
AATGGATAAT	GAGTACGTAA	CAAAAAAATT	TGGAGTAAAT	AGCTTTCAAA	TAAAAGATTA	350520
TTTAGCTATT	GTTGGAGACA	GGTCTGACAA	TATACCTGGA	ATAAAAGGCA	TTGGCGCAAA	350580
AGGAGCAGCA	AATTTATTAA	GAGAATTTAA	AACCTTAGAC	GGGATATATT	CAAATTTAGA	350640
AATAATAAAT	AAAAAACACC	GAGAACTTTT	AATCAAAGAA	AAAGAAAATG	CTTTTTTAAG	350700
CTATGAACCT	GTAAGTCTTG	AAGAAAATTT	AAAAATTTCCA	GAAATTGAAA	ACTTCGCCTT	350760
AAAAAATTTT	AGCGAAGAGA	TAATATCTTT	GTTTGAAAAG	CACTCAGCAA	TTGCCCTAAT	350820
AAAAACTTAT	AAAAAGGATA	TCTTAAACAA	AGAAAAAGAA	AATGCAGACC	AAAAAGTCT	350880
ATTTAAGCAA	GAACCTACTA	CCAACAGCTT	AGATGACATA	AATACAATTG	ACACAGAAAA	350940
TGTTAAATAC	CGCTCAATAA	CAACAAAAAT	AGAGCTTGAT	GATTTAATAG	AAAGCCTTAA	351000
AAAGGCTAAA	TACATATCAA	TAGACACAGA	AACGTCTTCG	CTTGATACTT	ACACAGCAAA	351060
ATTAATTGGG	ATTTCTATTT	CATTTAAAGA	ATTTGAAGGT	TACTATATTC	CAATCGAAGC	351120
CAAAGGAAAA	ATTTACATAG	AAAAAACTA	TATAATACAA	AAATTTAACA	ATCTTTTGA	351180
ATCAAATCCA	AAAATAATTG	GTCAAAATTA	TAAATTTGAC	TATAAAATAC	TTAAAAACAA	351240
TGGATTTAAC	CCTATACCAC	CTTATTTTGA	CACAATGATT	GCTGCATACC	TTATCGACAC	351300
AAACTCAAAA	GTATCGCTTG	ATTTTCTTGC	AGAAAAATAT	TTAATGCATA	AAAACATTAA	351360
ATATGAAGAT	GTGATACAAA	AAAATGACAA	CTTCGCAAAT	ATATCTTTAG	AAATGGCAAC	351420

AAGCTATTCA	TCCGAAGATG	CTGATATTAC	ATTTAGATTA	TTTAATATAT	TTACCAAAAA	351480
ATTAAAAGAA	GACAAACTCG	ACAAGTTAAT	GCACGAAATA	GAAATGCCTT	TTAACAAGGT	351540
GATTATAGAA	ATGGAAGAAA	ATGGAATTTA	CCTTGATAAA	GAATATTTAA	AAGAATATGG	351600
AAAAGAACTT	GGAAAAGAAT	TAGAAGCAAT	CGAAAACGAA	ATAATAAAAA	GCATAGGAAT	351660
TGATTTTAAT	CTAAATTCTC	CAAAACAAAT	GCATGAAATT	TTATTTGAAA	AATTAAATCT	351720
AAAATTACCA	GAAAAAATGA	AAAAAGATTC	AAC TGATATA	AAAGTGCTTG	AATCTCTCAG	351780
AGAACAGCAT	GAATCAATTG	AAAATCTAAT	AAAATACAGA	CAAATTGCAA	AATTGAAGAG	351840
TACTTACACA	GATAATTTGA	TAGAACTAAT	AACTATAAAA	ACAAACAGAC	TGCACACAAG	351900
CTTTATACAA	ACAAAAACAG	CAACTGGTAG	AATCACTAGC	ATAAACCCCTA	ACTTGCAAAA	351960
CATACCAATA	AAAGATGAAA	AAGGGCGAAA	AATAAGAAAA	GCATTTAAAC	CAGAAAATGG	352020
AAATATTTTT	ATTTTCAGCTG	ATTATTCTCA	AATTGAGCTT	GCTATACTTG	CTCATTTATC	352080
ACAAGATGAA	GTCCTTATTA	AAGCATTTGA	AAATAATAAA	GACATTCATA	CAGAAACTGC	352140
TTCTAAGCTT	TTCAAAATAG	AAGAAAAAGA	AATTACTCCT	AACTTGAGAA	GAATAGCAAA	352200
ATCTATTAAT	TTTGAATAA	TTTATAGAAT	GTCAGATTTT	AGACTTGCAA	AAGAACTGGG	352260
AATTACAAAA	GAAGAGGCAA	AAGGATTTAT	AAACTCTTAC	TTTGATTCTT	ATCCAAAAAT	352320
CAAAGAGTTT	ATAATAAATC	AAATAAACTT	CGTAAGAAAT	GCTGGATATA	GCGAAACCAT	352380
CTTAAAAAGA	AGAAGATATA	TAAAAAGAAAT	TAATAGCAAT	AATTATCTGG	AAAGATCTGC	352440
CGCTGAAAGA	ATAGCAATAA	ATAGCATAAT	TCAGGGAAGT	GCCGCCGATA	TCATGAAAAAT	352500
TGCAATGGTC	AAAGTATTTA	ATGAATTTAA	AAGTAAAAAA	ATGGAATCAA	AAATATTGCT	352560
ACAGGTGCAC	GATGAAATGC	TCATTGAATC	TCCTATTGAA	GAAGAAAATG	AAGTGAAAAA	352620
AATATTAAAA	ATTATGATGG	AAACTGCTTA	CACATTAAAT	CTGCCTTTAA	GAGCAAATAT	352680
TGAAACGGGT	AAATCGTGGG	GAGAAATCCA	TTAATCATTG	GAGTAACAGG	AAGAATTGCA	352740
TCTGGCAAAG	ATACTGTTTC	AAAAATAATT	AGCAATAAAT	ATGGATTTTA	CGAAATAAAT	352800
GCAGACAAGC	TTGGACATTC	AGTATTACAT	GAAAAAAAAG	AAGAAATAGT	TAAAAATATTT	352860
GGTCAAAAAA	TATTAAATAC	TAAAAATGAA	ATAGACAAAC	TCTTACTAAG	AAATCTTGTA	352920
TTTAATGACA	ATAAAGAATT	AAAAAAGCTT	GAAAGCGTAT	CACACCCAGT	CATACTCAGC	352980
AAAATAAAAA	AAATCCTAAT	CCAAAACCAA	TCTACAAAAA	TAATAATTAA	TGCTGCTTTA	353040
CTTTTAAAAA	TGAATTTGGA	AAAACCTTGC	GACTACATAA	TTGTGCTTAA	GGCAAAGAAT	353100
TCTATAATAA	AAAATAGATT	ATCATATTCT	ATACCAAACA	TTGATTCAAA	TATGATTAAT	353160

AAAATACTCA	AAATCCAAAA	AGATATTTTT	TTTGAAAAAA	ATATTATAAA	CTTAAAAATA	353220
ATCAATATAA	TTAATAACAA	GAATTATGCA	TATCTAGAAA	AAGAAATTGA	AAAAAAAATG	353280
CAGGGGATAA	TTAACTATGA	AAGATTTGAA	TGAAAACAAT	GATAATAATA	AAGGATTTTT	353340
TGTAGCATT	ACATCAATTG	CAACAGTTTG	TATCATAATA	TTTCTTGGGA	CAATTATTTT	353400
CTTTCCAAAC	AAAAATTTGG	CTTCAGACAT	TGCAGAAAAA	AATATTGTTT	TAGAAGAAGA	353460
TAAAGATCCA	AACACCTTAG	AAAAGGTTGA	CCAAAATGAA	AAATCTTTAA	AGGTATCTGA	353520
AACTCAAAAT	GAAATAATTA	TAGATTTAAC	ACAAGATTTA	AATAAAGAAA	AAAAACCTAC	353580
AAACAAAATA	CCTAATACTC	AGAAATCAAA	AATCATCGAA	AAGCCTCAAC	CCACAACCTCA	353640
AAAAATATCT	AATACTTCTC	AGAAATCAAA	AACCATCGAA	AAGCCTCAAC	CCACAACCTCA	353700
AAAAATATCT	AATACTTCTC	AGAAATCAAA	AACCATCGAA	AAGCCTCAAC	CCACAACCTCA	353760
AAAAATATCT	AATACTTCTC	AGAAATCAAA	AACCATCGAA	AAGCCTCAAC	CCACAACCTCA	353820
AAAAATATCT	AATACTTCTC	AGAAATCAAA	AACCATCGAA	AAGCCTCAAC	CCATAGCCCA	353880
AAAAACTTTA	AATACTGATA	ACATTTATGA	TCCTAATATA	GAATATTACA	TACAATTTGT	353940
ATCACTCTCA	GACCCAATCA	ATGCAGACAA	CTATATTCAA	AAATTACTCA	AATATAATAT	354000
AATTGCTAGA	ATATATTCTG	CAACAGTAGA	TAATAAAGAT	ATTTACAGAG	TAAGATCTGG	354060
TCCTTATAAA	ACAAAATCAG	AAGCAAAAGC	AGACTTTAAA	AAAATAGCAG	GAATAGGTGA	354120
ATTTAAAGAA	ACTTATATAT	TACCCGTTAA	CAAATAGACT	ATAATTATTA	ATATATTTTT	354180
GATATTTTTC	TAAATATTCT	TCATGAACCT	CAATAATAGG	CGAAACAACA	TGCTTAATCT	354240
TTGTAAGTTT	TAAAAAAGAA	TCATTTAAGC	TGCCAAATTC	TCTTAAAGAA	TAGAATGCTT	354300
GAATTGCTCC	CCCAATAATC	TCTGAATGCT	TAAAATCAAA	AATTTTAAAA	TCTTTGCCAA	354360
GAATATTTGC	CTTTATTTGA	TTTAAAAGCA	AATTATCAGA	ATTAGACCCA	CTAACAAAAA	354420
TGCTCAAAAT	TTCTTTATTG	CAGGCTTTTA	GCTCTACCAA	TCTGTTGTAA	AAAGCAAAAC	354480
ATACAAACTC	AAGTATTGAT	AAACCAATCT	CTAATGGATT	TTTAATACTA	CCAAAAATTC	354540
CTTTACTTAG	ATCTTTGCAA	AGACAAGGAT	CTAAAACAAA	TAAATCATTA	AAAAGTTTAA	354600
TTTGTCTTGG	ATAAAAGTAT	ACATTATTTA	AAGTGACACT	TTTAACAATT	TTTTTTAAGA	354660
GCAACTCAAA	AGTTAAACTT	TTTTTTATAA	AACTGTCTTT	TAATAATTGA	ATCAAATATC	354720
CAAAAGGAAC	AATTCTCCCA	ATAATAAAAA	ATCCTTCTAA	AAAATAAGGA	TATTCTAGAG	354780
AAAATCCTGG	TAAATATGTA	CTTGAAACAA	AATTAAACCC	TTCACTTGTA	CCCATTCTAT	354840
TTGACACAAT	TCCTTCTTGA	AAAGCACCAC	TTCCCACCAA	AGCATTCAAA	TAATCTGATC	354900
CCGCATTAAT	TACGCTAATT	CCACTATTTA	GCCCAAATTC	AATTCCTGCT	TTATAAGTTA	354960

CAACGCCAAT ATTTTCTCCC ATTTTACAA ATGGAGGAAA TTTATTCTTG TCAAGCCCAT 355020
ATTTTTTTAT CTCTATATCA TCCCAAATAA AAGGAATATA CTCCATGCTT GGAAAGCTTG 355080
TAAAAAGCTT TCCTGTAAGC AAATAAATAA AATACTCAAA ACAAGAAACA AAATAGCTTA 355140
TTTTAGAATA TGTTCCTCTT TCAACCGTAC TAAGTACATA GGGCAAAAAT ACAGACTTAC 355200
CCTTAAAATA AGACTTAATT TTAAAGGAAT TCCAATGCAA CACTTCCAAA GGAATTAAAT 355260
TTGAATTTAA AGCAATTAAA CATGGCGAAA TGCCGCCAAC AGAAATGCAA TCTATTTTGC 355320
TAGGCTTAAA ATTGGATATG GCTTTCTTAA AAGAAAAAAG CCATATATTA AAGTCAAAAT 355380
TTTCGAAATC AACATCAAAA TAATCTGAGT AACTAACATC AATATAACTT AAAACTCCAT 355440
TTTTAGAACT AACTAATGCT GCCTTTAAAA CACTGGTACC AATATCAATA CTAAGAGCAT 355500
TCATAAATTA ACCCTTGGTA ATCAATTTTT GAATATCATC CTTTCTATCA AGAATTTTTT 355560
GCAAACCAAC TTTATTATAA ATTGCAAATA TTGCCTCCGC AAAAAGAGGC GCAACATTAG 355620
CCTCATGATA CCAAGGTTTA TTTATTAATT CATCATATG ACAACAGCA TTTGTTCCAA 355680
TTATTTTATA AAAAAATCCC TCCTCATAAG CTTTATCAAA ATATTTAATA GCATCTCCAT 355740
TGAAAAACGG CAAACTAATC CCACATATAA TCTTCTTAGC ACCCATGCTT TTAAGTAATT 355800
TCATTGCCTT AATTAGAGTG CCCCAGTAG CTAACATGTC GTCATCATA AAAACATTCT 355860
TGCCTTCGAC ATCTCCTAAA AGCTTGGTTA CAGAAATATT TGAATCAGCA ACATCATTTG 355920
AAACTCTTGA ATAATCTCTC TCCTTATAAA GCAAAGCAAG AGGGCTCTTA AGGCTTGATG 355980
CAAAAAATTT ATTTCTACTT ACAGCACCTG TATCGGGTGA AACAATAACT AAATTAGAAT 356040
CTCTAATGTC GATTAAATCC TTAAGAGAAT TAAAGATTTT ATAAGAAACA TTTAAATTTT 356100
CAAAATAAAC TTTCCTAAAG ACATTCTCAA TAGCCTTTGA GTGAATATCT AGGGTTAAAA 356160
TATGTCTAAT GCCCAACTCT TCTAAAAATC TTCCAATAAG ACTTGCTGTT AAGCATCTCT 356220
TTGAATGCTT TTTATCTTGT CTTGAATAAG GATAAGACGG GATAATAACA CTAACAGAAT 356280
TGGCTTTGGC CTGCATACAG GCATCTATTG TTGTCATTAA ATTCATTATG TGATCATTA 356340
CCGTCATAAT TATTTTTTCG CTAAGTTTAA TCTCAACTTC ATAAGCATTA GCAACATCTT 356400
GAACAATAAA AATATCCTTA TTTCTGATTG TTTTAAAAAT TTCTGTTTTA AATTCACCAT 356460
TGGCAAATTT AACAAATTTT ACAGGAATTT CTAAAGGCTC TTTGCTTTTA AGAGTAGACA 356520
AACTAAGTCC TTCTAAAAAA GGAGATAAAA CTTTTTCAAT CTTAAAAATT TCTTCCTTTA 356580
AGGCTTTAGA ATCTTGGCAT ATGCTCTCTA TAATCTCATT TTCAATATTT ATAAATATTC 356640
TGTCAAGCTC TTCTATTATT TTAGTAGCAA AAACCCTACC CCCAGGACAA GCAATAATTC 356700

CTATTGATTT CTTTTTAAGT AAATTCACCC AGCTCCTCGT TCTTTTTTAG AAAATCTTAA	356760
CAATCTTAAT TTAATAATTA ATAAACTTA TACACACAAA TATGACTAAA ATTTTTTAAA	356820
GCAAGGTCAT TAAAATATTT TAGCTTTAAT AATAAAAATA AAAATCTAAA AATTCTATTA	356880
ATAGCAAAAA CAAATACTAT AACATAATCC TAAAAATAAA ATTAAATAAA CTACACAATT	356940
CCAAATTCAA AACCTATTCC AAAGTTGAAA TCAGAAAATT TAGGGTTTTT AATATTCCAA	357000
ACATAGTACC CTTCAAGAAT TAAAAAGAA AATGAAAGTC TAGCACCATT ATCCCAGCCC	357060
ATTGTTCCCA GTTCTGCTAA AACAGAATCC GCAGAAGAAG TCGCTATATT GATCTTAGGA	357120
CCTGTGAAAA ACGCTAAAGC TAAAAACAAA AAATCTAATT TTGTATAAAA TCTTGGTGTT	357180
ATTGCCATAA TAAACGAGAA ATTTTCATTT GCAGTTCCAT CCGAACGCTT TATTGCTTTA	357240
AGAAGATTAA TGTTAAACAA AAGCTCAAAT CCAATAGAAA CAAATCATC AAATTTAGCG	357300
CCAAATTGAG CGTAAGTTCC ATATCTTATT CCAGCTTTAG CAATATTGGC TAAATCGGAA	357360
AAATTTTGGG CTATCTCTTC TTTTCTATT GGGGATAAAT CTGAAGGCAA ATTTTGCTTA	357420
AGCTTTGCAT TAATCTCTAA AGCCTCATTG TAAAAGCTTG AAAAGGGACT AACAGGAAAA	357480
GCAACCCAC CACCAAAATT GAATTCAAAA TTAGTATCTG CAAAACCATT TAACACAAAA	357540
ATCCCAAATA AACACAAAAT TAAACTTTA AGCCTAATCA TATACAACT CTCCTACAAA	357600
AATTTATGAA AAATAAACA GGGTTTATAT TGCACACCTT ATTATATAAT AATTACCATA	357660
AAGATTACCA CAAGCAAAAA GTAAACAAAA AAAGTTAAAA ATTAAGTCTT AAGAATAGAA	357720
GAAACTATTT CTTCCGCACC ACTTGGTATA GGATGATTTA GCTCTTTATA TTTTGAGATA	357780
TATTTTTTTG CATTTTTTTT GTCACCTTTT AAATGATAAA TGTAATAAAT ATTAAATAGA	357840
GCCTCTTTAT TTGCAGGCGC AAATCTAGA GTTTTCAAAT AATAAATCAA AGCATTTGTC	357900
AAATCATTTT TTTTAAATAG CAAATATCCC TTAAGATTGA TTAACAAAAT ATTTTCTGGA	357960
TCTTCTTTTA TAATAGAATT AAGTTTCAAC TCAGCCTCAA CATATTTTTT CAAATTAATG	358020
CAAGCTAAAA TAAAATTGTA ACTTGAATCA TCACCAGCAT TAATATTAAA TTTAATAGAT	358080
TTTTCATAAA GCAAAACAGA AGTCTCATCA TTACCAAGCT CTCATTTTAA TTTAGCAAGC	358140
TTATAGTATT CACCTGATAT GTTCTGATAT TCCTTAAAAA TAGAGCTACA AGACAAAACA	358200
AAAACAATAA TAAACAACAA TTTATACATA AAAAATTTAC TTAAATCCTT AATACTATTT	358260
ATACTATTTA AATTATCCAA AGCAGCAAAA TAACACTAAA TCTAATAATA ATCAAAATAC	358320
AAAGCTTCAA TGCTGTTGAA TTTTAAATTT AAATAAACCA TCTTGATGAT TATAAAACAA	358380
AATTTATTAC TCTAAAAGCT AGTCATAAAC ATAAATAAGC CCTCCTGCTT TAAAAGCAAA	358440
AGGGCTTTTA ATACTATCTA AAAACAAAAT TAAAGCTTTT CTTGGTCATA TTTGTTAAAT	358500

AsGTTTTGCT GTTAAATATT TACCAACTGA TCTTCTGTCC TCAACAAGTT TAGATATTGC 358560
GCTAAAATGT CTTGGTTCAA TCTTAAAATA CTTATAAGCT CTTCCATCCT TAAAAACAC 358620
AGAAAGCTCA GACACAGAAG AATCGTAATC TACTTGTGAT ATTTTGCTCA ACTCATTAGA 358680
TATTGTTAAA GTTTCCTCACT CAAATTCCTC CAAATAATTA TCTTAGGAGT ATAATAATAA 358740
AGTAAGAGTT AATTCCTAA ATAAAAAGTT TTAATCAATA AAATCAAAAT CTACTAAATG 358800
ATATATTCCC TAATATAAGG ATATACATTA ATGCAAATTT AATCAAGCAA ACTGTCAAAT 358860
TTCATATAAA ATAGTTTAAA CTTCCAAATA TTTAATAATA TAAAACGATA TAAGATAGAT 358920
TTTTAAAAAA AAATTTTGTA AAATTACTAA GATAGTTAAT CTTCTACCCA CATATCATCA 358980
GGAGGGACAA AGTCTAATGG ACTATAATAA ATTACGAAAC ATAGGTATTA GCGCACACAT 359040
CGACTCAGGA AAAACCACTC TTACAGAACG TATTCTTTTT TATTGTAATA AAATTCATGC 359100
AATTCACGAA GTAAAAGGCA AAGATGGGGT TGGTGCAACA ATGGACTCAA TGGAACTTGA 359160
AAGAGAAAGA GGAATCACAA TAGCATCAGC TGCAACTCAC GTTGAATGGA AAGATTTTCC 359220
GATAAATATT ATTGATACAC CCGGACACGT AGATTTTACA ATTGAAGTTG AAAGATCTCT 359280
TAGAGTGCTT GACGGGGCAA TATTGGTTCT TGATTCTGTT GCAGGAGTTC AATCCCAATC 359340
AATAACTGTT GATCGACAGC TTAAAAGATA TAGCGTGCCG CGCCTTGCAT TTGTAAACAA 359400
GTGTGATAAA ACCGGAGCAA ATCCCTACAA TGTAAGAT CAACTAAGAT CAAAACCTGA 359460
CTTAACTCC GTTTTAATGC AAATTCCTCAAT TGGATTAGAA GACAAACATA TTGGAGTTAT 359520
AGACCTTGTA TTAATGAAAG CCTACTATTT TGAAGGAAAA GATGGAACAG AAATAATAGA 359580
AAAAGAAATA CCCTCAGATC TCTTAGAAGA AGCAAAAAGC AAACGAGAAA TAATGcTtGA 359640
TACTCTTGcT GACTTTAATG ATGAACTTAT GGAATTACAC ATGGAAGGAA AAGAAGTTCC 359700
TACTGAAATA ATATACAATG CAACTAGAAC AGGAACATTG GCTTTAAAAT TATGCCcTGT 359760
ATTTATGGGA TCTGCTTATA AAAACAAAGG AGTGCAATTG CTCTTAGATG CTGTAACCAG 359820
ATTTTGGCCA TCCCCTCATG ATATAAAAAA CACCGCTCTT GACCTAAATA ATAATGAAAA 359880
AGAAATCGAT CTTAAATTG ACAACGAGCT CCCAACTGTT GCTCTTGCAT TTAAACTTGA 359940
AGACGGACAA TACGGACAGT TGAATTATGT GAGAATCTAT CAAGGAATTT TAAAAAAGG 360000
ACAAGAACTT ATCAACTCAA GAACTTCTAA AAAATTCAAA GTTGAAGGC TTATCAGAAT 360060
GCATGCCAAT AATACAGAAG ACATTGAATT TGGAGGAAGT GGTGACATTG TTGCTTTATT 360120
TGAATAGAA TGTGCATCAG GAGATACGTT TTGTGATCCA TCGATCAACT ATTCAATGAC 360180
ATCAATGTTT ATTCCAGATC CAGTAATTTT TCTTTCTGTA AAACCAAAGG ATAAAAATC 360240

TGCTGATAAT ATGGCCAAAG CCCTTGGAAG ATTTACAAAA GAAGATCCAA CATTTAAAC 360300
TTATGTTGAC ATTGAATCAA ATGAAACAAT AATTCAAGGA ATGGGAGAGC TACACTTAGA 360360
AGTTTACATT GAAAGAATGA AAAGAGAGTT CAAGGCAGAA GTTGAAACCG GAATGCCGCA 360420
AGTAGCCTAT AGAGAAACGA TTACAAGAAA AGCTGAATTT AATTATACTC AAAAAAGCA 360480
ATCTGGAGGA GCTGGTCAGT TTGGACGAGT TGCAGGGTTT ATGGAACCTC TTGACAAAGA 360540
AGGAGAAACA TACGAATTTG TCAATCTAAT AAAAGGAGGA GTAATCCCAA CAGAATATAT 360600
CCCATCATGT GATAAAGGGT TCCAAAAAGC AATGGAAAGG GGAACATTAA TTGGCTTTCC 360660
AATAGTTGAC ATAAAAATTA CAATCAATGA TGGCCAATAT CACATTGTTG ACTCATCTGA 360720
TATTGCATTC CAATTAGCAG CAATTGGAGC TTTTAGAGAG GCTTATGAAA AAGCAAAGCC 360780
TACAATCCTT GAGCCAATAA TGAAAGTTAC CCTTGAAGGA CCTACTGAAT TCCAAGGCAA 360840
TATGTTTGGA CTTTAAATC AAAGAAGAGG AATAATAACA GGTTCCCTAG AAGATGGAAG 360900
TTTTTCAAAA GTTGAGGCTG AGGTGCCTTT AAGCGAAATG TTTGGATTTT CAACAGTCCT 360960
TAGATCCTCT ACCCAAGGAA AAGCAGAATT CTCAATGGAA TTCTTAAGGT ATGGAAAAGT 361020
TCCAAGCACT ATATTTGATG AACTTCGCAA AAAATTTAAC GATCAAAACA AATCTTAATA 361080
AAATAATAAG GAGGCTTTAT TATGATCGAT TTAACACAAG AAAACAAGA AATACTAATA 361140
AAAAACAAGT TTTTAGCCAA AGTTTTCGGG CTTATGTCAA TTGGACTTTT AATCTCAGCA 361200
GTATTTGCAT ATGCAACCTC AGAAAATCAA ACAATCAAAG CAATAATATT CTCAAATTCA 361260
ATGTCATTTA TGGCTATGAT ACTTATACAA TTTGGACTTG TATATGCAAT AAGTGGTGCT 361320
CTTAATAAAA TATCAAGCAA TACTGCAACA GCTCTTTTCT TGCTCTACTC AGCACTAACA 361380
GGAGTAACAT TATCTTCTAT ATTTATGATT TACACACAAG GATCAATAGT ATTCACATTC 361440
GGAATTACTG CTGGAACATT TCTTGGAATG TCTGTTTATG GATACACTAC AACAACAGAT 361500
CTAACAAAAA TGGGAAGCTA TTTAATAATG GGCTTATGGG GAATCATTAT TGCATCTCTT 361560
GTTAATATGT TTTTGAAG CTCAGGTCTT AATTTCCCTA TATCTATTTT GGGCGTAGTT 361620
ATATTTACAG GCTTAACAGC TTATGATGTT CAAAATATTT CTAAAATGGA CAAAATGCTA 361680
CAAGACGACA CTGAAATAAA AAACAGAATG GCGGTTGTAG CCTCACTTAA ACTTTATTTA 361740
GATTTTATAA ATTTATTCTT ATATCTTCTA AGATTTTGG GCCAAAGAAG AAACGATTAA 361800
AATAATAAAA AAATCATAAA AAATTCAATC AAAAATGAAT GCTTTAACTT TAAAGCATTC 361860
ATTTTLAGAG GTTCAATGA GTATAGATAG CTTAGAATTC GAAGAAAGTA GTACTCAAAA 361920
TGTAATAAAA AAAAATTTTG AGTTTGAAGG ATATATTGAA AGTAATAAGC CAATAATAAT 361980
AGAAGGAAAG CTTAAGGGT TAATAAACTC ATCAAATCA ATCTATCTAA GGGAAAAAGC 362040

TGATGTTGAA	GCTGAAATAA	AATGTCAACA	TTTGCTAAAT	CATGGCAAAA	TAAAAGGAAA	362100
TATTGAGGCT	TTAAAAACAA	TTAAAAATCTA	CAAAACCGGC	AAATTAATAG	GAAACATTAA	362160
AACCAAAGAA	CTCTTTATAG	ATTCTGGAGC	AATGTTTAAA	GGGAATTGTG	AAATGGAGGA	362220
TTTAGAAGAA	TGAAATTTTT	TTTTCTATTA	CAAATAGCTT	TAATTCTACT	ATCCAATTCA	362280
AGCTTGTTAT	TTGGACAATC	ACCGCCTAAA	GAAAAAGAAG	ACTCTCTTCT	TCTATATAAA	362340
GAAGGAAAAT	TTAAGAAGC	TATTTTAAAC	ACGTTAGAAG	AAATTCGACT	AAATCCTAGT	362400
AACTTAGATG	CTAGGACAAT	ATTGATATGG	AGCTTAATAG	CCATAGGAGA	ATACAAGAGA	362460
GCTGAAAAAG	AGGCGATTAT	AGGACTTGGC	ATTAAAAAAC	ATGACATAAG	AATTATTCAA	362520
GCAC TAGGAG	AAGCTTATTT	CTTTCAAAAA	AATTATGACA	ATGCATTAAA	ATACTTTCAA	362580
GAATACATTA	GCCTTGATTC	TAAAGGAGCA	AGAATAATAA	AAGTTTATAA	TTTAATTGCA	362640
GATTCTTTTT	ATGAGCTAAA	AAGATATAAT	GAAGCCGATT	TTGCATACGA	ACATGCATTA	362700
CGTTTTTCTC	CTAATAACCA	AAATCTATTA	ATAAAATTAG	CAAGATCAAG	AATAAATGCA	362760
AAAAATAAAA	TATTAGCAGA	AGAAGCACTA	ATTAAAATTC	TTACAATCTC	TCCTAATAAT	362820
CTAGAGGCAA	AAAATTTACT	AGAAGAATTA	AAAAAAGCA	ACAACAAACC	TTGACATTCA	362880
ATTTATAAAA	ACTTATTCTT	ATTGTTAGCA	AATTAATAAA	CTGGGCTGCT	AGCTCAAGTG	362940
GTAGAGCATC	GGACTCTTAA	TCCGCTGGTT	ACAGGTTCAA	GTCCTGTGCA	GCTCAAATTG	363000
TTAAATACAT	TTTGGTATAA	ATTATTAATT	TTATGCCAAT	TTAACTTGAC	ATTATTGGAA	363060
AATAAATATA	TTATTACTTT	CGATGGTCAT	AAAATGACTT	TTGGGCTCAT	AGCTCAGGTG	363120
GTAGAGCAGC	GCCCTTTTAA	GGCGTTTGTC	GTAGGTTCGA	GTCCTACTGA	GCTCACTTTT	363180
GTCCTCTTCG	TCTATCGGTT	AGGACTCCAG	GTTTTTCATCC	TGGCAAGAGG	GGTTCGATTC	363240
CCCTAGAGGA	TGTCTTGCTA	ATAAAAATAG	ACTAAACATT	CTTGCCTTCT	AGCAAACCCA	363300
GAAAACAAGA	ATGTTTTTTA	AGCAAACACA	AAC TATTCAG	GTATTAGCAA	TATTTCTGCT	363360
TTTTTCATCA	GATTAATTTT	CTTAAAAAAT	TCATTTATTA	AATCTTTGTT	TAAGTTTGTC	363420
TCTATAAACT	TAACACCAAA	ATTATTTTTA	AATACTCCAT	ACCAGGATAA	TGACGCCAAT	363480
ATATTTGAAA	TCCAATAACC	ATTCTTCTCT	GAATTTATTT	TTGTATTTTT	AATATAATTC	363540
TTCTTAACAT	AAGAAAAATC	TTTATCATTA	AAATCTATTT	TTTGCCTTTC	GATCATATAG	363600
CGATTAATAG	AATTTAAGAC	ATTGTCCAGC	TCCTTAGGCT	CGGTAGTAAA	AAAAATAGAC	363660
AAAATACCAT	CGGAATCTAC	ATTTTTTCTT	AAATTGGAGT	CAAAAGAGGC	TTGAATTGCA	363720
TAAACACTAG	ACATTTTTTC	TyTAATATTT	TTTATAAGCC	CATCCGTTAA	AAGATCCGCT	363780

AAAGCATTTA AATTTAACCA GGTCTCTGCT AAATAATTAA ATTTAAAAGG ATAAATTACA	363840
TAGGCAAAAC TAGTTGAATT TTTTCCCTTC CTTACAACCTA TTTTATTAAA ATTTTACTG	363900
TAAGAGTAAT CTAAATCTTT ATACTCGTTT ATTTCTTTAA AGTTAAGATT GCCCAAATAT	363960
TTCTTTGAAT AAGCCTTTAT TGTCTGAATA TCTGAGTCTC CAGCAAGACA AACTTAAAT	364020
TATTTGCATA AGTAAACCTT TTCTTATAAA AAGACAAAAT ATTTTCTTTT GTAAAATATT	364080
GCAAATCACT ATCTTTTGTA TCTTCAAATC TAGGATCATT ATTGTTTAAA AATTACTAA	364140
TGGCTTTATG AAAATGATAA TCAGAACTAT TTTTATTGCT CTTTATTAAT GCTTTTATAT	364200
TATTAATAGC ATTTTGCAAA GAAACATCAT CAATTTTGGG TTCCTTAAAA GTAAAATATA	364260
TAAGCTGAAA AAGAGTTTCA AGATCTTTTT TATCTGAACT TCCAGAAATA TATGATTCTT	364320
GAGCTCCAAC CCCAACTCTT AAAGAAACAG CTTTATCTGA TAAATATTTT TCAATCTGTA	364380
ATGCAGAATA ATCACCATAA CCCGAACCAG ATACTACTCC GGGAGCAAAA GATAAAACAG	364440
GAATAAGTTT TAAATCTTCA TTAATTAAAC CTCCCCAAGA AGTTGCACTA AAATCAATTA	364500
CACCTTTTTT TTGATCATT TATTTAAAT AACTTCAAC CCCATTTTCA AGAACAAATG	364560
ACGAAATTC ATTTTCAAAC TCATTTTCTC TAATAATATC TTTATCATCT AAAGACTTCT	364620
TAAAAAATTT ACCTTCAATT AAAGAATTCT CATAAGGCTT TAACTCTCTT TTAAAGCTA	364680
TCTTTTGAAG ATTGTCAATA TCTTCAAGAG TTAAAACAGG ATGTGCTCTT CCATGGTAAG	364740
AATAAAAAAT TGCACAATTT TTTACATCAA ACTCTCTTCC TACAAGATTG TTTATTGTTT	364800
TTAAATCAAT CTTTTCCAAA TATTGAAAAG AAAGATCGCA ATATTCATTC ATATCAAATT	364860
TATTAGAACC ATTAATAGCA ATTTCTATTA AATCCTGAAA AATAGCCCAT GAATTTGTTT	364920
TATTTATATT CTTTTTCCTT AATTCTAAAG ATTTGTAAAA TTGAGATCTA ACTTTTTCAA	364980
GCTCACCTTG GGTAAATCCA AATTTTCTTA TCCTCTCAAG CTCATAAAAA AAGTCTTGTA	365040
TTCTTCGTT CAAATGATCT GGATTAAAGT TTAAAGAAAT CGATTTTGCA ACAATGGTAT	365100
TGTTATCTGA TTAAATGAG AAAAAATCTT TATTTGAAAC ATTTTAAAT TGCTTTACCC	365160
CAGCAGTCTT TAATTCAGAA AATCTATTTT CAAAAGAGC GGCTAATAAA GACTTTTTAA	365220
TAGCATTTAA AAGGTCATCT TTGGTCTTTA CAAAGTTAAT AATTTCTTTT TTAAAGAACA	365280
TTAACTAGG CTCTCCAAC TCCAAATCTT CTAAAAGTAA AAATTTATCC TTAAGCTCTA	365340
CGTCTAACT TACTTTTACT TCTTTAATT TATCGGTTGG ATTTTCCAA GAAACAAATT	365400
GCTTCTTTAT CTCTCTTCA ATTTCTATAG GATCAATATC TCCTACCACA ATAACACTTG	365460
CAAGTTCTGG CCTATACCAC TTTCTATAAA ATTTTTTAAA ATCTTCTGGC TGAAAAGATA	365520
AAATTTGCTC TTCAAGTCCA ATAGGACTTC TAAATTCATA AAGACTTCCG CTTGTCAAAA	365580

ACTTATCCAT	TTTCTCATAA	ATTCTTCCAG	GATAAGTCTC	ACCAAGCTTT	TTTTCCTCAA	365640
TAATAATATT	TCGCTCTAGA	TCTATTTCTT	CTTTCATGAA	ACTGATTTGA	GAAGCCCAGT	365700
TTCTCAAAAT	ATTTATAGAT	TCATCAATTT	CATCTTTATT	ATTACCATCT	GACAAATCAA	365760
GTCTATAATA	AGTGAAATCA	AAACTAGTAG	CAGCATTAAAT	GTCAGCACCA	AATTGCATTC	365820
CAAATTTTTT	AAGAACATCA	ACTATAGAAT	TCCCTGGATA	ATCTTTTGTA	CCATTAAAAG	365880
CCATATGTTT	AAGATAATGC	GCTATTCCCC	TCTCATTATC	TTCTTCATTA	AGTGAGCCCA	365940
CATTAAAAAC	AATTCCCATA	TTAACGGCAT	TCTTTGGGGT	TTGATTTTTA	TAAATATAAT	366000
ACCTTAGCCC	ATTGACAAGT	TTTCCTTTTA	CCAACTTTTG	ATCTAACTTT	AACTCATTAG	366060
AAACACAGGA	AAACAAAAAA	AATAGAAAAA	CGCTTGTAAT	TTTACAATAA	TTCTTAATTC	366120
TTTGATAATT	CATTTGCACT	CCTCTTTTAT	GAATTTATTT	TTTCAGAATA	AATTTTATTC	366180
AATGCTTTTG	AAATAGATGA	AAATCCAAAA	TCATTCCAAT	CTTTTAAACT	CTTTAGCTTA	366240
GAAACTGGAA	ATAGTTCATA	AAATAAAAAA	AATAACTCTT	CTTTGCTTAA	TTTTGGAATA	366300
TCATTTAAGT	AAACGTTTTT	ATTAAAATCT	TCAAGATAAA	TAAAAGGATT	TAAGCGCTTA	366360
TCTAGAAGAA	ATTTATTTAA	ATTGGGCATT	AAAATGCTTT	TATTATAAAT	TTCAATAGTA	366420
GTATATTAC	TTGGAACATC	ATCATAAAAA	TCGTTATTCA	AAAAAGAATC	TAAAATAATA	366480
AATTTATTAT	CCTTAACCCC	TACATTTCTC	CCATCTAAAG	TCTTTAAAAG	ACCATCTTTG	366540
CCAATATGAA	CCAAAGTATT	TAAATCCTTT	GTAGCATTAA	AGATAAGCCT	TGCATTGTTA	366600
TATGCCTTGG	ATTGCACTAA	GTGCTCAGTA	TTATTATCTA	CTGCTAATTC	TTTGTCATTT	366660
TTTAATAATA	AATTTATATT	TTTTTCTTTT	AATGCCTTAT	AGGCTAATTC	AATATACTCT	366720
AAAGCGCAAC	TATTTTCCAA	AACAAGTTGC	TCCCTCTTTA	ATAAGTTAAT	AAAAAATATC	366780
AATTCTTCCT	TTTCAAGACT	ACGGTAAAAA	TCAAATCAT	TTAAATCAAT	TCCAAAACCTA	366840
AAATTAACAA	TAAATATTAA	ATAAAAAATT	GCAATGTTTT	TTTTCAATCT	AGCCTCCTCC	366900
CTTTAGCTAA	CTACATCAGC	CAACTCTAAA	AAAACAGGGC	AATGATCACT	TCCCATTACT	366960
TTGTCTAAAA	TTAGAGATTT	TTCAACATTT	CTCTTGAAAA	ATTCATTAAC	AATAAAATAA	367020
TCAATTCTCC	ACCCCATATT	TCTCTCTCTA	GCTCTTGTTT	TATAGCTCCA	CCAAGTATAA	367080
TAACCAGGAT	CCTTATTAAA	TATCCTAAAT	GTATCCACAT	ATCCTTTGTT	TAAAAAATCA	367140
TCTAACCAAG	TAGTCTCTTC	AATATAATAT	CCCGGAGAGT	CTCTATTAGA	ATCGGGACTT	367200
ATAAGGTCAA	TCTCGGTATG	AGCAATATTA	AAATCACCAC	AAATTACTAC	ATTTTTACCA	367260
TCACATACAA	GAGAATCTGC	AAGATTTTCA	ACATAAGATA	AAAAATCAAG	TTTATACCCA	367320

AGTCTTCTTC	TTAAAACTTG	AGAATTGGGG	AAATAACCGT	TAACCAATAT	AAAATCGTCG	367380
TAGCATGCTA	CAAGCCCCCT	ACCCTCATTG	TCAAAAATTT	CTTCTCCAAG	CAGCCTTACA	367440
GAGATAGGCT	CAACTTTTGA	ATAAATGCAA	ACACCACTAT	AACCTTTAAT	CTTTGAATTT	367500
GAAAAATAAG	AATAATAATT	TTCAAGAATT	AAATCCTTTG	GCAACTGTTC	TCTTAAGGCT	367560
TTAGTTTCTT	GAATACATAA	AATATCTGGA	GTATATTCTT	TTACAAACTC	AAGAAAACCT	367620
TTCTTTAAAA	CAGCTCTAAT	TCCATTTACA	TTCCATGAAA	TTAATTTCAT	AAATCCTCTC	367680
TAATAAAGT	TAAATCAAAT	ATAAATCTTT	AATCCATCAT	AAGCTAAATA	GATATTATCT	367740
TTTTCTAAAT	AATCAAATTC	TTCATGCATT	ATATCGTGTG	CAATATGTGT	AAAGTAAGAA	367800
ATTTTAGGAT	TGATCTTTTT	AATTACACAA	AAAGCCTCTG	AAAAATTTAA	ATGCGCAGGA	367860
TGAGGCTTAA	TCCTCATAGC	ATCTATTATG	AGTAGATCTA	AATTTTTTAA	ATAATCATAA	367920
GACGCTTCGG	GAATAAATTT	AACATCAGTA	AGATACGCTA	AATTGCCTAC	CCTATAACCT	367980
AAACTAATTA	TATCCCCATG	AATCAAAGGA	ATTGGCACTA	TCTTTAGACT	TTTAAAAAAA	368040
AAGGGCTCAA	AATCCCTAAT	AACATTGGCA	ATAATGTCTG	CCTTTCCACT	TAAAGAGGGT	368100
TTGGATGTAA	AATTATACGG	AAAAGCATTC	CTTATGTGAG	CCATGGCAGT	ATCTCTAGCA	368160
TAAATGTTTA	AAGGGGCACA	TCGTGTATAG	AACTTAATAT	CATCAAAACC	CATAATATGA	368220
TCATAATGTT	CATGCGTGTA	AAGCACTAAA	TCAAGCCTAT	CTATTTTCTC	TCTTAAAAGT	368280
TGCTGTCTAA	TATCAGGACC	TGTATCAATC	AACAATTTGA	TGCCAGAAGA	TGACTCAAGA	368340
AAAAAAGAAC	TTCTCAATCT	TTTATTTTTTA	CTATAACTTG	AAGTACAGAC	TTTACAGCTA	368400
CAATTTAACA	TAGGAACACC	ACTTGAAGCC	CCCGTTCCCA	AAAAGGTTCC	AACCATATGT	368460
TACTACCTTT	CGCCTGTAAA	CATAATCTAT	TTTAACACAA	CATTTTATAT	TAAACAAAAA	368520
TAACTTTTCT	TAATCAAACA	ACTCTTATTA	AATCTAAAAT	TAGATTAACA	CTATTTAATA	368580
ATCAATTCTG	TAACTATTT	TGGAAAAATT	GCTTTTATGC	TTATAATTAT	TTAAGGAAAA	368640
ATTATTTTTTA	TGGATACGCA	AATTTATGAA	CTCATTTTCT	TAACCAGTTT	TAGCATATTT	368700
TTAATAGTAA	ATTTATTTAA	TTTTAAAAAA	GAATTTACTT	ATGAAGACTA	CTTCATAATA	368760
TTTCCAGGTA	CGTTTTTTGT	AATAACTTTA	TACTTTACAG	AAATCAGACC	GTAAATGTTA	368820
TATATTGGCA	GTATATTCTT	AATCTTTATG	ATAATCATCT	TCTTTAAAAA	CATCAAAACA	368880
ATAGTAAATA	GTAGAAGAAG	AATCAACAAT	AGGTCTACAA	AACAATCAAA	AGGAATATTT	368940
CTTTCAATTT	TGCTAAAAAC	AATACTTGTA	ATGCCTGCTA	TTTAACTGT	TATTATTGCA	369000
ACTATTTTTT	CATACTTAGC	ACTTTTTATA	AATTATCCCA	AAGATGAAAA	CAATAGCTAT	369060
CAACTTGGAT	TCGCAAGAA	TAAAGATCAC	AAAAATGATT	TAACTTATC	GATTTGGTAC	369120

CCTGtAAGCT CAACATTGGG CCTTAAAAAA CAAAATCCAT TTCTTTTGTA CGAATTTAAT 369180
CCTTTTTTCA TAAACGAAAT GAATTACTTA TCAAAACAGA ATAACATATA TAAAAAAGCC 369240
CTTATTAGCA ATAACCAAAA ACTATATGAT TCTGTTTTAC TTATACTTCC TTATTATTCT 369300
CACGATTCAA TGTTCAAATC TCTAGTTAGC AGGATTGTGA AGAAAGGAAA AATTGTTTAT 369360
TTATATTCGC CAAAATATAA ACATATGAAA AGCTACGATT TTATTAAAAA TAGCCATAAA 369420
AGTATATTTA GCTATGTAAT CAATAAAAGC ATTAGCTATT TAATTGAGCC TGCCAATATC 369480
CTTAATGAAA AAGCTGATAT TGCATCTACT GAAACTGATA TTCAAAATAT GTATTGAACT 369540
AGCAAAATCA AGCCAAAATT TGGAATTTTT AAATTCAAAA ATGAACCTTA ATAAACTAAC 369600
GTTAATTACA CTAGGAAATC AAGCAAATAT TGTTAATTTT ATCCTTGCAA AAAACACAAA 369660
CATAGCAAAA TATATCAATA TAGGGGGAGA ACCGCAACA ATAAGAAATT TAAAAAATT 369720
ACAACTAATT CTAAAAGAAA ATGAAAAGAA CCTCCACACA AAAGTTGCTA ATACAAAATC 369780
TATAAAGCTA ACAGGCATAA GCAATATTGC AGAAATTTCT GATCTTATTT TTAGCAGAAA 369840
CTATTTAAAA AGTTTTAATT TCTTAAAAAA CAAAAATCA ATGTTATCAA GATTTAATTC 369900
TATAGTTAAT GAAATTAATA AATTTATTGA AGAGGAAAAA TAATAATGAT AAAAAATTC 369960
TTGCTATTTG CAATGCTCAA CATCTTTTTA ACAAATAAAG CTCATAGTAA TGAAGAGATA 370020
ATCGAAATAA GACTGAAAT ACAAAGGAA AAATATATTC CCTTTTAAAT AAGTAGAGGA 370080
AAAACCAAC TAGAAGACCT TGTAATATAT ACTCTAGAAA TAAATCCAGA GCTTGACAAA 370140
AACTATGTAA ATACTGTTGC TAAAACCTAT ATAGACGAAT CTTTGATTGA AGGGGTTAAT 370200
TATGACATTG CCTATGCTCA AATGTTACTA GAAACAGGAG CTCTAAAATT CAATGGAATA 370260
GTTTCAAAAG AACAACACAA TTTTTCAGGA ATAGGCGCTA CTAATAATCT TACAAAAGGA 370320
AATTCTTTTT CCAATATTAC AGAAGGAATT AAAGCTCATA TTCAACATTT AAAAGCTTAT 370380
GCTTCAAAAC AAAATATCAA ATCAAATATG GTTGATCCTA GATTTTACCT TGTTAAAAGA 370440
GGATCTGCTC CAACAATATA TGATTTGACT GGGAAATGGG CAAAAGACAA ACTTTACGAC 370500
AAAAAACTTA AAAAAATATT ATTAGAATA TTAGAATATA ATAATGCAAA TAAAAGCTAA 370560
AAGCTCGCTA TATGATTTTC TAGAAAAGAT ATATTCAAAA TACAATAAAA AAAAATTTAT 370620
ACATCCTGAT CCTTTAGAAAT TTCTATACAG GTATAAAGAA AAAGAAGACA TTGAACCTGt 370680
AGGCCyAatt aGTTCTTCAT TGTCGCTTGG AAGAGTAGAA AGAATTTTAG AAGCAATCGA 370740
GACAATACTT AAACCACTTG GCAAATCCCC TTCTGAGAGC CTTAAGCTGG CAAATGAAAA 370800
GGACTTAAAA GAAATATTTA AAGGATTCGT TTATAGATTT TTCAAAGGAG AAGATATTGT 370860

AAGGCTACTG	TGCACCCTTA	AGATAATAAA	AGAACAGCAC	CATACGCTTG	AAAATCTTCT	370920
TTACAGTATT	TATTATAAAA	ACCAAGATTT	TATACTTAGC	ATAGATGAAT	TAATAAAGCA	370980
TATGGAAAAA	ATAAATGGGA	GAGAATTTGG	CATGCTACTT	CCAAAGCCTT	CAAAGGGAAG	371040
TTCTTGCAAA	AGGCTTTTTT	TATTCTTAAG	ATGGATGATA	CGCAAAGATG	AGGTCGATTT	371100
AGGCATTTGG	AATAAATTCA	ATCCCAATAA	GCTTATAGTG	CCAATGGATA	CTCACATGAC	371160
AAGCATTGCT	TCAAACTAT	TTAAAATCAA	AGAAATAAAA	AACGTAAATC	TTAAACAAGC	371220
AATAAAAATT	ACAAGCTATT	TTTCAAAAGA	AAATAATGAA	GATCCTGTAA	AATACGATTT	371280
CTCTTTAACC	AGATTTGGAA	TAAATAGAGA	TTTTAATAAA	GAAAAATTGC	TAAAAAATAT	371340
TAACAAACTA	TAAATTTTA	TTTATAAAAC	TTTTAAATA	AGACATACTT	AAATCATCAT	371400
TAAAACAAAA	ATACCAATTT	ATCGTAAAT	AAAAAGGAGA	ATCTGTGAAT	AATCTTAAAG	371460
ACAAGATAAA	TACTTATAGC	AAATTAATTT	TAGGGTCTTG	GCAATTCGGA	GGAGGATATT	371520
TTAAGCAAGT	CGAAAAAGAA	ACTGCTAAAA	AAATATTAAA	AAAAGCATAT	GATCACGGGA	371580
TCAGAAATAT	TGATACTGCA	AGAGCTTATG	GAAATGGAAT	TTCGGAAAAA	ATAATTGGCG	371640
AAATAATAGA	AAAAGATCCA	ACAATAAGAG	AAAATATTTT	AATTGCAAGT	AAATGCTACC	371700
CAATGGAAAT	TTCAGAATAT	AGAGAGAACT	TTAATGAAAG	TCTTAAAAAT	TTAAAACTG	371760
ATTATATAGA	TATTTACTAT	ATACACTGGC	CTAAAGCCGA	TTTTGACCTA	AGACCAATCG	371820
CATCATTTCT	TGAAGAAATG	AGAGTAAAAG	GAAGAATAAA	ATATGTAGGC	GTAAGTAATT	371880
TTGAAATATC	ACACATGGAA	AGCATAAAAA	AAGTTTGCAA	AATTGACGTA	AACCAAATAG	371940
GATACAACCC	CTTATTTAGA	AATAAAGAAA	AAGATGTAAT	TCCTTACTGT	GAAGACAACA	372000
ATATTGCCAC	CATATCATAT	TCAACAATTG	CTCAAGGACT	TTTATCTAAA	GCTAATATAA	372060
AAGACAAAAA	CAAATTTAAT	GATATTAGAA	CAGAAAAATT	GATACTTTTC	AAAAAAGAAA	372120
TTTGGCCTTA	TACTTTGAAA	ACCATAAATA	AACTTGAAGA	GATAGCAAAG	ATAAATAACT	372180
TAACAATTTT	AGAATTAACA	TATTCATGGC	TTAAAAAAC	AAAATTAAGT	GGATTTATAG	372240
TGGGCTTTAG	CAAGGAAAAT	TATGTAGAAT	CAAACGTAAA	TTCATTTAAA	GCAGAAATTA	372300
ATGATAAAGT	ATATGAAGAG	ATTACATCAA	TTTtagataa	TTTCAATCAC	CAAACAAAAA	372360
ACTTCCCAA	TTTATTTAAC	AAAAAAATTT	AAAACTTTAA	AAACAAATAT	TTCAATTAAC	372420
AACTTAAAG	TCAATAGAAT	TTCCTAAAAT	TCTAACGCCT	TCTACAGTTA	AATGAATATT	372480
AAAAATAAAC	TCTATCTCAA	TTAATGACAA	AATTAGGTCC	GCATTACCCC	CAGTAATTAT	372540
TAAATTAAAT	TTTTTTTTAT	ACATCTGCTT	AATATCACGA	TAAACACCTT	CTATTAAATA	372600
CTTATATTGA	TAAATAAAC	CGCTGTTTAC	ACTCCCAGAT	GTCGTTCTCT	CTAAAAGATT	372660

ATTTGGAGTG CTAATGGGGA ATTTTTTGAT AAGATAGGCA TTATCTAATA AAGAATTAAA	372720
ATTTATCAAA GGACCAGAAT TTATAATACC ACCGAGTATT CCATCTTGCC TGCTAACAGC	372780
AAAAATGGTG CAAGCAGTTC CAAGGTCTAC TACTAAAACA TTTTCAAATG AATAATTTTC	372840
AATGGCTGCA ACAAGATTGG CAAAAACGTC TGAACCTAGC AAAAATTTAT CGCTTTTGTA	372900
AGGATTAAAT GTCAAATCAT AATTCAAATC AAAACCAATA AACAAAGGCT TTATCTTAAA	372960
AAAAGAAAAA ATGACATTTT TAAATGTTTC ATTAAGAATA GGAACAACGC TGCTTATAAA	373020
AACTTTATTT ACATTAAAAT CAAAATTTTC TTCAAAAAAG CTATAAACCT CATCATACCT	373080
TAAACATAAGA TTTGTTTTCA TTTTAATAAA TAAATTAACT TGATTATCTT TAAATAAGGC	373140
AAAAGCAATG CTGGTATTTT CAATATCAAT TATCAATTCT GATAATAAAG GTTTATTTCAT	373200
AAATATTTAT TTTTTTTGCA ATTTTGTCAA ATCTCAATAA AAGATTAAAA GTTCTCTTTT	373260
TCTTGGGCGT TGCTTTAATA ACCAAAATTT TGTTTAAAGG ATAATACTTC CAACCATCAG	373320
AATATACGTA AAACCTTATA TCTGTAAACC AATCAATTTT TCTAAATCTA ACTAAAGTTG	373380
GATTTAAAAT GTTCCAAAAA AATATATAGC TTGAATAATT AATCTCTTGA TCAAAATCAA	373440
TTGCAACTTT AGTATCAGTA ATTTCACGAT TTAAAACCCC AGAAGCAGCA TATATCCACC	373500
TGATAGATCT ATAGCTAGAA ATAAAGATAA ATTGGGGCAT ATATTGATTA TCAATAATAT	373560
CAGAATAATA GCTTTCATAA GGAATTCCTT TGGCATAATC ACTCATTAAT GAATAATAAA	373620
TTGCATTCAA TGAAAGCTTT AATATTAAGC TATCTTTTAA ATAAGATGCC ATTCTTTTAA	373680
GAACCCGAGA AATCTTTAAT GCATGCTCAA CAACATCAGA TGAATTAATA TTATTATTTA	373740
AAATATACAT TTTTCCTTCA TCTGTAACGC CAAATAAAGT AAATACAAAT TTATAAAGCT	373800
CCTTTTTTAA ACTTAAATAA AAAGAATCGT CAACTCTAAT CTTAAGAAAA GTAAGATAAT	373860
TAGATAAAAT GTTGTAGGCT TGGTTAAAAT TAAAATTAGA ACTTAATATT TTTTTAGGAT	373920
CTTTGAGAAG ATTTAAAGCA CCATTTAATT TAGAACCGTT TTCTGATAAA AAAATTTTTT	373980
CCAAAAGACG AGGATCTTCC TTTAAATAAA CCATAAGCCT GTCTTCTTCA AGAGAATCAA	374040
TAAAAGTTTT ATTCCTTGAT AAATAAGAAA AAAATTTATC AAATTGATCT GAATTAGCGT	374100
AATAACATAA ACTTAAATAA GTCAACTTAT GTTCATTTTT GGCTAATAAA GAATCTAATT	374160
TTAAAAATAT TGA CTGGA TCCCTCTGA TTAAAGATTC TGCTAAAAAA CAAACCATTA	374220
AATTTTCATC AAAGCTATAA ACACCGTATT TAAGCCATCC TCCCTTTGAA GCATTAAAAT	374280
TAACAGAATT GTTCCAAGAA TCATAAGCAT TTTGTCTAAA ATTGCTTAAA ACATCATTA	374340
AAATCTTATT ATCCACCTCT TTAATTTTTG AATGCACAAT AGAATAATCT AATACATTAC	374400

TTTTATTAGT	TTGGTTGCCC	TCCATAATAG	AATTTGGAAT	ATTTTCTTT	GGTGAATCGA	374460
TATAAATAGC	ATTGCCAATT	CTAAATGCTG	CTTGAGGAGA	AATCAAAATA	TCTTCTCTC	374520
TTATCTTTAC	ATTTTCTCCT	AAAAAGATTT	TATATTCCAA	ATTCTCCCCT	TGTCTTATTG	374580
AAATAGTAGG	CTTATCTAAT	AAAACCTCTAT	AATGATCTTC	AACTTCATAA	CTTAACAAAA	374640
AGCTCTTAGA	GAGATTTGAT	TCAATGCTAA	AATTATTTTC	CGAATCAAGC	AAAAATCCGA	374700
GAAAAATATT	ATTCTCAAAA	TAAACATAAA	TACCCATGTC	TTGCAC'TTTA	TAAGAGATGG	374760
GGAAAAGATT	TAAACCAGTT	TCTAAAACAA	CAAGTGGATT	AAGC'TTGGAC	AAAAATATCC	374820
TAAGTCCCCT	AACATTAACA	ACCAGATCAT	TTAAAGTATA	TTCAC'TATTT	AAAACCTTAT	374880
TATTTACTTC	TAATTTTATA	TCTTTTAAAA	AAAATATATT	TAAGTTTAAA	TTTCTAAATT	374940
GTAAAAAAT	AACAACAAAC	AATATTAAAG	CACCAAGCAA	TAAATTAAAA	GCCCCTACCC	375000
TTAAAACTC	CTTCATATGA	TGATTCTAAT	CATAAAAAAT	CAAAATATCA	ATATTGATTG	375060
CATAAAAAACA	AAAAAATAA	TAGAATTATA	GGTTAGCTAG	TTAAATAGGA	GTAAAATATA	375120
TGAAAAATCC	TAAAAATTAT	ATTCCAGGAA	CAAACCTTA	CAAGTCTCTA	CCTAAAAAAC	375180
CTATCATTGA	AAACAAGAAA	AAAATTACTA	AAAAACAAGA	ACAAATTAAT	TCAGAAATCA	375240
TGAAATCTCA	AGAGCGTATT	TTGAAGCTAT	ATATGAGGCG	CCTACAAAAA	AAAGATCAAA	375300
TAAC'TCTTCA	AAATTTCA'TT	CTAGAAGGAC	ATAAAATAGG	CTCCAAAATT	TTCAATAATT	375360
TACCAAAAAAC	ACTAAAAGAA	ATAATAGCTT	TAATGAATAT	AGAATCGTTA	AAAGTGCTAA	375420
AGAAAAATAC	AAAAAATCCA	TTTAAATGTC	TTTACATAAA	ATTTTCAAGC	TGGACCTTAA	375480
ACAAGCTAAT	CAAAACACTC	GACATTGAAT	CTAATAACAA	CAAAACCGCA	AAACATAAAT	375540
AACAATTTTC	AAGTTTTTTA	TACCTTACTT	ATTGATTTTT	TTATTTGCAT	CTTTTCTTAT	375600
AATGTCTATT	GTTGATTTAT	TATCAGAATA	AATAAAAAAA	TCTTTCAAGG	ACCATCTTTT	375660
ATGATTATTA	GGCTCTAAAA	TATACATTGA	ATCTAAGATA	TCTAATGTCA	TTTTATTACC	375720
ACAATAAAAT	TCGCCAACCA	TGCCCAATTT	ATTACCAATA	GCTAAACACG	CTGCAATATC	375780
CCAAAGTCCT	ACAAAAGAAA	AGTAGGCCTT	ATAAGAACCT	GTAAAAAGTT	TAGCAAAAGA	375840
ATATACACAA	GAACCATTA	TATGAATATG	AGAAGAAATA	TCAAGATTAA	ATAACCTTAT	375900
AATAGACCTT	GAAACTGCAA	GTAAACTATG	AATATTGTAA	CATTTAGAAT	TATCAAAAAT	375960
AAATTTATTA	AAATCCTTTT	TTAAAGGATA	GCTACCAATG	TTTTTTTTAG	CATAAAATAC	376020
ATTATCTTTA	GAAGTAATAA	AAAACCTCTC	GCTTAAAGGA	AGAGAAATGG	CTCCTTCAAT	376080
AATTTTGCCG	CCACTAGCAT	ACGCTAGCGA	TATTCCATAT	GAAGGAAGGC	CTGCTGCAAA	376140
AGAAGAAGTT	CCATCAATAG	GATCAATAAT	AAAAGTACTC	TCTGATATTA	AAGCATCTTT	376200

GATATACTCT TCTTTATAAG TAGATATTGT CTCTTCTCCA AGAACAAAAT TTCCAGGCTT 376260
TTTGATCTCT TTGAATAAGA ATTGCTCAAT TTGCTTATCA ACCTGAGTTA CAATAGACCC 376320
ATCAGATTTA AAATCTAAAA TTAATTTAGC ACAACCACTT AATGCAAGCC TAGTTGATTC 376380
ATTTAATAAA AATATAATTT TTTCAAAATC CCAATCCATT TTTATCTTAA TTCTCTTATT 376440
AATAATAAAT TCTAAAATTG AAAAAATCATC TTTAAAAGCA TTATACTTTG ATAAATTAAA 376500
TATTTTTTCAA TAAAGCACCT CTAAAAAATG CACCAAATTA GAATAACTTT TACTAAACAT 376560
AGTATAAAAA TCATAAATAT CTATACTTAC ATTTTTTTTAT TTTCAATCTC AAAGATTCTA 376620
TTAAATATCA AAAGCTAAGA AAATTTATCA AACACAAACT CTTTCTTCTA ATAGAAATAC 376680
ATAAATCCCA ATTAAAAACG ATGTCCTTTG TTTAAGTGCC AAAATCCCAT TAAATCCCAT 376740
TAAATTTAAA AACTGAAGT TAAAGCATT GAACAAATCT CATTTTTATA ATTTTACAT 376800
TCAAAATTCT ATACAACAAT GGAATACACA TATCACTTAT AAATTCAATA AATAATTATT 376860
GACATGATTT AACACTTAAA AAGGACTTGT GTTATTTAAG CTGTCACAAC ATAAAAATTA 376920
ATAATATTAA TACACTAAGA AATAAAAAAG CAGATCCTAT ACTATGACCA GATATGTCTA 376980
TTAAACAGAT TTAAAGGTAT AAAAATTTAA TTTTAACTTA AAAAGCTATT TTTCAATTTT 377040
TCCAGCAAAA AATATTATTA ATAAAAATTA AAAAAAGAAA AGAATTTCAA AATCTCAAGC 377100
TCCAATCATA ATTTCAAAT ATATTATTTA AAATAGGCAT TGAAAGCTCA AAACCAAAGG 377160
TTTTTTCAGA AACTTTAACT ATAGGAGCTC CCTGTCTTCT TTTGTATTCA TTTTAAAAAT 377220
AAAGATTTAA AACTTTATCA ACTATACCTT TTTCAAAAT AAGATAAAT GAATCTACAG 377280
ATTCATTGCC AATCAAATAT CTATTTAAAA TAACATCAAG AACTTCATAT TTTGGAAGAT 377340
AATCACTATC TTTTGTATCA AACCTTAACT CAGCTGAAGG CTCCTTTAAA ATAATATTAA 377400
CAGGAATAAT ACATTGGTCA AATTTTGCAT TAATATAATT TACAAGATCA TAAACCTCAG 377460
TCTTAAAAAG ATCTCCGATC AAAGCAAGCC CTCCGCAAGT ATCCCCATAA AGGGTACAAT 377520
AACCAACTGC AATTTGCTT TTGTTACCAG TATTTAAAAG CAAAGAATTT TGAGAATTAC 377580
TATAAGACAT TAATAAAAGC CCTCTTAACC GAGCTTGCAA ATTTTCTCCA GTAACACCTT 377640
TAATATCAAA ATATCCTTCA AAAAATCTAC TGCTTACCTG AAATAAATCT TTTATTGGCA 377700
TTTCAATCAA TTTAAAACCT AATTTTCTAG AAAGTTCTTT AGCATCAGAA ATAGAACCTG 377760
CTGATGAAAA TTTACTAGGC ATAGAAATCC CAACAACATT CTCAGCGCCC AAAGCAAAAC 377820
ATGCAAGATA CGCAATAAGA GCAGAATCAA CACCCCCAGA TACTCCCAA TGAACCTTGG 377880
AAAATCCTGA AAAAGAAACA TATTTTCTTA AAACAAGAGA TATTGCTAAA ATAATTTTTT 377940

CAAAAAGCTC ATTACATGTA TCAAATTTTA AATCTTGAAA TGTATCATTA GATATAAAAT	378000
CAAATTCAAA TCCTTTGGCT TGCTTTACCT TGCCAAAACCT ATTAATAAAA AGCTACACCC	378060
ATCATAAACT GCAGAATCTT CAACTCCATA AAAATTTCGAA TAAATAACAT CTAGATTATT	378120
CTCAATAGCA ACTCTTTGAA AGAATTTTAA CCTAAGATTA TTCTTCTCCT TAGTGAAGTA	378180
AGATTGAC GGTATTATTA AATACTGTGC TTCTTTAAAT CCTCGCCAAA TTTGGGAATT	378240
ACTTCTTTAA ATAACAAAGC ATCCTCAAAA TTTAATACAG CAAATAAATT GTCCTTATAC	378300
CTAAAAAACC CAGGCAAATT GCATTGTGAT ACAGTTAGAA TAGCTTTATG ATTACTGATG	378360
ACAGAAATAA CATCTACAAA TTTACCACCC TCATAAACAC TATGACCAAA AACAATTAAA	378420
GTGTTATCAT TAACCTGTTC TTTCATAAAT TCAATGAACT TACATATATT TTGAGAATAT	378480
TTAGAAAGCC CAAAAAAGCTC ACCATACTTA GTATTGCCTA AAAACATAGA AGGAAAAACT	378540
AAAACGTCTG ATCCCCCTAG CAAAGCTTCA TAATAATTAA TTTTAAAATC AGCAATACAT	378600
TTATCAAAAT CTAAAGCTCT GTATTTTGCT TGAGCAATGC TTATTTTCAT AGGTAAATAA	378660
TAAGCAATAA TACATTAAAT TACAACAAAA AAATTAATAG CTTGGCAAAA ATAATACTCA	378720
CCCATATTTT AAAAATACCC TAATATTAAA GATGTCTAAA AGCACTAAAA ACACAACAAA	378780
ATCAAAAAAT GATACCAAAA ATATTCTTAT AAATAAAAAA ATAAAATTTT TTATTTTGAC	378840
AAAAAATAC ACACGAACAT TTTACTAAAT AACAATATGT ATCAATATAA CACTATTACT	378900
GAAAGCTTAA GAAAAATATA CATCTTACAA ATGCTCAAAA TGAATCAATT TTATTAAATT	378960
TCAAGAAAGA AAAAAATTTG TAAATATTTT TTTTTAAAGA TAAAATGCTT TATCAAAGGA	379020
GGAAAAATGG AAAAAAAGA AACTAAAAGC GAATCTGAAA AAACCAACAA ACAAGATAAT	379080
AAAAATACAA AATCTCAAAA AAAAGAAAAC TTAAATTTAG TAAATTCTGA TAAAAAATT	379140
GCTGAACTTG AAAATGAAAT CTCCAATCTT AAAGATTTGT ATTTAAGAAA ACAAGCAGAA	379200
TTTGAAAACCT TCAGAAAAAG ATTAGAAAAA GAAAAAGACA ATTTTGTTAA ATTTGCAAAT	379260
GAAACCATAA TGAAAGATGT CGTTAATTTT CTTGATAACT TAGAACGAGC TATTAACTCT	379320
TCAAAAAAT CTAAAGATTT TGATACTTA TTAACAGGAA TCAGTATGAT TGAAATGAA	379380
ATACTATCAA TCTTTGATAA AAAATATAAT TTAAAAAAT TTGGAGAAAA TGGCGAGAAC	379440
TTTGATCCAA GTCGTCATGA AGCAATAAGC ATTGAAGAGA AAGAGGGTCT TAAAAATCCA	379500
GAAATAGTAG AAGTATACCA AAAAGGATAT TGCTACAACG ACAGAATATT AAGAACAGCG	379560
AAAGTTAAAG TTGCTCAAAG CAAAAATTAA TTAGAAAAAA GGAGGTTTAT AATATGGGCA	379620
AAATAATAGG TATTGACCTA GGAACAACAA ACTCATGCGT AGCTATAATG GAGCATGGAA	379680
AACCAGTTGT AATACAAAAT TCAGAAGGGG GAAGAACTAC TCCATCTATT GTTGCTTACA	379740

CAAATAAAGG CGAAAGACTT GTGGGGCAAG TTGCAAAAAA CCAAATGGTT ACAAACCCTG	379800
AAAACACAAT TTATTCTATT AAAAGATTTA TGGGAAGAAG ATTTGAAGAG GTTGCAAGCG	379860
AAATAAAAAT GGTTCCTTAT AAAATAGAAA AAGGACTAAA TGGCGATGCG CGAGTAAACA	379920
TTTCAAATAT AAAAAAGCAA ATGTCACCGC CTGAGATCTC AGCAGCAACT CTTACAAAAA	379980
TGAAAGAAAC AGCAGAGGCT TATTTAGGTG AAAAAGTTAC AGAGGCTGTT ATCACAGTTC	380040
CTGCTTACTT TAATGATGCT CAAAGACAAG CCACAAAAGA TGCTGGAAAA ATAGCAGGTC	380100
TTGAGGTAAA AAGAATTGTT AACGAGCCAA CTGCTGCTGC TCTTGCTTAT GGAATTGAAA	380160
AAAAACACGA AGAGATCGTT GCTGTTTACG ATCTTGGTGG GGGAACATTT GACATTTCAA	380220
TATTGGAAct TGGAGATGGT GTTTTTGAAG TAAAGTCAAC CAACGGAGAC ACACATCTTG	380280
GTGGTGACAA TTTTGACGAC GAAATAATAA AACATTTAAT TTCAGAATTC AAAAAAGAAA	380340
GCGCTATTGA TTTATCAAAC GACAAAATGG CTCTTCAAAG ACTCAAAGAA GCAGCTGAAA	380400
AAGCTAAAAT AGAACTCTCA GCGCTCAAG AAGCTTCAAT AAATCTTCCA TTTATTACAG	380460
CAGATGCAAA TGGTCCAAAA CACTTACAAT ATACTCTAAC AAGAGCAAAA TTCGAACAAA	380520
TGGTAGACCA CTTAGTTCAA AAAACAAAAG AACCATGCCT TAAGGCTATT AAAGATGCTG	380580
GGCTTAAAGC TTCTGATATT AATGAAGTAA TACTTGTAGG TGGATCAACA AGAATTCCTG	380640
CTATTCAAAA AATTGTAAAA GATATATTTG GACAAGATCC TAACAAAGGA GTAAATCCAG	380700
ATGAAGCTGT AGCAATTGGA GCTGCTATTC AGGGTGGCAT TCTAACAGGA GAAACTAAAG	380760
ACATGGTACT CCTTGACGTT ACTCCACTCT CACTAGGAAT AGAAACACTA GCGGGGGTTA	380820
TGACTAAACT TATTGAACGA AACACCACAA TTCCTACAAA AAAAAGTCAA GTATTCTCAA	380880
CAGCTGCTGA CAATCAAACC TCTGTTGATA TTAAAGTCCT TCAAGGTGAA CGTGAAATGG	380940
CAGCACAAA CAGAATACTT GGTAATTTTA TACTTGATGG AATACCAGCA GCACCAAGAG	381000
GAGTGCCTCA AATTGAAGTT AGCTTTGACA TTGATGCTAA TGGAATAGTT CATGTGTCTG	381060
CAAAAGATAT GGGAACGGGC AAAGAACAAA AAATTAGAAT TGAATCATCA TCAGGACTCT	381120
CTGAATCAGA AATAGATCGA ATGGTAAAAG ATGCAGAAGC TCATGCGGAA GAAGATAAAA	381180
AATTAAAAGA AAATATTGAA GCAAAAAATA CAGCTAATTC TTTAATTTAT CAAACAGAAA	381240
AATCATTTAA AGAATATTCT GAAAAATTT CAAGCGAAGA CAAAGAAGCT ATTGAAAGTA	381300
AAATAAAAGA ATTTAAAGAA AGTCTTGAAA AAGAAGACAT TTTACTTATA AAATCTAGAA	381360
CAGAAGAAct TCAAAAAGCT TCTTACAAA TAGCTGAGAT GATGTATAAA GATTCTTCCC	381420
AGCAAAATGC AAACAGCCAA CAAGAAAATG GCCCACAAAG CAATACAAGC GAAGAGGCTA	381480

AAGAGGCTGA TTATGAGGTT GTTGACGAGG ATAAAAAATA GTGAAAAAAG ATTATTATGA 381540
AATTTTGGGG CTCTCAAAAG GAGCCTCAAA AGATGAGATA AAAAAAGCTT ATAGAAAAAT 381600
AGCAATTAAA TATCACCCAG ACAGAAATCA AGGGAATGAA GAAGCCGCCT CTATCTTTAA 381660
AGAAGCCACT CAGGCTTACG AAATTTTAAT AGATGACAAT AAAAAAGCTA AATACGACAG 381720
ATTTGGGCAT TCCGCTTTTG AAGGAGGAGG ATTTGAAGGA TTTTCAGGTG GATTTAGTGG 381780
ATTTTCAGAC ATCTTTGAAG ATTTTGGCGA TATTTTGTAT TCATTTTTCCTA CTGGAACAA 381840
AGGACAAGAA AGAAATAGAA AACACGCAAA AGGTGAAGAC TTAGGATACA ACATAGAAAT 381900
ATCTCTTGAA AATGCCATAC TTTGGGTACA AAAAAATAACA TAAACATAAC AAGACAAATG 381960
CTCTGTGATT CTTGTCTCGG GAAAAAATCC GAAAAAGGTA CAAGTCCTTC GATATGTAAC 382020
ATGTGTAACG GCAGCGGAAG AGTAGTGCAA GCGGAGGAT TTTTCAGAGT TACAACAACA 382080
TGTTCTAAAT GTTACGGAGA AGGTAAAATA ATATCAAACC CTTGTAAATC CTGTAAAGGA 382140
AAAGGAAGTC TTACAAAGCA AGAAACCATT CAATTAAACA TTCCCCCAGG CATTGATAAT 382200
AACCAACAAA TAAAAATGAA AGGCAAGGGA AATGTTAATC CAGATAATCA AGAATATGGT 382260
GATCTTTATG TAAAAATATT GATAAGATCT CATAAAGTAT TCAAAAGAAA TGGTAAAGAT 382320
CTCTATGCAA TGCTTCCAAT AAGCTTTACT CAAGCAGCGC TTGGAAAAGA AGTGAAAATA 382380
AAAACAATCG CTTCAAAAGA GATTAAAATA CACATTCCAA AAGGAATAAA CAATGAAGAA 382440
CAAATTTTAA TTAAAAATGC AGGGATGCCA ATTCTTCAAA CCGAAAAGTT TGGAAATTTA 382500
ATATTAATCA CAAAAATAAA AACACCTAAA AATTTAAATT CTAATGCTAT TAAACTTTTT 382560
GAAAACTTGG GCAAAGAATT AAAAGATGGT GATGAAATAG ATTTACTCAA AGCATAATAT 382620
GTATATAACT CATGCCAATT CAATAATTGA AAGCATAAAA AATAACAAAG GATTTGAACT 382680
TTATATATCA AAAAAAAGT CCAAAAACTA AAGAAATTGA ACAGCTAGCT AAAACACAAA 382740
ATATAAAAAT AATAAGAATA AATACAAATG AACTTGACAA AATTCTTAAA AACAAAGACC 382800
ACAGAGGATT TGCATTAAAA TTAAAACTTG AAAAAAATAA AAATGTAAAA ACACAAACCA 382860
AAGATTTTGA AAACCTACTA GAAACATTTA AAAAAAAGA AAATGCTTTC ATTTTACTTC 382920
TAGATGAAAT AGAAGATCCC CAAAACCTTG GAGCAATCCT TAGAACAGCA GAACAGTTTA 382980
GTATAGATCT TGTAATTACT ACTCAAAAAC GCAGCGCAAA AGACAATTCA ACAGTTTTGC 383040
GCACTAGCTC TGGCGCAAGT CAATATGTAA AAAAAATGAC AGTGACAAAC ATAAACAACA 383100
CAATAAATCT TTTAAAAAAC TATGGCTTTT GGATATATAC TGGTGATATT AAAGGACAAG 383160
ATATAACAA AATCAAAATA AACGATAAAA AAATTGCACT TATTTTAGGA AATGAAGGAA 383220
AAGGTGTACA TAAGCTAATA AAAGAAAATT CTGATTTTTT AATAAGGATA CCAACCAGCG 383280

GAAAAATAGA CTCACTTAAT GTCTCTGTAT CTACAGGCAT TTTAATTTTT GAAATCAAAA 383340
GACAATTAAA TCTACTCTAA AGCATTAAAT TATATAAAAA CTTCATTTAA AAAACAAAA 383400
ACATCTTAAT AAAAATATT TTAAAAATT TCCTAACTCA ACAGATGCAA TAAACCCCTC 383460
AGCAGCAGCA GTAATGGCTT GAGCATAAAG TTTATTGCTA ACATCTCCAC ATGAAAAAAC 383520
ACCATCAACG CTTGTTTTAA CAACATCTTT AGTGACAATA AATCCCTCTT CGTCCAAATC 383580
CAAAAATCCC TTAAAAATT CTGTATTTGG CTTATAGCCA ACAGCCATAA ATACAGCACT 383640
CACTTCTAAT TCATAAACAA CATTATCTTT TTTATTAAAA ATCTTAACCG AAGAAACAGA 383700
AGATTTACCA TCTACTTCTA TGGCTTCTGA ATTATACAAA ATTTCAATAT TAGGTAACCT 383760
AGCAACACTA TCTCTTAACA TAGCAATAGC TCTAAGATTA TTTTTTCTTA CAATAAGATA 383820
AACCTTGTC ACCAATTTGC TTAAATAAAT TGATTCTGAA AGGCAGTGT TGCCTCCACC 383880
AATTACTGCA ACCCTTTTCC CTTTAAAAAG ATGTCCATCA CAAATAGCAC AAACAGAAAT 383940
ACCTTTATTC CAAAATAAAC CCGAATTTTT AAGAGTTTCA AGTTTTTTGG GTTTTGATCC 384000
CACAGCAATA ATAACAGCTT TACTTTTATA AATATAATTT TCTGTATAAA GGTAAAAAAT 384060
ATTACCCTTC CTTTTTATAG AAAAAACGGT TTCGGGAAAA GTTTTAGCCC CAAGATTTAC 384120
TACTTGCTCC CTCATATTTA ACATCAAATT TCTACCACTT ATTCCATTTT TAAAGCCAGG 384180
ATAATTGTAA ACTTCTGTGG TTGTAGTAAG CTGTCCCCCG GGTTCAGGAC CTTCCAAAAT 384240
AGCAGCCTTA TAATTACTCA TAACAGAATA AATCCCAGCT GTTAGTCCAG CCGGGCCAGA 384300
TCCTACAATT ATTACATCTT CAATAAAATC TACCTCTTTT TGAGATAGAT TTTTCTTCTT 384360
GGTTAGATTT ATATCAATAG TTTCAAATTC CAACATATCT AAACCTCAGG CCTCTCTTAA 384420
AAATTTGAAT ATTAATCTTA ACATTGCTAA AACTAATATT CAATGCTTAA GATCGACTCA 384480
TAAGTTTGT TATATTAACC TCAAAAACAG AACATGGAAT AAAAATACCA AAATTATTTA 384540
ACACATAAGG TGAAATTTTCG CCAAACCAC CTATATTAAA ACCTTCAATT ACAATATCCG 384600
CTCCCCTGCC ATTAATATAA AAAGTGGTTT TTGATTCTAT TAAATTAATC TCAATATTTA 384660
AATAATAAAA AAGTGTTGCA ACAATTGAAT TAATCTCATT AAAAGAAATT TCTTTACCAG 384720
ACATTAAAAA AGCTAAATTA GTAAAAGTAC TTGTTCTTCG GTAGTATCCA GATTCTTTAA 384780
AGCCACCTTG CCAATTTCAA AAATTTTATG TGGATAGGGA AAATTAGAAC TAACACTTTC 384840
TGATTTTAAT AAATTAGGAA TTATTGATGC TCTAATATAT TCATAATTCT CTGTCATTGG 384900
ATTAGATACT TTAAAAAAT TTTGATCATT AATATTCATT CTGTCAATAA AATCTTTCTT 384960
AGAACCATA TAATTATAAA TCATCTCTTG AAATCCATA CCCACCATA AATTTCTAAC 385020

ATTCTTGAA AACTCTTCTA AAGGACTAAG CCTTCCCCT GCAAAAAGCCT TGGGAAGCTC 385080
CGGATTAAAA CTTGAAAGAC CCTCCCCTAT CATTACATCT TCAATTACAT CAACCTCATG 385140
AAGAAAATCG TTTCTATAAA AAGGTGGAAC AATATAATTC TTAAAATCTT TGGAATAAGA 385200
ATTTACTCCC ATTTTTTTTA AACTAAGGCA AATACGCTCT AATGTTAAAT TGCTTCCAAG 385260
CAGTCTATTA ATATTTTCAA CATTAACTC CACTTCTTCT TGAAAATAAT AAGGACATAC 385320
CAATCTTTTA AAATCTAAAT TAAAAGGCTC TCTAAACACA GTTTTTACGG GCAAAATTTT 385380
AAAACCCATA TCATAAAAT CACAGGCTGC TATAGATAAC GCTAACAAAG TTGCTTCAAA 385440
ATCAATACCT GTAACCTCAA CAAATAAATC AGTATCACCA ACCTTTAAAG ATCCAATATT 385500
GTTAGAATTA ATTATTGGAG GATAAGAGAC TACATTATTA TTATCATCTA ATAATAACGG 385560
AAACTTATCA AAATTTTTTA TAATATGTGA ATATTCCAAT CCTTTGGGAT GCTTTTCATT 385620
TATCTCTAAA AGAGAAAGCT CATAATCCAT TCCAAAGGGA ACAAACCTGT GATTAGGAGA 385680
TGAGGCAATA TAACTTATTG GGAATTTAAT AAAATTAGAA TTATACATCC CCATTGCAAT 385740
TCTTCTTCTC TTTTGTCCAT AATTCTGACA AAGTTTTTCT TGAAATTGAA TTAGTGTCTC 385800
AAGCATTTTA TCATTAATAA TCAATCCTTT TGCTAAAAAT CCAAAAATAA ACGGTCTGAT 385860
TTGAGACATT TTGCCATCAA CTAAAATTTT ACCATAAAAC TTCTTAAAT CTCCCTTTTT 385920
TGAAAAAAAA TCATAATAGG GCATTTCTCC AAAAAAATAC GTTTTTATCT GACGAGCAAG 385980
TCCTAAATAA GACCACAAAT CTGGCCTATT TGTATCATTA AATTCATTT TGATTTTTTC 386040
CGAACTCTCA TCAAACCCAT CAAATCTGC CTTAAATGGT TCAAGTAATT CTGAAATCTC 386100
TAAATTTGTA AAATTTTTTC CTATTTTATC TAAAAAAGA TTTTATAAA TTTCTAACTT 386160
TGGCATCTAT CTTTCCTCGT CTTAAAATAA CATCACCAAT ATCATAAGTA AATAGATCTC 386220
TCAAATCATT TAGACCTAAG TGCATTAAAG CCATTCTATC TATTCCAATT CCCAAGCAA 386280
TAACAGGCAG ATCAATGCCT AAAGGCTTTG TAACTTCTGG TCTAAAAATT CCACTTCCTC 386340
CAAGTTCAAA CCAACCAAGA ACAGGATGCT TTACATGTAT CTCAATCGAA GGTTCAGTAA 386400
AGGGAAAATA TGCGGAACA TATTTAATTT CTGTAGCGCC CGCAAGCTCT TTGGCAAAAA 386460
TTTCAAGAAG GCCTAGCAA GTTTTAATGC TAACACCATC CTCAATAACA ATCCCTTCGG 386520
TTTGATAAAA ATCTACTCCG TGAGTTGCAT CTACTTGATC ATACCTAAAA CATCTAATAA 386580
CTCCAAAATA TCTGCTTGGA TTTTGGCAT TAATTAATTG TTTTGCAGAA AGAACGGTAC 386640
CATGGGTCT TAAAACCAAT CTCTTAGAGA GATCTTCACT AAACTATAT CTCCAGCCTC 386700
TTGAACCTGT TGCATATCCT GTTTCATGGG CTAATTTTAC ATTAGAAAA TAAGGCTCTG 386760
GCAAAGATTC TTGCATGCTA GGATCTGAAA TGTAATAAAC ATCTTAAATA TCACGAGAAG 386820

GATGAAATTG GGGCATAAAA AGAGCATCGT TGTTAAAAAA TTCTGTTTCT ACCAAAGGAC 386880
CATCAAATC TTGAAAGCCA AGACCTACTA ATTTATCTTT AATTTTAGAA ATATAATCTA 386940
AATAAGAATT GGCACGCCCC ATAAAAGTCT TAGCTGATGG AATATGAATA TTGTAAGCTC 387000
TAAATTTTTT GTTCTCATAC GTTTTATTTT TAAAATTTT GGGAGTAAGC TTAGTAAGCT 387060
CATCTCCAGT CAATTTGCTT TTCATTAAAA AATTTTAAAC TTCCAATCCA AAAC TAGATA 387120
ATCTAAACTT TAAATCAAGT TTTTCTATTA TTTTAAAAAA TACAGAGTCT GCTCCTTTTT 387180
TCTTAGCAAA ATTTGATATT AATAAAAGCT CTTCGGTTGT CAACTTTCT CTAAGAAGAT 387240
CGCTATTTTT TGCTCTTTCC AACAAAACAC GTACTTTTTG ATAATTAGTC TCTGTGCCAT 387300
CTAAACAATT TATAATAATC TGTTTATCTA AATCAAGAGA AAGAATGCCC TCTTTTAAAC 387360
AATTACCAA GGCTTTTCTT ACTTCTTTAA CATCAATATC AAGCTCTAAG GCTAAATTTG 387420
AAGCCAACAC TGCCTTTTGA GATACTAAAT TTATTATTTT TTCTTCAACA AAACCATCTC 387480
TTAAAGCACC AAGACCCCTT TCTGTTGCTT TATAAAATAC ATTTAATTTT CTATAAATCT 387540
CTTCAATAAT CCCTTTAGAA TTAAACCATT CAATTGTTTT ATTTGCTTGA CCTTCATTAA 387600
ACCCCAATTT TTCAATAATA ATTGAAGCAG AAATATCATC CTCTTCTTCA TTATTTACAA 387660
TTACTTTTAT CTCAAGAGGG TGCAATGTTT TTATTAAATT TAAATCTGCC TTCATAAATA 387720
TAACCTTCAA TCACCTTTAT TACTTATACC AAGCTCTAAA ATAAGCTCAA CTTCCCCAAT 387780
AGATAATTTG GTAGCTCTAG AAATTTCTTC AGCACTCCAT CCCTGCCTCA TTAATTTTAT 387840
TACAGAATTC CTAACAGTTT CATTATTAAG ACCAACATTA TCTTGATATT TAGAATCAGT 387900
TTTGACAAGA ATACCAAGAG TTTTATTCT CTCTTCTGCT GCAATATTTA AATTCTCCAA 387960
CCTTGCTCTA GATTTACCA CCCTCTCTCT CATAGTCAAA GTATTTTCA ACTTATTTTC 388020
AATATCTAAT AGCATTTCTT TTAAATTTTG AGCATTAATC AACACTTCTT CTGACAACCC 388080
TTTGTTTAAT AAGAGACTTG AAACAACATT TTCCATATCC TTGAGATTGT CTTGAATCTT 388140
AGCACTCTCT TTGCTTAAAT TATTAAATCT TTTCTCCACT TCATTTATTA AATCAAAATT 388200
TTTATCAACA GACTCTATAG TACTCTTTAA TATGCTCTCT TTATTGCTAA TTCTTTCATA 388260
ATTATCAAGA ATAGTTCTCT GCTCGTCAGC TATCTCTTTT ATTTTAGCTT TATATATCTG 388320
CATTTTCATCA TAAGATTCAA TTAACTCTT ATATCTACTA TCAAATGAAG AGTAAAATTC 388380
AAAAATCTA TTAAATCAT TTTTAATAGA TTTAATTGAT TCTTGTTCTA ACTTTAGCTC 388440
ATTAAAAATT TCAATAATAC CCAATGTTTC TTTTGAATA TTATAAAATT CTTTGTTAAC 388500
GTTTTCAAAA TTATTTTAT ATTCTGAGC AAGCCCTATC TCATTTTTTA AAGTTTCCCA 388560

TAATTTTCC AACTTGTCCCT TAAGAGAATA AGCCTCCAAA AATATTGAAT TATTCTTTTC 388620
AAGTTCAGAA TCTAATTTT TAAAATTTTC AATTGATTT TCGATTTGAA AATTTATTTT 388680
ATCATAACTA TCTTCAAATT CTGCTCTCAA ATCAGATTTG TATTCAACTA AATTGTCTTT 388740
AATCTCACTA ATAAATTTGT TAAATTGAAC ATCACAATTT AATATTTTAG ATTCAAGTTC 388800
TAAAATATTA TTATCAACTT CTTTAAATAA TTCTTTATGA TTTTCTTAA ATTCAACCTC 388860
AAATTTATCA ATTTGTTCTT GCAAACCACT CTTTATGGTT TCAATCTCTG ATGTTGAATG 388920
TTTTAAACTT TTTTAAAGCT CATCTTCAAG TAAGCCGAGA TCTGATTTTA TAGATTTAGA 388980
AAACGAATTA TATTCATTCT CAATTGATGT CTCAATATTA TTTCTGTATA AACTAATTTT 389040
CTCAGAAAAT TCTGAAATAT TTTTATTAAT TAATTCAATT TGCCCTTCAA AGCTTTCTTT 389100
ATCACTAGAA ATTACATCAA CCATTTCCCG CCTTACTTTA TCAAGATTAG AAGACAAGGT 389160
TGTAATTC A TGCTCTAATT TCTGATTAAG CTCAAAGATC TTATCTTCAA GATCCTTTTG 389220
CTGAGTTAAA AATTTCACTT CTGCTTGAAT TAAGATGTCT TCTGTTTTTT TATTAACCTT 389280
TTCATCTATC TTTTCTAATT TAAAATCAAC AAATTTTTC AAGATCTAAA CTTTAAGATT 389340
TAATGATTCTG CCAATATTTT TAAAATCAAG ATGAACTGAT TGTTCATTT TTTTAGCCTC 389400
GTTTTGCAAA TTGCTAAAAA TCTCCTCAGC CTTAATCTCA AAACCATCTT TAAAAGATTC 389460
TAAACCAATC TTAACATTAA AAATATCATT CTCAAATGAT TTAATTCCAA GCTCAGCAAG 389520
ATTTATTCTC TTCTCTATTG TGCTATAAGA TTTTCTTGC CAATCTTTTA CATCATCTTT 389580
AATATTCAAA AACCAAGAAT CAATAATACT TTGCTTATTA TTTACAAAAT CAACAAATTC 389640
ATCTACTTTT CCGGTAATAT TGGTTTCCAT TAAAGCTATC TCGCTCTGCA TATCTTTTTT 389700
TTTAGAAGAA AATTCTTTAG TAAAATCTAA ATAAAAATTC TCTTTATCAT CTTTCATTTT 389760
TTGTTCAATA TCTAAACGGA AACTTTGAAT AAGTTCTGTT TTGTTTTCCA AATTTTGA 389820
CAAATCATAT TCTAAATTTT GAATTTTATC ATTATATGAG GCAATAAAGT TTTCTAAAGA 389880
ATATTTAAGC TCTTCGCCTC TAATTTTTAA ATCTTTAAAA AAGTCTTCTT CTAATAATTT 389940
AAGATGTGAT GAAACATTGT GATAAGACTC TTCTTTTAAT CTAATAACAT CCTTTTCAAC 390000
ATTATTTAAA TCAGATTCAA GATTTTTAAG ATTTTTCAGT TGAGATTCAA GTTCAAAAAT 390060
CATCTCTTTA TTTGAACTCT TAAACTCTC ACTTAAAGTT GCAATATAAG AATTTAATCT 390120
CTCTGAAAAC TCATCGTACA TATCAGCATA CTTTTTCTCA AGTCCATCAT ATTGACTTAA 390180
AGCTAAATTA TCAATGGCTT TAATTTTGTT GTCAATTTTA TTCTCTAAAT TTAATTGCCC 390240
TTCATTACAC CTTTCTTCAA GTTCAATATA CTTAAGATTA AAATCATTAG CTATTTTATC 390300
AATACACCCA CTCACCTTAT CATTTAAATT TTTCTCTATG CTATCAAAAG TACTCTCAAT 390360

CGATTTTAAA GAATCAATTC TCTTGTGAAT TTCATTTTCA TACTTTACAA TGTCATCATC 390420
AATCAAGGTA TTTACCTTTT TTATACAAAC ATCAAAATGA TTTTATATAT TCTCTTCAAC 390480
ACCTGCCTTA ATCTCTCCAA ATTGAGAATT TATAAAACCG TAACAATCTT TAATTTTATC 390540
TTGCAATTCT TTTTCAAATT CTAAAATATC TTTTGATCTT TGCTCTATTA TCTCAAAATT 390600
TTGATCCATT TCAGAAATCT TAATTTGCAA ATTTTCATCA TTAAGTTGTA GTGTTTTATA 390660
GATTTTCATCT CTAATTTTTG AAATAGCTCC CTCGCTTTCA ATTAAAAATG TAGAATATCT 390720
CTCTTCAAAA TTAAGTTTAA TAAAGATCGT TTAATAACTC 390780
AGACTTACTC TCAATATTAT TTTTAAGCTC ATTTGTTATC TCCCAAATC TCTCTTTTGC 390840
TTGCATAATA TCGTTATCAA TCGTTCTTCT ATAATCAATT GCTTCTTCTA ATCTAGATTT 390900
ATAATACTGT TCGATCTCTT TAACAAGCTT GTTAATTTTT GCTTCTCCAT CATCTGTAA 390960
ATCTTTAACT TTCAATTCAA ATTTTTCAC TTGATATTTT GATACATCAA AAGATTCCTT 391020
AAGTTTTTGA AGATTTTCAT CCATACCTTT ACTAAGACTA TCTATTCTAT CTGTCAATCT 391080
TCTGCTTAGA TTTTCAATCT CATGCATTAT TTCATTTTCA AGTTTACTAG AAATATTCTC 391140
TGAATACCCC CTATAATTAG ATATCACCTC ATTGTATTTT CCATTAATTT CTTTGTTTAT 391200
ATCATTAAAC TTCACATTAA GAGAATCAAG AGTAATATCT ATGTTAGCCT GAAAAGAAGC 391260
AATATCGGTT CTTTGTCCCT GCAATAAACT ATCAACCTCT TTAACAAATT CCTCTGAATT 391320
ATTTAAACC GCAGCAAATT TTTTGTGATA ATTTTCTTCA AGTTCTCTAG TCTCTTTATT 391380
AAAATGGTTC ATTATGTCTT GCAAAAGCTC ATCAGAGTAT ATGGCACCTT GATTTCTAAA 391440
CTCATCTATT TTCTCAAGAT AATAACTCTC AAGGCTTTCT ATAGAAAATT TAAGCTCTTT 391500
AATTTTTGTA GTCACCTCAG AATCTATTAA ATCCAGATCA ACTTTACCTG AAGACAATAA 391560
ATTTTCAATT TTAACAGTTA TTTCAATTAA TTTACTTTGC CAATCACTAA GCTTGCTATC 391620
TACTTCATTG TTAATTGAAT CTTTCCTGTT TAAAATATCT TTAGAAATTC TATCTAAAAA 391680
ATCATCAATT TGCTTTTGAT TATCCGATTT TATATTAGAG ACAATTTGTA GTTTTGACTC 391740
AATAAATTCA TTAAGATCAG ACTTAAATTT ATTTAAATA TCTTCTGATT CAATCTTGAA 391800
ATCTTTTAAT TTATAATCAC ATTCTTCAAT CTTGCTTATA ACAAATTTAT TCTTATCATC 391860
AAATTTTTTA TTCAAATCCT CAAGCATAAA CACGCTTTTA TCTTTAATTA TTTCTGTTTG 391920
TCTATTAATA AACTCTTTAA TTCCTAATAT AGCCTCATCA CTTTGTGAAT ATGACATATC 391980
TTTAAATTCT TTGTATTTTT CTATCACTAA ACTCTCAATA TCGCCTGTTT TTAATAAAAC 392040
ATATTCCATT CTATCGTTAA CATCTTTTTC TAACTTTTCT ATTTTAAAG TAGCAGATGA 392100

AAGTAGCTCT TCACTAGAAA CCTTAATATC AAGCAAAGAT TTATTTAAAG CAATAAGCTC 392160
ATCTTTCCAA CTGCCATGCA TATCAATAGC TTTTTTTTGA ATATGATCTG ACAGATCATT 392220
AAAAACGCTC TACTAAGCT CTATTCCTTT GTCTTTTTGA ATCTGAATTA AACTTAAAAA 392280
TTCTTCATTT GTTTTATTTA TTTGAGATTC AATATTCTTT AAATTAGAAT CCATTTACCC 392340
TTGCCACTTT GAATATTGAA GCTTGCTTTC TTCTAGCTGA GTAACAAAAA TATTTACCTC 392400
ATCGTAATAA CGATCCCTAA ACTCTACTAT ATTTTACCA ATTCATCTT TAATATTAAT 392460
TAAACTAGTA TTAAAATCTA CCTTTAAAGT CTCTGGGTT TTTCAAACA TATTATAAAA 392520
AGATTCAATT TCATTTTCTA ATTTTTTGTT TAAATCTTGA AATTCTTGAT AATTATTAGT 392580
CGCCTCTTGA GAGAGTGTCT CAAATTTCTC ACCATACATT AAAGAAAATT CATCCATTCC 392640
TGCTGTTAAT TTATCTGTAA AGCTCTTATA TTTAGATTCC ATTTGATTTT CAAATTTAGA 392700
GCTGCTAGAA TCCAAAGATT CAAAAGAGC TGTGTA CTGCTTATAT TATCATTTAA 392760
ATTTGAGTAA TTATTATTAA ACCTACCATT AATTTCTTCA AAATTAGAAA TCAAATTATC 392820
ATTAAGCTTA ATAAGCTTTT CTTGAATATT TGAATCAACA TCTAAGAGTT GGGATTCTAA 392880
CTGCATCTTA AGTTGATTAA TATCACCTTT AAACTTTCA CTAAAACTT CAATATCTGC 392940
CCCAAACCTA CCTTTAAATT CAAGATATAT TCCATTAGAA TCATCTTCAA GCCTCTTTAT 393000
AAAATCAATA GCACCAGACT GAACACTTTC CATTTTAGAA TTCAAATCTA ACAAACCTAAG 393060
CTCTACCCTT TCTCTAATGT TATTATCAAC TTGACTTATT TTATCTTCAT AATCCTCATA 393120
AATATTTTTTA AGATTCAACT CAACTTGAGA TCTAAATTTA TCAAAAACAT CATCAACTTG 393180
CTCTTCATAC TTTCCCATCT CTATTCGCAT TGACTCCTCA AGTGAATTAA TTCTTGAATA 393240
AACATTGTCT TTAAAGGAAG AACTCATAGA AGAAATTTCA TTGTCCACCA AAACCAATTT 393300
ATCTTCAAGC TTATCTTTAA TTTCCCTAGA GCGATCATCA ACATATACTA AGATATCCTT 393360
AAATTTATTT TGCAATTCTT CATTCAGTCT ATTTAAAATA AAATCTTCTT TTTCATTAAT 393420
TTTATCTTTC AACTCTCCA TAATAAGCTC TATAGAATTT TCTATTAACT TATATTTGTT 393480
TTCATAAAAA TTAAAAGAAC TTTCAATCTC TTTGCTGTAT TTGCCAATAT TAAATTCGAC 393540
CTTTTCAAGA AAATCGCTAA ATTCTAAATC TAATTTCTCA TTACCCTTAA CTAAAATATC 393600
ATTTTTTCTC TCTTCAATAT TTGCTAAATC TTTTTCATAA AGACTAATCT CTTTATTTAA 393660
ATTATCTATT TTAAAAACAA GTTCCTTAAT ATTAGTGTCA AACTTTTCCC AACTAGCAAT 393720
TTTAATAGAC TCGAGATTTT CTTTATTAGC CTTGTCAAAT TTTTCTAACA CTGAATTCAA 393780
ATTTGATTCA ACCGAATCAA TCTGAGTATT AAATCCTTTT AAAGTTTTTG AAAGTTTATC 393840
TACTATTTTC CCATCAACTT GCAATCTTTG TATATTCTCT TGAACCTTAA AAGTCATTTT 393900

ATCAAGATCC TTAAGCATAG AATCATGATA GGCTATCTTT TTTTCAACCT CTGCAAAATC 393960
ATTGCTTTTA TTTTAAATCT TTTGCTGAAC TTCCTCAATC TTTTTTATTA TTTCTATACT 394020
AGATCTTTGA TAAGCTTCCA TATCAACAGC AAGATCATT AATCTCTTTG TCTTATCTTC 394080
AATAAAATCT TCAAGATTAA CCTTTGTAAG ATCAACGAAC TTTTAAATTT TATCTAATGC 394140
TCTAGAACGT TTATCGTATT GCCTATAAAC AAATAAACT ATTGAAACCA AAAAAAGGTT 394200
AACTAAAATA GTCGCAAAAT CTATCATAAA ATATTTTACC CATATTCTAT ATATTCAAAC 394260
GTATATATTC TCTTAAGTCT TTATAATCAT GAAAAATAAA GTCAATCATT CCCTTGTAAT 394320
TTATATTCTT TTTTGTGAA AAAAAAGCTG CTTTCATTGA AACATTTCTA GCACCTAAAA 394380
TGTCATATTC ATAAGAATTC CCTACATACA AAATATTATT ACTCCTTAAA TTTAAATCCT 394440
CAATAACTTT TAAAAAAGGT GCTTTATGGG GCTTTAAATA TCCAGTATCT TCTGAAGAAT 394500
AAAGAATATC CCAAAAAGT TCTTGAATGC CCAATAAATT TTTGACACGA CCTAAAATAG 394560
GAAAGTCTGA CATTACACCT AATTTTATTC CTTTGAATTT AAGCCAATAG ATTAAATCTT 394620
GCAACTCCAA GATATGGCTT GAGTTTTTTA AACTTATCGC TAAAAATTTG ACTATAATAT 394680
ATTTTATTTA ACAAAAAAGC ACACCGATTC TCATCAAGGA TTTAAATACT CAGAAAGCAT 394740
TTTGAACCTG CAAGGTAAAA GAGTTCATCC CTATTTGAGG GTGAAAATTG ATTGCTTTGT 394800
AAAATTCGTA TTTTTTTCCT AATCTGTTTA AAAGCTAAAA AAACTTAAC ATTAGTTAAA 394860
AATTCAAAAA ACATTAGCTT ATTTCTATCC GCCTCAGGAT ACAAGGTGCC ATCTAAATCA 394920
AATACTACAG CTTTAATCAT GATGATTGAT TATTTGCCTT TATAGGTATA GGCATATTG 394980
GTAAATTTTC AGGAACTTTA ACTCTAACTA AATGAATATA AGATTTTGGA TATCTTTTCT 395040
GGAGAGACTT GATTGAAGTT TCAGCATTA CTTTCGTTAA AGAAACCCTA AAAATCCTAT 395100
TTTCATCAAG AAATGGAAGA AACAAAACAA CATGTTTATG AAGCACCATG CTTGATAAAT 395160
TGTTAACACC CGTGCTAATA GATCCTAAAT AAATATATCC AGGCTCATCT AAAGCCAGAC 395220
TATATAATAA AAACTCTAAA TTTTCAATTT TATAACCACG ATTGTCAATA TAATCAAAAA 395280
ACTTAATATT ATTGACATCA TTTTCCTTGA TTTTAGATAA ATTTAAATCT ACATTAATAT 395340
TATTTATCCT ATAAGCAATA TTACGAATCC AATCAAGACC AAAAAAGGA TCCTTATTAA 395400
ATTCCTGACT TCTAGTAAAA CCACTGCCTC TAACGCCAAT ATGTCTAAGC TTAAGATCAT 395460
CAATTTTTTA AAGTCTTCCC GTCATTGATT TATAAATCGA ATCCGCTACC CATTTAACAA 395520
ATCCTGAGCA ATTAAACCCT ACAGGATCTT TTTGCAACAG CCCAGTTTCT ATATGCACCA 395580
TTTTACCATA TTCATTCATT GCACCATCAG CAACCTCAGC AATGGGAAAA GATCTAAGAG 395640

ATTTTCTTAA	ACTAATTACC	ATATTAGAAA	TATTTTTTATA	AATATCAAAA	TATTCAGGAA	395700
TAAAATATCT	AAAATCAACA	ACCTTGCCAA	TATAATTTAT	TATATTGGCA	AGAGAAATTA	395760
CCGCAATGTC	TTCAATCTTA	AAGGGCAATT	TAACGTCTTT	ATAAATCAAA	GTATTTACTA	395820
AATAAAAATC	AGCAATAGAA	GAAAATTTTG	AAGACTTTAT	TCTAATAAAC	GTATCCCCTC	395880
TGTTTATAAA	AAATATTTTT	ATCTGCTCAA	TACCCTCTTT	GCCCACTTTA	ATCACGTAAG	395940
ACCCTGGAAA	AATATAACCT	ACATTCTTTT	TTTTATTAAA	AAAAGAATAA	TAAACATACT	396000
CAGAAGAAAT	TTCACCTGAA	ACTTCAATGT	AACAATCTTC	TGTAATAAAA	TGTTTTATTG	396060
GGCTTATTTT	TTTTTGCGCA	TAGCTTGAAT	TAAAATATTT	TAAATATTTA	GTCCTTACAT	396120
CAAATCATA	AAAAAACTC	TCAAGCGCAA	AAAGATTTAG	ACTCTTAAAT	ATTAAGAATA	396180
AAAATATATA	TCTCACTTTA	AATCTCTTAT	TTTTTCCTTT	AATTCTACTA	AAATTGGAAT	396240
ATTTTTATAT	CCAATTTTAC	GCAAATTATT	TACTAAATAA	TTATAGTAAG	AATTTGGAAG	396300
ATTCTTTATT	TTATTTGCAA	AAAGAATAAA	CTTAACAGGA	TTAGTACTAA	CTTGTGTAAT	396360
ATATTTGATT	TTATGAGAAA	TATTTAAATG	ATAATCTTTG	ATCCATAAAT	TTAACATTTT	396420
ATTTAGATCT	GGAGTACTGG	TTTAAAGCTC	AAGCTGATCT	TTTAACTTAA	AAGATTCTTT	396480
AAAAAGAGAA	TCTAAACCTA	TCCTTTTATG	AACAGAAATT	CTAAATATAG	GAGCAAAATT	396540
TAAAATAGGA	AAAAAAACT	TCACATGGCT	CTTTAAGGCT	TCAAATAAAC	CTTTAGACTC	396600
ATCCACAAGA	TCCCATTTGC	TAAACACAAT	AACAATTCCT	TTCCCCTTTT	TAGTAACATA	396660
ATGAGCAATT	TTTTTATCCT	GAGAAGTCAA	TTTTTCTTGA	ACATCAATCA	ATAAAAACAC	396720
AATATCTACC	ATGTCAATTA	CTTTTAGGGC	CCTATTAACA	GAATAATATT	CAACAATTTT	396780
ATTTACTCTT	GCCCTTCGCC	TTATCCCAGC	TGTATCAACA	ACCTCAAAAA	CTTTCCCAT	396840
TCTAGTAAAC	TTAGTTTTAA	TAAAATCTCT	AGTAGTACCA	GGTTGATCAG	AAACAATTGC	396900
AATTTCATTT	CCAGATAAAT	AATTAATAAG	GGTAGATTTG	CCTGAATTAG	GCTTGCCTAT	396960
AATCCCAACC	TTAATATCAG	CGCCACTCTC	AATGCCAACT	TCACCAACTT	CTACTTTTAA	397020
AAAATCTCTA	AGCTTAGTAA	TGCCTCGACA	ATGGGCTGCA	CTAACCAGAA	AATAGCGCTT	397080
GAATCCTAAA	TTATGAAATT	CGTGAGCTAA	ACATTCCTTA	TCCTTAGTAT	CTACTTTGTT	397140
TAAAACCAAA	ACCACCTTAC	TACTATATTT	TCTCAGTCTT	TCAATAATCT	GATAATCTTC	397200
AAGTAAAATT	TCATTAATAT	CTAAAACCAA	TAAAATTAAA	TCAACTTTTT	CTAAAGAGCT	397260
TAAAACCTTT	TGCACAACAA	TTTTGCTAAT	CTCATCTTTC	AAGATAGTAA	ACCCACCAGT	397320
ATCGATTAAT	TTAAACTTAA	AAGAATCAAC	CTTACAAACT	TCTTCAACTA	AATCTCTAGT	397380
AACACCGTAA	GTACTCTCAG	TAATACTTCT	TTTTGTATCT	AAAATTCGAT	TAAATAAAGC	397440

AGATTTACCA	ACATTTGGTC	TACCAACAAT	AAGAACCCTTT	TTATAACTAA	GCAAAGCAAA	397500
TACACCTCTT	TATTTATTCC	GATATTTCCA	TTATAATAGC	AAATATTAGT	ATTTATGCCA	397560
ATTACACATG	AGTGTTTATA	TTGAAAAGAA	AAAAAAGTTC	AAGCTCAACC	AAATCAGACA	397620
TACTTTTAAT	TTTAATTGCT	ATTGTTTTAA	CAATAATTAG	TGTGCTATTA	ATAATTAAAA	397680
ATTCACTTAT	TATACATATT	TTTAAAGAAA	AAAATTATGA	TAACAGTTTA	TTCGAATCAA	397740
GTCAAACACA	AGATAATAAA	TTAATTGAAG	CTAAAAAATA	CACCAATAAA	AATACAAATG	397800
TAAAAATACT	TAAAAATGAA	AGTTTTTTAA	TCCAGCCACC	AGAAATAAAA	AAACTTGAAG	397860
AAGAGCTCAA	GCAAAACCAA	AGAAATAATA	ACCTTAAAAA	CAAAAAATTT	ATTAAACTTT	397920
ATTTTATAAA	AGTAACCCCA	GAAGGTATT	TTTTAAGACA	AACTGTAAAA	AGAGCTATAT	397980
ATTACGACAA	AAATATTCTT	GAAGAAACAC	TAAAATCTTT	AATCAAAGGA	CCAAATGAAT	398040
ACGAGCTAAA	AAATAATTTT	TTAAGTTTAA	TCCCTATAAA	AACCAAGCTT	TTAAATTTAA	398100
GCCTAAGCGA	AGGAATTGCC	AAAATAAACT	TATCTAAAGA	ATTTTATGAA	AATAGTTTTG	398160
GAATTGAAGG	AATAATTAAT	CAAATCGCTC	AAATAACCTT	AACATGTCTT	GAAATTAAAG	398220
GAATTGATGG	AATAATTTTA	ACAATAGAAA	ATAATCCAAT	AATACTTGAA	GAATTAAACT	398280
TAAATTTCTC	AGGAATATTA	AACAAAAGG	CTCTGGACAA	ATATTAAAAT	TCAATATTGC	398340
TAAGCAATTG	CATAGAGCTT	GCAATTCTTA	AAACACTTGA	CTTAACAAC	AAAAACATGA	398400
ATTCTTGATT	GCCTTTTTTA	CCTTTAGTTT	TTAACTTTAA	TATCTTTTTA	ACTTGTAATT	398460
TATTTTTATA	GAACTTTCA	ATTACGCTTT	GCAAAATTAT	CTTCAAATAC	TCACCACTCA	398520
CAACACCATT	AAAATTTTTT	ATATCTAAAT	TTAACTTTTT	AAACTCAAAC	TGAGGTTTAA	398580
TCAAAACTAT	AATAAAATTA	TCAGAAAGTT	TATCTATTAA	ATTACACAT	ATACTTATTG	398640
ATGATCTAAA	AGAAACATCT	ACAACGGCAA	AATTGGGAAC	AATCTTAAAT	TCTGTAACAT	398700
CAAAAATATT	AGTTCTCTCT	AAAACTTTAA	CTCTTGGATC	AATTCTTAAT	TTATAAGAGA	398760
GTTGATTAAT	GCCTACATCA	ATTGAATAAA	CAAAATTGGC	GCCACACTGC	AATAGACAAT	398820
CGGTAAAACC	ACCAGTTGAA	GAGCCAACAT	CAACACAAAT	TTATTTTTTA	ACTTCGATTT	398880
CAAAATCTTT	AAGAGCCTCT	AAAAGCTTGT	AACCTCCTCT	TGATACAAAT	GTTTGACAAG	398940
TATTCTCAAC	TAAATCTATT	TTACTTGTTT	TGTTTATTAA	TATTTTAGGA	TTTTTyTCTT	399000
TATGAGAATT	TACATATATA	TTGCCTTTTA	GAATTAAGAT	CATTAATTCT	TTTCGTGTTT	399060
TTTCTGGATA	CCTTTTACAA	AGTATATTTA	ATAAATTATT	TCTGAATCCT	TTCAATTTTT	399120
AAAGCGCGGC	CTGTCTTTAA	ATTAGAAGTA	ATAATAACTC	CTTGTAATAA	TGTGTCATCT	399180

TCTACAACCTT	CAGCTCTCAA	GGGGGTATAT	TCAAGTAAGC	CCTTAAGAGA	AATGTCGGGA	399240
TTAAATCCTA	TTACAGAATT	TAATCCACCT	GTCATCCCAA	TATCACTAAT	ATAGGCTGTC	399300
CCCTTTGACA	ATATTCTTTC	ATCTTGAGTC	ATAACATGGG	TATGAGTACC	AACCACACCT	399360
GTTACAAAAC	CATTTAAAAA	ATATCCAAAA	CTTTCTTTTT	CATAATTACT	TTCAGCATGA	399420
AAATCTACAA	AAATGGTTTT	GGCTTTATTA	CTCAGCATAT	TAACCAATTT	TTTTGTATTA	399480
TCAAAAGGAT	TTTTAACAAT	AAAATTCATA	TTTAAAACCC	CTTGAACATT	AACAACAGCA	399540
ACTTTTTTCAT	CTCTAATAGT	TAAAAACAA	TAACCATGCC	CATCTAACAA	ATCTGAAAAA	399600
TTATTTGGCC	TTAAGATATA	TGTTTGCTTA	TTTAGGTAAT	CATTTATTTT	GCAATTAGAA	399660
TACACATGAT	TACCGGTAGT	AATAACATTA	ACCCCCGATC	TAAAAAGATT	ATTTGCTATT	399720
TCTGGAGTTA	TTCCAAAACC	ATTTGAAGAA	TTTTCTCCAT	TAGCAATTAC	TAAATCTATT	399780
CTATATTTAT	TCTTAATGTT	TTTAAGATTA	AAAAAACTT	TTTTTAATCC	ACTCTCGCCT	399840
ATTATATCCC	CAATTATCAA	GGTTTTAATA	GTGCTATCTT	GCATATTCAA	TAACCTCGGT	399900
TTGCGGAATA	ATTGTAACCT	TAATTTTTCC	AGGATATCTC	ATTTGAGCTT	CTATCTTCTT	399960
AGCAATATCT	CTTGCAAGTA	AAATTGACTT	TTCATCATTA	ATTAAAGCAT	TGTCAACAAT	400020
AATTCTAACT	TCACGACCTG	CCTGAATAGC	ATAACATTTT	TGAACACCCT	CAAACTATA	400080
CGCAATGTCT	TCAAGTCTTT	TAAGTCTATT	TATATAGTTA	TTTAACTTT	CCCTTCTTGC	400140
TCCAGGACGA	GATGCTGAAA	TGGCATCTGC	TATTTGAACC	ACAATAGCCT	CAAGACTCTC	400200
GGGTTTCACC	TCATTGTGAT	GCGCAGCAAT	AGCATTAACA	ACAATTTTCG	TCTCTCCGCA	400260
ACTTTGAGCA	AGTTCAGCAC	CAGTAATAGC	ATGTCCCTCG	CTATTATCAG	AAATACTTTC	400320
CATCCCTTTC	CCAATATCAT	GCAAAAGGCA	TGCTCTTTTT	ACTACAACAG	GATCTAATTT	400380
CATCTCTTTA	GCCAAAATTT	CTCCTATTAT	AGCCGTTTCT	TTAGAGTGGC	TTAAACATT	400440
TTGACCATAA	CTGCTTCTAA	AGTAAAGCCT	TCCCAACCCC	CTAATAAGTC	TCTTATCAAG	400500
CCCATGTATA	TTAAGGTCAA	AAACCACCTT	CTCACCTCT	TCTTGAATAA	TGCTATTTAT	400560
CTCATGGTA	ACATTATACA	CAACTTCTTC	AATCCTAGCA	GGATGAATTC	TGCCATCTGT	400620
AACAAGCCTT	TCTAAAGTCC	TCTTGGAAG	CTCTTTTCTT	ATTGGATCAA	AGCAAGATAT	400680
AACAACAGCT	TCAGGCGTAT	CATCAATAAT	GATATCTGCT	CCTATTAAAG	TCTCAAGAGC	400740
CCTAATATTG	CGCCCTTCTT	TACCTATAAT	CCTACCTTTC	ATCTCATCAT	TAGGTAGCTC	400800
AACAGAAGCC	ACTGTAAACT	CAGAACTCAC	CTCCGTAACA	ATACGCTGCA	TAGTAGATAC	400860
TAAAATATCT	TTTGCAACCT	TATCTGCTAA	TAGCTGTGCT	TCCTGCTCAC	TTTTATTGAT	400920
AATAACTTGA	GCATCTCTTT	TGACTCATG	CTCAACTTTT	TCAATTACAA	TTTTTCTTGC	400980

ATCTTCTCTT GTAAGACCAG AAATATTTTC CAATCTTTTA ACAAGATCGG CCTCTTTTTTC 401040
TCTTATTACT TTTTCTTTTT GTTCAAATTC TTTAATTTTA AAATCAACTC TAGACTGCTG 401100
TTTGTCAAGA GCAGATATTC TCTTATCTAA AGTTTCTTCT CTTTGTAATA ATCTTTTTTTC 401160
TAAATTAACA ATCTCATTTT TCCGATCTCT TATATCCCTA TCTTGCTGGT TTTTTCTTTT 401220
AAGCATTTGA GATTTTGCAT TAGCAATAAT TTGCCTTCTT TCATTTTCTA TCTCTAATTG 401280
TGATTCTACT CTTACTTTTT TCAGATTTTT TTCTAAATCT AATAAAGACA ATCTACCTAA 401340
AAAACTCTT ACTAAAAATC CTAATATAAA GCCAGCAAAA ATAGAAGAAA AAATAATATA 401400
TATCATATCA TTTAACTCCT ATGCTGTTTA AAAGCAATTT AAAATTTAAT CTTTAAAACA 401460
GTGCCCTCAA ATTATTAATT ATTCAACTTT TAAAGGCTTT TCAACTAATT CTAGGATAGC 401520
CATTTAGCC GCATCTCCAT ATCTTTTTTC TAATTTAATC ATCCGAGTAT ACCCACCCT 401580
TCTTTGTCTA AAAACAGGAG AAATTTTGGT AAATAGCTTA TTTAAATAT GCTTATCATG 401640
TATAAATTTT GATAATTCTC GCCTATTATG CACAGTATCA ACTTTTGCCC TTGTAATCAA 401700
TCTTTCAGCA AATCTTTTAA CTTCGAACAA TTTTGTCTTA GTGGAAGAAA TTTTTTCATG 401760
CTTAAAAAAA GAAATTACCA TATTTTTTAA AAGCGCTCTC CTGTGACTAG ACTTCCTACT 401820
TAATCTATTA AAACCCAATT TTGTTTTCAT GAAATAGCCT AAATCTCCT TTTATTCAGA 401880
TATTTTAACA TTCTTACTCA ATACAGATAG AGCATCTTCT TTAGACATTC CTAAATATAA 401940
TCGATAAGAA CCAAGTTTTT CGATTATCTC TTCCAAACTT TTTTCCCAA AATTTCTAGC 402000
TTTAGAAAGC TCTTCTGCGT TTTTACTAAT AAGTTCTCCT AAAGTCCTAA CATTTTCTTT 402060
GGCCAAACAA TTTAAAGATC TGAAGTACAA ATTCAATTTT TCAATACTCA TATCAAGCAA 402120
GTTAGAAGTT TCTGATTTTG ATTTCTCAAA AGATGTATTA ACATTGTCTT CAAAATCAAC 402180
AAGAGGAAAC AAAAATCTC TTAATATTGA TGCAGCCTTT TTTATTGCAT CTTTGGCAGA 402240
AATCACACCT GTAGTCCAAA TTTCCATTAC AAGCTTGTC TAATCTGACC TTTGACCAAC 402300
CCTAGTATCT TCTACAGAAT ACGAACTTT CTCTATAGGA GAAAATATAG AATCTAAAGC 402360
AATAACATTA ACCTCTTCTA AATACTTAGA ATTTTGCTCA GAAGACACAT AGCCCCTACC 402420
ATAATTAATT TGAAATTCAA GATCTAAATT AACATCATGT GATAAAGTAG CTATAACTAA 402480
ATCTTTATTA AAAACCTCAA CTCCATCTCT TTCAAAATGA GAAGCTTTTA AAACATTGGT 402540
GTCTTTACCG CTAACACTAA AGCTTATTGT CTTTCTTTGC TCTCCTTCTC CAAGTTTCAA 402600
ATGAATATTT TTAATATTAG CAATAATCTC AAGAGTATCT TCAGAACTC CAGGAATCAA 402660
ATCAAATTCA CTTGAAACAA CCTTTGACGA AGAGTCTTTA TTGTTAGACT GAACTCTCAT 402720

AGCAGTAATC GCATACCCTT CAATAGAAGA AAGTAACACA CGTCTTAAAG TATTACCTAT 402780
AGTAATTCCA AAGCCTCTTT CAAAAGGATA TATCGTAAAT TTACCATAAG ACCCATCACC 402840
TTGGCTTTTC AAAAATTCAA TTTTTCAGG TATAGTGAAA TCTTTCAAAA ATTTTCCAC 402900
AAGCATCATA ACTCCTTCTA GCTAAACTCG TCTGGTTTTT TTCGGTCTGC ATCCATTATG 402960
AGGAATGGGA GTAATATCTG AAATTGATTT TACAGTCATA CCAATCGAAC CAATAGCTCT 403020
TATTGCAGAT TCTCTGCCAA TGCCTGGCCC TTTTATATAC ACATGAACAT AATTAATTCC 403080
AAAATCTCTC ACTTTATTTA AAGCAGACTC TGCTGTTATT TGAGCAGCAT ATGGGGTCGA 403140
CTTTTTCAGCA CCTTTAAAAC CCATACCACC AGCACTTGCC CAAGCTAAAG CATTTCCCTT 403200
TATATCAGAT ACAGTAACTA TGGTATTATT AAAAGTAGCT TGTATATAAA CGTTTCCTTC 403260
TCCGATATTT CTTTAAATTT TTTTTTACT ATTAGTTGAT AATTTTGCGC TCAACTTGCC 403320
CTCCAAATCT TAAAACTAT TTATTTGCTA GCTATTTTCT TGTTAGCTAC AGTCTTTCTT 403380
TTTCCTTTTC TAGTTCTTGC ATTCGTTTTA GTTCTCTGTC CTCTCAAAGG CAATCCTTTT 403440
CTATGCCTAA CGCCCCATA ACACGCTATA TCCATAAGTC TTTTAATAGA CATTGCAACT 403500
TCACTTCTAA GTTTTCCTTC TACAATATAA TCGCTCTCAA TTACCTTCCT AAGTCGATTA 403560
ACTTCATCAT TATCTAAATC TTTAGCAATT TTGCTTGGAG AAATACTTGA TTTATTGCAA 403620
ACTTCCAAAG CTCTTGTCT ACCTATACCA TAAATAGAAG TAAGAGCTAT TTTTAATTGT 403680
TTATTATTTG GTAAATCTAT TCCCGATATT CTAGCCATTT TATTTCTCT AATTTTTACT 403740
TTTGTCTTTG TTTATGCTTT AAATTATCAC AAATAATTCT TAATACACCT TTTCTTTTTA 403800
TAACCTTACA TTTTTCACAA ATTGGCTTTA CACTTACTCT AACTTTCATA ATCAAACACT 403860
CCTAAATTTT TTGCAAAAAT GCATAATTCT TTTTATTTCC ATGAGAAAAT CCTTGAGTTT 403920
TCAAATAAGC ATCAATATGA ATTAATGTAT CAAGAGCAAC CCCTACCATA ATAAGCAAAG 403980
AAGACCCCCC CATTATTCTA GAAACATCGT GTGGAAATCT AAAAATATTT TGCACATAAA 404040
ATGGAATAAT TGCAATAATT GACAAAAAAA TAGATCCTGA AAATAAAGTT TTATTCATAA 404100
TTTCATCTAA ATATTTTTC ATCTCATCAG ACTTTATTCC TGGAATAGTG CCCCCATTCT 404160
TACGAATATT ATTACTTATG TCTTTAGGGC TTAAGTGAAT CTTAGAATAA AAATACGTAA 404220
ATCCAATTAT CAAAATTACA TTCAAAAAAG TATAATAAAA ACCATTAGGC CTTAAATAAG 404280
ATAAAATTTG CCTGGCTATG GAAGAAGTTT CTGCGAAGCC ACTTAAATTT TGTAAGGCA 404340
GAGTAATTAA AACAGAGGCA AAAATAACAG GCAAAACGCC CGATGGATTG AACTTGATTG 404400
GCAAAATATGA ACTAACTGTA TTATTAGAAT TTGCTCTAGC ATAATGAATG GCAATTCGCA 404460
TTTGAGCCTT ATATTCATAT ATAATCAATA TAACAACTAA AATAAATATA CTTATAATAA 404520

GTATAACAAA AACAGGATTA ACATTTTGAG AAGGATCCTG CATGCTTTGG AATAAGTTAA 404580
ACAAAGCTGC TTGAAGTCTA ACCACTATGC CAGAAAAAAT TATCAAAGAT GTTCCATTAC 404640
CTACACCTCT TTGATTAATT TGCTCTCCAA ACCACAAAAG GATAAATGTC CCCGTAAGTAA 404700
CCGTTAAAAAT AGCAACAAAT ATATATCTAT AAAAGGGAAT GGTAACAGCA CCCGGAATAC 404760
CTTTAGCATA AAGGCTTGTT GCGTATCCTT GAACTACAGC TGCAACTATT GTTAAATATT 404820
TTGTATATTT TTTAGTCTTT TGTCTTCCGC CGTCACCTTC TTGCATTTTT TTCAAAGAAG 404880
GAAAAGAATA AACAGAAGC TGAACAATA TAGATGCCGA AATGTAAGGC CCTATACTAA 404940
GCATAAATAT AGAAAAATTA CTAAAAGCTC CCCCTGAAAA AAAATCAAAA TAATTAGCAA 405000
TTGAAAAATC TGATTGCGAC TTGAAATAAC TTTTAAGAGC TACAGAATCT ATTCCTGGTA 405060
TCGGCAAATA TGAACCAACT CTAAAAAGAA AAAGAACAAA TAAAGTAAAC AAGAACTTAT 405120
TTCTCAAATC CTTAACGGTA AATAAACTTA AAAACAATTC TTTCATCTTT ATTCCACTTT 405180
AAACTAATTG AATAGTACAA CCAATTTTTA TTACAAGGCT TTCGGCAGAT TTAGAAATTT 405240
TAGAAACCTC AAAAGAACT TTTTTTGTA GCTTACCATT AGACAAAATC TTAATTTTTT 405300
TATTTTTCTT TTTTATAAGT TTATTTTCAA GCAAAGTATC ATAATTGACA ACTTGTCAT 405360
CCTTAAATTT TTTATCTATA TCTCCAAGAT TAACAATTGC ATATTCCAAT TTATAATCAC 405420
TATTAGAAAA ACCTTTCCTT GGCAATCTTC TATAAAGAGG AGTCTGCCCA CCTTCAAATC 405480
CAAGTCTTGG CGAAGTATTT CTGCTTTTTT GCCCTTTTTG ACCTCTCCCA GAAGTTTTGC 405540
CAAGTCCTGA ACCTGGACCT CTGCCAACAA TTTTACGTCG CTGCTCGCT CCCTTAGGCT 405600
TTAACAAGTT AAACATTACA TTACCTCGCT TAATAAAATC ATATTAATAG TCTCGTTAAG 405660
CATACCCTTA ATAGATTCAT TTAAAAATG AACCTTTTTA TCGCCTATTT TATTTAAACC 405720
TAATGCTTTT AAAACTTTGA CCTTTTTATT TAATTTCCCA ATAAGACTTC TTACAAGAAA 405780
AACTTGCACA TTAATATTGT TTTTAGAAAT AATTTTCTA TTATTTTCCA TTCTTTTAAT 405840
AAAACATTTA TTCTTAGATC TAGACCTTGA AGCATTAAC CTAGCTTTCT TTAGTTGTAA 405900
TCTTAATTTT CTTTTAATCA TACATTAACC CCATAAAGTT TTCAAAGTTT TTCCTCGCAT 405960
TTCTGCTACT TTTTCAGCAT TCAAACTAA ATCAAATGCC TTAAAAGTCG CCTTTACTAC 406020
ATTCATAGAA TTATTAGAAC CAAGAGATTT GCTCAAAATA TCATGCACTC CTAAAGCCTC 406080
CATTACAGCA CGAACAGGGC CCCCTGCAAT AACACCAGTA CCATGAGTAG CTGGTTTGAT 406140
TAAACCTTA GCTTTTTTAA AGCAGCCAAT AACCTCATGT GGCAATGTTT CTTTTCGAAT 406200
AGGAACAAAT CTAAATTCT TCCTAGCACT TGTAAACTT TTTTTTATTG CATCACTAGC 406260

ATCATTAGCT TTACCAAAGC CCCAACCAAC ATGTCCTTCT CCATCTCCAA CAACCATGAA	406320
AGCAGCAAAA GAGAATCTTC TTCCGCCCTT AACAACTTA GTAACCTGT TGAGTGATAT	406380
TAATTTTTCT ATCTGCTTTC TTTGAGCATG AACATCTACC ATAAATACAC TCCCTTAAAT	406440
ATTAATACCA AACTCTCTCA AAGAAGTTGC AAAACTTGCA ATAAGTCCAT GATACTTATA	406500
ACCATTTCTG TCAAAAATAA GATTATTTAT ATTTTCTCC TTAAGCCTTT TAGCAAGAAC	406560
TTCTCCAAGT TTTTTTACAT CATCAATATT TTTGCCTAAA TTAAGACTTT TTTCAATAGT	406620
AGAAATACTT GCAATAGTAT GTCCCTTACT ATCATCTATA ACTTGCGCAT AAAAATACCT	406680
ATTAGATTTA AATACAGTAA TTCGTGGCCT ACTAGCTACT CCGCGCCCTA TTTTGTCTT	406740
TATTCTTTTT TTACGTCTAA GCTTTCTCTG TTCTGCTTCT TTTATTTTTT TCATAATTAT	406800
TAACCTAAAA TTTATTTTTT TACACCAGAT TTTCCAACCT TTCTTCTAAT AACTTCATTA	406860
TCATACTTAA TACCCTTTCC TTTATACGGC TCTGGTTTTT TTAACTTCT AATCTCAGCA	406920
GCAACCTGAC CAACCTTAA CTTGTCTATT CCTTCAACTG AAATTTTAGT ATTCCCATCA	406980
AGCTTTACGC TAATACCATC TGGAATAACA TATTCAACT GAGTTGAATA ACCAAGGCTT	407040
AAAAAAGGC TATTGCCTTG TTGCTCTACC CTATATCCTA TACCATTTAT AGTAAGAGAC	407100
TTAGAAAATC CTTCAATCAC TCCTTTTACC ATGTTAAAAA TTAACTTCT GTAAAGACCA	407160
TGGTAGGCTT TTGCTTTTTT ATCATTTAAA ACTCGATCAA CAATAACGCT GCCATTCTCA	407220
ACTTTAACAT TAATACTGTC TTTTATATCT TGAACATACT TTCCCTAAT ACCTTCAACT	407280
ATCACTAAGT TGTCTTTAAC ATCAACCTTA ACAGCATCTG GAATCTTTAT CGGAAGTCTT	407340
CCAATACGTG ACATACATCC CCCTATTAAA CTACCAAACCT GAGCAAATCA ACTCACCACC	407400
TATTTTTTTA TCTTTAGCTT CCTTACCAGT AATAACACCT TGAGAAGAAG ATATAATTAA	407460
TATTCCATAT CCATTCTTTA TTCTTGGCAT ATTTCTATAT GAAGAATAAA TTTTCTACC	407520
AGGAGTAGAA ATGGCATCTA TTTATTTAT AACAGGATTT CTTTGTGTGT CATACTTTAG	407580
CAAACCCCTA ATAAAAGCAA TTCCTTTCTT TTCTAAAAAA TTAAATCCT TAATATAACC	407640
CTCTTCTTTA AGAATGTTTA ATATTGATTT ATTCATATTA GACATCTTTA AATCTACAGA	407700
TCCATGCCCA ACTCTGCTTG CATTTCTTAA TTTAGTTAGC ATGTCTCCTA TTGAATAAGT	407760
AATCGCCATA AAATTCCCTT ACCAACTTGA TTTTGAAACG CCAGGAATTA ATCCTTCAGA	407820
CGCATACTTT CTAAACATA TTCGACACAT AAAAAATCT CTTAAATATC CTCTTGACG	407880
ACCACATAAT TTACATCTAT TATTTTGCCT TGTTTTATAC TTAGGCTTTC TTAAAGCCCT	407940
AATAATCATT GATTTTTTTG CCATATACCT TATAAATCCC CTAATTACTA AACGGCATTC	408000
CAAATTTCAA AAGCAAAGCT TTACTTTCTT TATCATTTGA AGCTGTTGTC ACAATTGTAA	408060

TATTCAAACC AGATATTCTC TCTATTTTAT CATAGTCTAT TTCAGAAAAT ATTATTTGTT 408120
CCGTTATCCC AAAAGAGTAA TTTCCATTGC CATCAAAAGC ATCCCCATTG ATTCCCCTAA 408180
AATCCTTAAC TCTTGGCAAT GCTAAATGAA TAAGCTTATA TAAAAATTCA TACATTGCAT 408240
TGCCCCTAAG TGTAACCTTA GCACCTATTT CTTGTCCTTG TCTAATTTTA AACCCGGCTA 408300
TTGCTTTTTT TGCTTTTGTC TTTACAGCTT TCTGACCAGT GATCTGAGCA AGCTCTAAAA 408360
CAGCAGAATC TAATAACTTC TTATTCCTAA CAGCCTCCCC AACACCTACA GAAATCACTA 408420
TCTTCTCAAG CTTGGGAAC TGCATTATAG ATTTATATTC AAATTCCTTA ACAAGCTCTT 408480
TTATAACACT GTCTTTTATA TATTTCTTCA ATTCAGGAAC ATAATTCATA AACTCTATAT 408540
CCTCTGTCCA TTTTTTTTAA GATACCTTAT TTTTTCATTA TTTTCAAATC TAATGCCCAA 408600
TCTTGAAGAA GTTCCCTTGA CAAATATCAT CACATTTGAA ATATCTATAG CGGCCTCCTT 408660
ATCTATTATT CTGCCTTTTT CTTGGGGTGT CCTAGCTTTA ATGACTTTTT TAACCATATT 408720
GCAAGATTCA ACAATAACTT TATTTTTTTT TCTATTTATA CTAGCAATCT TACCTATTCT 408780
ACCCCTATCT TTTCCAGAAA GAATTTTTTAC GCTATCACCT ATCTTCAACT TTGTCTTCAC 408840
AAAACCCCT TTTGCTATAT AACCTCTGAA GCCAATGATA CTACTTTCAT AAAATTAGCA 408900
TCCCTAAGTT CTCTTGCAAC AGGCCCAAAT ACCCTTTTGC CCCTAGGACT TAAATTAGCA 408960
TCAAGTATCA CACAAGCATT ATCATCAAAC CTAACATAAG TTCCGTTTTT ACGTCTTACT 409020
TCTTTAGAAG TCCTAACAAT TACGGCTTTA TAAACATCTC CTTTTTTAAC AGAAGAATTA 409080
GGAATTGCTT GTTTTACTAC AATGGTTATT ATATCCCCAA TTTTGGCATA ACGCCTTTTA 409140
CTGCCACCAA GCACCTTAAT ACATTGAGCC ACCTTGCCAC CAGTATTATC CGCAATTGTT 409200
AAATAAGTTT GCATCTGAAT CACAATCAAC CTCCTTTAGA AAAATCAAAA CTATTTTAAT 409260
TTTTCTAAAA CCTCAACAAG AGACCATCTT TTATCTTTAC TAATAGGTCG AACTTCAATA 409320
ATTTTACCT TATCGCCAAC CTTTGAAACT TCTTTTTCAT CATGTGCTTT AACTTTTTTA 409380
CTAACCTTTA AATACTTATG ATAAATTGGA TGCATCTTTC TTTGAACAAT TTCTACTACT 409440
ATAGTCTTAG ACATTTTATC ACTAACAAC TTACCAATTA ATTCTTTTTT ATTTTCTCTT 409500
GCCATATCTA AACCTTTCTA ATACCTAATT CATATTCACA AATCATTGTA TTAAGCCTTG 409560
CAATAYCACG TCTAATCTCT CTTTTCTTTA AAGGATTTTC AACATGACCA ACAACAGATT 409620
TAAATCTTAA ATCTAAATAT TCTTTCTTTA ATTCTAGCCT TTTAGCCTTC ATGTCCTCAA 409680
GAGTAAAATT TTTGAAATTT TTCAACATAA TTACCTCAAA TCTCGCCTTA CAACAAACAT 409740
GGTTTTTACT GGAAGCTTAG AGCTTGCAAG CGACATAGCC TCTTGAGCAA GTTCCTCAAC 409800

AACCCCTGAC	ATTTCAAACA	TAACAGTGCC	AAGCTTAACA	GGAGCATTC	AATGATCAAC	409860
ACCCCTTTG	CCCTTACCCA	TTCTAGTTTC	AGCTGGTTTT	TTAGTATAAG	GAATATCAGG	409920
AAATATTCTT	ATCCAAACCC	TTCCGCCTCT	TTTTATTTTA	CGAGTCATTG	CAATACGAGC	409980
AGCCTCAATT	TGACGAGCAG	TAATAAAATT	TGTTTCCAAA	GAAACAAGTC	CATATTCACC	410040
AAAAGAAATT	TTATTGCCCT	TCTGGGCCTC	TCCAGACAAT	CTTCTCTCT	GCTTCTTTCT	410100
ATATTTAACC	TTTTTTGGAC	TTAACATCTA	ATTATCCTCC	AATATCCTGC	TCATTAGAAT	410160
CGTCTCTTTC	TTTAGAAAAA	GACGCACTAA	ATTTTTTTTT	GTTTAAAAGA	TCTACTTCAT	410220
CTTTAGACAG	CCCATCTTTT	TTATCCAAAA	GCCTAGTTTG	CTTTTCATTA	GCCTTTTCTC	410280
TATTATTTAA	AGTTTTATCA	AAATTTTTTA	CAGCATCGCC	TCTTTCCTTA	AAAGGCTTTT	410340
TATTTATTAC	CTGGCCAGCA	TCAGAATTAG	TTTGTCTCCC	CAAACTTCA	CCTTTAAATA	410400
ACCAAACCTT	AACTCCAATA	ATGCCATAAG	TAGTTTGAGC	CTCAGAAAAT	CCATAATCTA	410460
TATTGGCTCT	AAGAGTGTGC	AAAGGAACCC	GACCTTCCTT	AACCTCAAAG	CTTCGAGCAA	410520
TTTCCGCCCC	ACCAAGTCTA	CCAGCAATTT	TAATTTTTTA	CCCTTGAGCA	CCTTTTAACA	410580
TAGAGGTAGA	AAGAGATGAT	TTTAAACTT	TTCTATAAGA	CGCCCTATTT	TCTACTTGCT	410640
TTGCAATCCC	ATTAGCAATA	ATTTGAGCAT	CAAGCTCAGG	TCTTTTAACC	TCTTTAATCT	410700
TAATGCTAAT	CTTTTTAGAA	ATTTTTTTAG	TTAACAATTG	ACCAATCTTT	TCAAGATTAG	410760
AACCTTTAAG	CCCTATCACA	GAACCAGGCC	TTGGAGTAAC	AATTACTACT	GTTACTTTTT	410820
GGGGATTATT	TCTAATTATT	TCTATATCAG	AAATATCAAA	TTAATCCCT	TTAAGAAATT	410880
TCATAATTTT	TCGCCTTATT	AAAAATCTT	CATGAAGAAT	TGCAGAATAC	AATTTTTTAT	410940
CAAAATACCA	TTTTGACTTC	CAATCCTTAT	TAATTTTTTAC	CCTTAAGCTA	TATGGATGTA	411000
CTTTTGGGCC	CATGCTTTAT	CCTTTAATAT	CTTTTTTTTC	ATCAACTTCA	ACAAAAATAT	411060
GACAATTTCT	ATTAACAAGC	CTATCAGCTC	TACCCCTAGC	TCTAGGCCAA	ATCTTTTTTAC	411120
GACGACGCCC	ATCATCAACC	ATAACTGTTT	TAACAAATAT	CATGTCCTCG	GAAAGATTTT	411180
TATTGTGATA	CATAGCATTT	GATGCTGCTG	ACTTAACAAC	TTTTTCTAAA	AGCTTAGCTC	411240
CTTTATTAGG	CATAGAACAA	AGCACTGCAA	TAGCCTTAAT	ATAAGACTCT	CCCCGGATAT	411300
TGTCAGCTAT	TGGCCTAACT	TTTTTTGGAG	AAGAGGGTAA	ATTTTGGCCC	TTTGCCGTAT	411360
ATCTTCTATT	TACCAACATA	ACTACTTACT	TCCTTCCCTT	TTTATCTGAC	TTAGCATGCC	411420
CTCTAAAAAT	CCTTGTAGGT	GAAACTCGC	CAAGCTTATG	TCCCACAAGA	TCCTCGGTAA	411480
TATAAATAGG	TATAAAAGTT	TTGCCATTGT	AAACAGATAT	AGTAAGGCTT	ACCATTTTCAG	411540
GAATTATTGT	TGAAGATCTG	GAGTAGGTTT	TAATAACAAC	CCTCTTCTCA	CTTCCAAAAG	411600

ACGATAAAAC TTTTGTGATAA AGACTCTTTT CTATAAAAGG TCCTTTTTTA ATAGATCTTG 411660
CCACTATACT CTCCTATTTA TTTCTTCTTT TAATAATAAA TTTATCTGAA TATCTCTTTT 411720
TCTTGCGAGT CTTATAACCT TTAGTAGGCT GTCCCCAAGG AGACACAGGA TGACGACCTC 411780
CAGAAAGTTTT TCCTTCACCC CCACCATGTG GATGGTCAAC AGGATTCATA GCAACACCTC 411840
TAACCTTGGG TCTTCTACCA AGCCACCTAC TTTTACCAGC TTTCCCTATA GAAATATTGG 411900
CATAATCTTC ATTTCCAATT TCACCAATTG TTGCAATACA TTTTTTAAAA ATCAATCTCA 411960
TCTCGCCAGA TGATAATTTT ACAGTGACAT AATTCCCGTC AGAAGCAAGT ATCATAGCAT 412020
ATCCACCAGC ACTTCTTATA AGCTGTCCAC CCTTTCCAAC ATTAAGCTCA ATATTGTGAA 412080
CGGTTCTTCC AATAGGAATA TTTTCAAGAG GTAAGGCATT GCCAATTTTA ATTGGAGCAT 412140
TAGGACCACT TTCCAAAACA TCTCCAACCT TAATGCCTTT AGGAGAAATA ATATACCTTT 412200
TTTCTCCATC TTTATAAACA AGCAAAGCTA TATTAGCACT TCTATTAGGA TCATATTCAA 412260
TAGAAGCAAC TCGAGCAGGA ATGCTAAATT TATCTCTTCG ATTAAAATCA ATCAACCTAT 412320
ACTTCTCTT ATGCCACCA CCTCTTCTTC TAATACTAAT CCTACCAGAA GAATCTCTGC 412380
CCGATTTAAA TTTTTTACCT TTTGTTAAAG ATTTCAAAGG ATCATTACCT TTGCTCAAAT 412440
CATCAAAAAGA TAAAGTCGTC TTATAGCGCA AAGAAGAAGT TTTTGGCTTA TAAGCTTAA 412500
TACCCATATT TATTTTCTC CAAAACCACT AAAAAATATC TATTTTATCT TCCTTTTTGA 412560
GATAAACATA TGCCTTCTTC CATGAAGAAG TTTTCCCTT ACCTATAGGG TACCCTTTTC 412620
TAGACACCAC AACCTTGGCT TTACTTTTAA TATTGAGCAA ATTACACGAT ACTGGAGTAA 412680
CATTGAAAAG TTCTTTTATT GCTGCACCAA CCTCTTTTTT ATTTGCTCTC TTATTAACCT 412740
TAAAAACATA AACATTAATA CTTTCCCTTT GAGTATTAGT TTTTTCAGTA AGCATAGGTG 412800
AAACTATTAT ATCATAAGCC TTCATACTTA TCCTCAACAT CCTTTTTATT TAATGTAAAA 412860
CTCATTGAGC TTGTAAACAG CGGATTCTAG AGCTATTAAA TTCTTAGCAT AAAATAAATC 412920
AACAACCCTA AGTTTATCAA AAGATAAAAT CTTTAAATCT CTTATATTTT TACCAGCCCT 412980
TTTTATCATC TGATCATCAT TGCCCCAAAG AATAACCACC TTACCATTAA AACTTGCAAA 413040
ATTTTTTATT ATTAAAGCAA GATCTTTCGT TTTTCCAGAT TCAACATTAA AATTCTCAAT 413100
AACTTTAAAA CTATTTTCAT CAGCAGCACG CAACTTAAT ACAGACTTAA ATGCAAGCTT 413160
TTTTACCTTT TTAGGCAATC TATAGCTATA ATCCCTAGGC TTTGGCCCTA ATGCTATACC 413220
TCCGCCAATC CAAACTGGAT TTCGCTTTGT ACCAACCCTA GCTCTACCGG TTCCTTTTTG 413280
CTTCCAAGGC TTTTLAGAAC TACCCTAAC CTCTGATCTG GTTTTAGTTG AAGATGTTCC 413340

AACCCTAAGA TTAGACAACT CGTTTTTTTAT AGCATTATAA ATAGACCCAT GACTAATTTTC 413400
TATATTAAAA ACTCTATCAT CCAAATTTAT AGTTCCAATC TCTTTCCCAT CTTTAGAAAA 413460
AACTTTTCTT TCCATACTAA ATACCTACTT TTTAGATTTT TTAACAACAA CAAAAGAACC 413520
CTTAGCACCA GGCACAGCCC CTTTACTAG AAGGGCTCTT TTTTCTTCAT CGATTAAAAC 413580
AACTTCAAGA TTTTGAATAG TTTGTTGATT TCCGCCCAT CTACCAGCCA TTTTGGTCCC 413640
TTTAAATGTT CTGTCAGGAG TAGTAGCTTG TCCTGTTCCA CCAAGATGTC TATGGAATTT 413700
TGATCCATGA GAAGATGGAC CACCACTAAA ATTATGCCTT TTCATAGCCC CTTGAAAACC 413760
CTTGCCTTTA GTAGTCCCTG TAACATCTAC ATACTTAACT GACTTAAAAA CATCAACCTT 413820
AATCTCATCG CCAGCATCAT ACCCGTCAAG CCCCTTAAGC TCTATCACAT ATCTTTTAGG 413880
TTCAATATCT TTTAAACTTT TATATTGACC TTTTATGGGC TTTGAAACTT TAGAACTCTT 413940
AAGATCAACA GAACCTGCTA TAAGAGCACT ATAACCATCT CTATCGACTG TCTTCTTCCC 414000
TATAATATAA TTGGGCTGAA ACTCTATAAC AGTAACAGGA ACCACAATGC CATTTTCTG 414060
AAATATCTGA GTCATGCCAA CTTTTTTTCC AATCAATCCC AACATTAAAA TACCTCAAAT 414120
TCATATACTT AAAATATCAT TTAAGTCTTA ATATCTACCT CAACACCTGC TGGAAGCTCT 414180
AATTTCATTA AAGAGTCCAT TAAAGCAGAA GTAGGTTCTA AGATATCAAT AAGCCTTTTA 414240
TGAGTTCTCA TCTCAAATTG CTCTCTTGAT TTTTATTGA CATGAGGAGA ACGTAAACA 414300
GTATATTTTT TTATTTTTGT CGGCAAAGG ATTGGACCCT TAATCTGAGC CTTAGCCTTC 414360
TGAACAGCTT TAACAATAGA TTCGGCACTC TGGTCTAATA TTTTAACATC AAAACTAAAC 414420
AATCTTACGC GTATCTTATC TTTAGCAATC AATTTATTCT CCTAACTTT AGAGAGTATT 414480
AATATATCCT TAAAGTCTTA ACCTATTCCA ATATCTCAAG AATTCTTCCT GAAGCAACGG 414540
TTCTTCCACC TTCTCGAACA GCAAATTCTA CATTCTTATC CATAGCTATT GAAGAGATCA 414600
GCTCAACAAT AATATCAACA TTATACCAG GCATAACCAT TTCTTTGCCC TCTAAAGCAA 414660
CAACTCCAGT AACATCGGTT GTTCTAAAAA AGAACTGTGG TCTATACCCT GGGAAAAATG 414720
GCTTGTGCCT ACCGCCTTCT TCTTTAGTCA AACAATAAAT TGAAGCTTTA AATTTCTTGT 414780
GTGGAGTAAT TGTACCTGGA GCTGACAAAA CTTGCCCCCT CTCAATGTCT TTTTATCAA 414840
CGCCTCTCAA AAGAAGACCA ACATTATCCC CTGCTTGACC TTgCTCAAGA ATTTCTGGA 414900
ACATTTCAAC ACCAGTAACA GTAGTTTTTC TGGTTTCTTT AATTCCAACCT ATTTCAACTT 414960
CTTGACCAAC TTTAATAATA CCTCTTTCAA TACGCCAGT AGCAACAGTG CCTCTTCCTG 415020
AAATAGAAAA TACATCTTCA ACAGCAAGCA AAAATGGCTT GTCAATATCT CTTTCTGGAA 415080
GATCAAAATA ATTATCCATA GATTCAAGAA GTTCTTTAAC GCATTTTGTA GATTCAGGAT 415140

CTTCTGGATT	TGACATAGCC	CCAAAAGCTG	AACCTTTGAT	TATTGGAGTA	TCAGCTGAAA	415200
AGCCATATTT	TTCAACAAGT	TCTAAAACCT	CAACTTCAAC	AAGCTCAACA	AGTTCAGGAT	415260
CTGCTAAGTC	CAATTTATTT	AAAAAACTA	TTATTTTCTT	TATTCCCATT	CTTTGAGCAA	415320
GAAGCAAATG	CTCTTTTGTT	TGAGGCTCAG	CACCACTATC	AGCAGCAACT	AAAAGTATCG	415380
CTGCATCCAT	TTGAGCTGCT	CCTGTAATCA	TATTTTTTAT	ATAATCGGCA	TGGCCTGGAC	415440
AATCTACATG	AGCATAATGT	CTATTAGCTG	TTTCGTACTC	AATATGCCTA	GCATTAATTG	415500
TTATTCCTCT	TGCTTTCTCT	TCAGGTGCAT	TATCAATATC	TTCATACTTT	AATGCTTTTG	415560
CATCTTTATT	TAATTTTGAA	CAATAAATAC	TAATAGCCGC	TGTTAGTGTT	GTTTTACCAT	415620
GATCAACATG	ACCTATTGTT	CCAACATTCA	TGTGCGGCTT	TGTTCTTTGA	AAAACCTCTT	415680
TTGCCATGAC	TAACCTCCTA	AATTTTCATAT	TCTAAATAGC	TACTTACATT	TAATCTCTTT	415740
AAAAAATTTT	TAACAAATTT	ATTCTTATTA	AAATAAGAAA	ATAGCTACAA	ATAATCAAAA	415800
AAATAAAAAA	ATCAATTTT	TAGAAATTGA	CCCGCACTAC	GTGTTTTTCT	AAAAAATTTT	415860
AATAGCTTTA	AAATTCTACA	CATTTTACAA	AATATAGTCA	ATACGCTTAA	ACTTTTAAAC	415920
TCAATTCACT	ACACATATAA	TAGCATTAAA	AATTAATATA	AACTTTACAT	TAATTAAAGA	415980
AAAGCACAAA	ATATTAAAAA	ATAAAGCTTT	AAAAGCAACC	ACTTAAAATA	AGCAATGCTC	416040
AACTAATACA	TTTAAAAACA	TGAAATTTAA	AACAATAGTA	AATACTTTTT	GAAATCTAGT	416100
CACTATTTAA	AATTGATCAA	AAACCTTTAT	TTTATCAAAA	AGGTAAACAC	TTTCCCCGGT	416160
AAAAAAATAT	AATAAAAAATG	ATGAAAGCTC	AAAAATTTAA	GCTTAAATTA	TTACCAATAC	416220
TTGTAATTTT	TGGCATTTTA	ATTGTTTTTA	TGTCTTGCAT	GAAAACAAGC	ACAATAAAAT	416280
CAAAAGAAAA	TGCAAAAGAA	ATTACCTATC	TTATTAGCAC	TATAAAAATC	AACCAAAAAG	416340
TAGAAATAGT	AACTACAAA	TCCGACAGCA	AAAATAATCT	AATAATTACT	CTTAAAAACA	416400
AAAGCACAGA	AGATATAAAT	GCAAATTCAT	TGGCAATTTT	TAAAGAAGGT	AGCAAAACAG	416460
GTGAATTAAT	AAGAGAAAAA	CTTAATGGGC	TTGAAACAAA	AACTTTTCAT	TTAAAACTA	416520
AAATCAATAC	TAAAAGAAAA	ACCACATTAT	ACATTTTGA	AAAACAATAA	CAAATAGAAA	416580
TGATTTAAAA	CCTAAAATTA	TTAAAAATTA	TTCTACTTAA	ATAAGCTTTA	TTGCAAACAA	416640
ACAATTACAC	TTAGAAATAG	ATTAACAAAG	AATCTAAAAT	CTATTTTAA	GGCCAAAAC	416700
ATTAAATTTA	TTAAAAACAA	ATAAGCCATT	TTTTGGCAAA	ATGTAAATAT	AAAATAAATC	416760
TTAATTACTA	TTTGTATTTT	TTAATTAAAA	TAGGCTTAAC	CCAATAACGA	GTGCAAGTAA	416820
AAGCAATTAA	AATTATAATT	GCCAAATAAT	TTGAAATTAT	AAAAGCATAA	CCTAAAGAAT	416880

TTTCCATTAT	GCCAAAATAT	TGAAAAATAA	AAACTACTGG	AAGACGAATA	AGCCACAGCC	416940
TAATAAAAAT	AACAATCATT	GCAATTTTTG	TCCTGCCAGA	CCCAATAAGT	CCCCCAAAAA	417000
ATACTTGTTG	GAGTCCATAT	CCAAAAGTAC	CAATAGTTGT	TAACAATAAA	TAATTATTAG	417060
CATAATTTAA	AACTTCTAAA	TCATTTGTAA	ATAACCTTAG	TATAAACTGT	TTATTAAAAA	417120
TAACAATCGA	ATTTATTATC	AATAAAATTG	CCAAAGAAAT	AAAAAACCT	TTTTTCAAAA	417180
CTTCTTCCAC	CCTATTGACT	TTCTTAGCGC	CAAGATTTTG	ACCAACAATT	GAAATAATTC	417240
CAGTACCAAT	TCCCATAGCA	GGAAGAAATA	AAAAAGAAAT	AATGGTGTTT	GTAAGTCCAT	417300
AAGCCGCCAA	AAATTTTGGA	CTAATCTCAA	TAACTATATA	ATTGAAAATA	AAAAAGACA	417360
ACGAAACCAT	TATTTGCCCA	AAAGTTGAAG	GCAATCCCAG	ATTAACAATT	TCTTTAATGG	417420
ATCTTATATC	TATCACTAAA	TCCTTCAGAT	GAATTTTTAA	TCCATAATTT	AGCCTGTAAG	417480
TCAAAAATAA	ATAAAAGACA	ACGGTTAACA	ATTTTGAAAA	TAAAGTGGCC	CAAGCAGCTC	417540
CAGTAATGCC	CATATTAAAA	CTAAATATTA	AAATTGGATC	AAGAATAAAA	TTACAATAT	417600
TGGCAAATAA	AACTATTGTC	ATTGAAAGGA	TAGTTTCTCC	TTGAGCATTT	AAAATATATG	417660
TAATTGAAAT	ACTTAAAAAC	ATGATAGGTA	TTGCAAAAAT	TGTCACATAA	AAATAAACTC	417720
TTGAGAGTTC	TTTAAGCTCC	CCTTTTACAC	CCAACAAATC	TAAAAGATGA	TCAATAAAAA	417780
AAAAAGCACA	AATAGTAACA	AATAAGGATA	AAACAAAGTT	TAAAACAATA	AGTTGCCCTG	417840
CATATCTTGA	AAAACGAGAA	AAATTTCCCT	CTCCTATGCA	TTTTTGACATC	AAAGAAATGC	417900
TTCCCGTAGC	CATTCCCATA	GCAATAGCTA	TAATAAAAAA	ATTTACAGGA	CCAGCAAGTG	417960
AAAGCGCTGA	CAAAGGCATG	GCTCCAAGTT	TACCAACATA	AAACATATCA	GTAAGATCAT	418020
AAAAAGCTTG	AATAATATTG	GTTATAACAA	TAGGAAAACT	TATTAAAAAA	AGAACCTTGT	418080
ATAAATTGCC	ATTTAATATT	AATTCCCTAG	TCTTACTCTT	ATCTGTAGAC	ATAAAATTTT	418140
ATCCTCATCT	AAAACATTTT	TTATAAAAAA	TTTAAATCA	AATTTATTCA	TCAGTAATAA	418200
ACAAGTATTT	AATTTTTAAT	TTCAAAAATT	AAAAATTAAT	ATACAATATC	AAAACAATTA	418260
ACAGTCAACA	TGTTATGCAT	TAAATGACCA	AGATATAAAAT	AAAATCTATT	AATCTGCCAC	418320
AACAAAAAAA	TCATAACCAA	AAACAGAAAA	ATTAAACCA	GATATAATAA	ATAATAAAAA	418380
TTTATAATTC	TAATACTAAT	CATAAATAAA	CAGTAATTAA	TAAAATTAAA	ACCATTCTAC	418440
GAATTAAAGC	AGAGAAATAA	ATACTTTATT	TAAAAGAATA	ATTAATATTA	TAAAAATAAA	418500
AATTCAAAAAT	CAGAAATACC	TCTCTGCAAA	TTTTTATCAA	TCTTTCAATA	TTATTTTTTTA	418560
CACTAAGATC	TTTAACTAT	AAAATAAAAA	AATTAATAAT	ATTAGATAAA	AATACTAAAA	418620
CCCTAATAAT	ACTTCAAATT	ACAGACTAAC	TAAATAAAAT	AACAAAAAGT	CCCAACAATA	418680

AAAATTAATG	TAATATATTT	TCATTCACAA	TTCAACCTCT	TAATACCTTA	TCCTTACCTT	418740
CTATTAAGAA	CATTTTCCAC	AAATCATACA	TATAATAAAG	CCCAACAACA	AGCTATTGAC	418800
TTTTAACTTT	CTTGATTTTT	GCACCCAAAT	TAATCAATTT	GTAACTACA	TCTTCGTATC	418860
CTCTTTCAAT	TTGATAAACA	TTTTGAATCT	CGCTGCGACC	TTCAGCAACA	AAAGCAGCAA	418920
TAAGAAGAGA	CATTCCTGCT	CGTACATCCG	GAGAAGACAA	AACATTGCCT	TTAAGAGAAG	418980
ATTTGCCCCG	AACTACTACG	CGGTGTGGAT	CACAAAGCAC	AATTCGAGCA	CCCATTTTTA	419040
TTAATTTATC	TACAAAAAAC	ATCCTAGATT	CAAACATCTT	CTCAAAAAC	AAAAGTGTGC	419100
CTTCTACTTG	CGTTGCAGTA	ACTACAATAA	TACTCATAAG	GTCTGTTGGA	AAGGCTGGCC	419160
ATGGGCCATC	ATCAATTTTT	GGAATGTGCC	CACCAAAATC	TAAGTTAACT	TTTAATTCTT	419220
GTTTATTTCT	TACATATACA	TTTTCCCTGT	CATATTCAAA	ATTAATGCCA	AGTCTTGAAT	419280
ATACATGCCT	AATTAATCTG	AAATGTTGGG	GATCTGCTTT	TTTAATTTCC	AACTCACCCC	419340
CTGTTAATGC	AGCAAGGCTA	ATTAAAGAAC	CAACTTGCAT	GAAATCGGCT	CCTATTCTAA	419400
ATACGGTCCC	ACTTAATTTT	TTTACACCTT	TTATTTCTAA	AACATTTGAA	CCAATTCCTA	419460
AAATATTAGC	GCCCATTGAA	TTTAACATAT	TACACAAATC	TTGAACATGT	GGCTCACAAG	419520
CAGCGTTCAT	AATAACAGTA	TTTCCTTCAG	CAAGAACTGC	AGCCATAATG	ATATTTTCTG	419580
TGGCTGTAAC	AGAAGCTTCA	TCTAAAAACA	TTTCAGCGCC	AACAAGCTTG	TTAGCCTTTA	419640
AAACAATCCT	TCTATCTTTT	GTGCTTAACT	TGGCCCCCAG	CTTGCAAAGC	CCGTAAAAAT	419700
GAGTATCAAG	CCTCCTCTTT	CCAATCACAT	CTCCTCCTGG	AAGCGCCATA	TCTATTTTTC	419760
CAAACCTAGA	AACAAAAGGC	CCTAATAAAA	GTATGGAAGC	CCTAATTAAA	TCTGTAAAAG	419820
AAGAATCTAT	TTCTGTTTTT	ACAATATTTA	AACTTTTAT	TTTTAAAGTA	TTTCCCTCTC	419880
TTGCAATATC	TGCTCCTATG	TCATTTAAAA	TATCTAAAAC	AACTTTTACA	TCATTAATAT	419940
TAGGAATATT	TTCTAAAATA	ACCTCTTCAT	CGGTAAGTAA	AGCAGCCAAA	ATACAGGGTA	420000
AAGCAGCGTT	CTTATTCCCA	CTAGCTGTAA	TTTGACCACC	TATCTTATAG	CCGCCTTCTA	420060
CAATATAACT	ATGCATAATC	CATCCTCCTA	TATATAAAAA	CTTAATAAAA	TTAAATCGCA	420120
CAGATAAGAT	TATTAAAATT	TAAAGAATAT	CTAAAGATAT	GAATATCAAA	CAATATCCAT	420180
ATCTTTTAAA	CTTGATTTAC	AATCTATATA	TTCTCTAACA	ATCTCTACAG	AAAAAGAATG	420240
GCCATTCTCA	TCGATATCAA	TTAAAACACC	GTAAAACCA	AGGCCTTCCC	AAGATTCATT	420300
AAATTTCTGA	TTTAAAAATC	CTTTCAAAAA	TTTATCCACC	TCTAAATCAG	GAGAATATCC	420360
AATAACACTG	TCCAAACTCC	CAACTCTGCC	CAAATCAGTT	ATAATAGCAG	TATTATCTAA	420420

AATTCTCAAA	TCAGCTGTTA	AAATCCTTTT	CCCGGTTCCA	AGACAAGCAC	TAACTCTTGA	420480
TTTGTAGATA	AAAAACAAAG	CATTAACCTC	GGCTGTAGTA	TTTGAATCAA	AAAGAACAAT	420540
AATATTATTT	GTTTGCATCT	TGATTCTTTG	ATAAAAAAAA	TCAAACTAT	AAAAAGGATG	420600
ATTAAATTTA	TATTTAGTTA	TTCCTGTTTG	ACCTACAATT	CTAATCACAG	CCAATTTTTT	420660
GCCATTAATA	TTATAAATA	AATAAGAATA	TCCCTTTAAT	TTTGCAGGAC	AATTTAAAGG	420720
CTTTAAAATA	AAATTATACT	TATCAAGATC	ATCAGATAAA	TCAGGCCTTG	CAAAGCATT	420780
TTACCTTAAA	GTTACACATC	AATTCCATAC	TTTTTTAATA	AAAAGGCATG	CTTTTTTGCCA	420840
AGACCTCTTA	AACCTGTAGT	AAAATTATTG	CCAGATATTA	CAAAATCAAT	CTTTTTTTTCC	420900
ACCTTAAAGG	ATGATAAAAA	AGATTTTATA	ACAATAATCC	CAGCTTTGCC	GACAACCTCG	420960
CCAGTAATTA	AAATCCTTAA	AGACACAAAG	CCTCTCTTTT	TATTGATCTA	GTTCAAACAA	421020
CTTAATAAGT	AAACTTTTTA	CAATAAAAT	TGACACAAAA	TACCCACCA	AAACAGCGAA	421080
AACAATCATC	ATAAAAATCA	ATATAAATTG	CAAATAGGGC	TTTACAATAA	TGCTAAATTT	421140
AACAATAAAA	AAAAACTCTA	AAAAGAAAAC	TAGAAACATT	AATGATAAGT	TCATTAACAT	421200
ACATAAAATA	AAACTCAAAA	TCTTCATTTA	TTAAGCACTT	TTCTTTTTAT	AAAAAAATCA	421260
TAAACCAAAA	ATAAAATCAT	ACCTATAACA	ACATAGCTAT	CTGCAAAATT	AAAAGTAGGC	421320
CATCTATCAA	GTCCAAAAAT	TCCATAAAAT	TTCAAATCTA	AAAAATCTAC	AACTCCAGAA	421380
GGTCTAAACA	ATCTATCAAT	AACATTTCCCT	ACTCCTCCTG	AAAAAATTAA	TAAAAGTGAA	421440
ATTCTGGCAA	TACAATTTCT	TTCTTTCAAA	GAAAGATAAA	AAACAAATAT	TAAAATGAAA	421500
ATAGGCATTG	CAAGAAAAAA	AATTTTTTTC	AAGCTATAAT	GGATATTAGA	GCCCATAGAA	421560
AATAAAATAC	CTGTGTTTCT	TACATGTATT	ATCCTAAAAA	AATCATCAAA	AAAGGAAAAA	421620
TATATTGAAC	CTAATTTAAC	ATACTTTGCA	ACCAAATACT	TAGAAAGTTG	ATCAAAAAAA	421680
ATCAAACTAA	TAATAAATAC	AAAAATATTG	AAATATTGCT	TACTTTTAGC	GCTCATACAA	421740
AAATCCTTAT	AAATTAGTAT	TTTTACAAAT	AAATTTAACC	TCTAAATCTT	CTTGAATTTT	421800
GAAATCTTCC	ATTAATTTAA	TTAAACCAAA	AGTTTCAGTA	AAATAATGAC	CTGCAAAAAT	421860
CAAATTCACA	CCGAATTCTT	CTGCCAAAAG	ATATATTTGA	TGAGAAGTGT	CGCCGGTTAT	421920
AAACAAATCT	ACATCATGAC	ATAAAGCTTC	TTCAAAAAAA	GAGTATCCAG	AACCACTAAC	421980
AATTGCAACC	TTATTACCG	ATTCTTTGAA	CTTTTTTCGA	AAAAGAATAT	GTTTATTTTC	422040
CTTTTTGATT	TTTTCTAAAA	TTTCAGAAAA	GCTAAAAACA	GAATCAGCAA	TAATCCCTAG	422100
ATTAACCTCG	CCATAATTTG	CAAAAGCAAA	AGAATTTTTT	AATCCTAAAA	AATCTGAGAA	422160
CACTTTGCTG	TGCGAATAAA	CAGAATGAGC	ATCCATAGGC	AAGTGCACCG	AATAAAGAGC	422220

TAAATTATTT TCAATTAAAA ATTCGTTTT ATCATACATA TTAGAAACAA TGCGCTCTTT 422280
TTTTGACCAA AAAATACCGT GATGAGTAAT TAAAAAATCA TTTCCTTTTG CTTCTTTTAA 422340
AGTTGAAAAG CTAGCATCAA CAGCAAAGGC AACCTTGTTA ACCTTAGCAT TAATATTCCC 422400
CACTTGAAGC CCATTTAAAT TTTTATCAAT ATGCTCATAC TTATTTATAT CAAAAATTGA 422460
ATTAAGCTTA AAAGACAAAT CTCTTACATT CAAATTAAAT TCTCCAAATT AAAGCATAAC 422520
TTTGACTTTC TCTTAATCTT CTATAAGAAT AAAGATTTTT CAAACAATAC GTACAAAGCT 422580
TTGAATTATA AATATTTAAA TTAAACTAG AAAGTAAATT TAAATTAAAA CTAGCATTAT 422640
CAAAGTATAT TTACCATCT CTTGTAACAA AAGAAGCATT TAATAAATCT TTGCTAAATT 422700
TATTACTTAC TTCTTTTAAG AAAATTCAG AAACCTTCATA ACAACAAGAT CTGTTATAAG 422760
GCCCAAAAC AATTTTCAA TCCTTCAAAG CTGATCCCAT TTTTCAAAC ATAAATAACA 422820
TTTTTAAAT AATCAAATTA AAGCTTCCTT TGTATCCACT GTGAATAAGC CCTATAATTT 422880
TTTTCACCGA ATCATAAAAG TATATTGGAA GACAATCTGC AAAGTAAGCA ACAAGGGCTA 422940
CATCTAAAGA GCTAGATATA AGACCATCTC CTTCTTGAAA ATTAATAAAA TCATCTTCAA 423000
CTTTATAAAT AATATCTGTA TGCAATTGCT TTAAATATTT TATTTTCTTA GACCTAGGAA 423060
CAAAGTTAAA ATTATCATTA CTAAGTTCTT TTAATTTTAG ATTAAGGC TTTTLAGTAT 423120
AAATCATTTT AACATCATCA GCTATCCTAA ATTCATAATA AAGTTCGTGC TCTATTGTTT 423180
TCATAATCTA AATCTTCTC CCAAATAAAG CTTTTTGGCT TTTTCACTGC TTATTATATA 423240
ATCAACATCA CCTCATCAA GCACCTGCCC CTGATAAACA ATATAAGCTC TGTCTATTAT 423300
ATCAAAAGCA TCTCTTACAT TATGATCGGT AATAAGAACT CCTATGTTTT TCTCTTTTAA 423360
AATTTTTATT ATATTCTTTA TATCCCCAAT CGCAATAGGA TCAATACCAG CAAAAGGTTT 423420
ATCTAAGAGT AAAAAATAAG GATTACAGC CAAAGCTCTT GCTATCTCTG CTCGCCCTCT 423480
CTCTCCACCA GAAAGAGTAT ACGCTTTTTG GCTTTGTATT CTTTTATCT CAAATTCTTT 423540
AAGCAAATTC ACAAGCTCTA TTTTGCGCTC AGCTTTAGAT AGATCTTCTC TTCTCTCTAA 423600
AGCAACCATG ATATTCTCTT CAACTGTAAG TTCTCTAAAA ATTGAAGCAT CTTGGGGAAG 423660
ATATACAATT CCTATTCTGT CACGCTCATA CATATTAAGA GATGAAATGT TATAATCATT 423720
TATTAAACT TTGCCTGCAT TAGGCTTAAT AAAACCTACA ATAGTATAAA ATGTTGTTGT 423780
TTTGCCAGCT CCATTTGGAC CAAGAAGCCC CACAACCTCA CCTTTATAAA TGTTAATTGT 423840
AATACCGTTA ACAGCAAGCT TTTGCCATA CTTTTAATA ATGTTGTCTG CTTTTAAGAC 423900
AACATTATTG ACAGAATCAA GGTAAAGCT TTCCTAATC TCTTTATTT TATTTTTTTT 423960

CTTCAGAAGC	ATCATTTTCA	ACTTGAGTAA	ATTCTCCCTC	AACACTTCCC	TCAAGTTTAT	424020
ACCTATTAGT	TTTTGTATTG	AAAATTATTC	TTGAAGCAGA	ATAATAGTTG	TCTTTCTGGT	424080
AAATTACTGG	AACCCCTCA	AGAATCATTT	CTTTTCTTTC	TTTATTATAA	GTCCCATTTT	424140
CAGCTCTTGC	AAAAGTATCA	TCCTTATATA	TTTTAACAGA	ATATTGCATA	ATATAAACAT	424200
TAGTTTTTATT	GCTGCCTTCA	ATTCTTTCTG	CTTTAACAAAG	CATATTGTTT	TCTAAGTCTT	424260
CAAGCTCAAC	CCCTTTTGA	AGATAAAAAT	TATCCAGCTT	TCTATTAAAA	AACAAAAACT	424320
GAGCTTTAAC	ATTCATTTTA	TTCTTATAAT	CTTTATAAAA	AACATTGCCT	CTAGCTTCAA	424380
GATAAGAGCC	ATTTTCTCCA	TAAATTTCAA	TTTCATCTGC	TCTAAGATTA	AAATCCGAGG	424440
AAATAACCTC	TGAATTCCTT	TTTAAAACAA	TTTTTTTATA	AAAAGAAGAC	ACTACTCCTT	424500
GTGCAAAATC	TGACTTAAAA	GTAAAATTAG	TGCTTTTCTC	ATCACTTCCC	TTAATCCTTT	424560
CAGATTTAAG	GCTGGATTCT	ATTTGTGTTG	CTTGAATATT	GTTAATAAAA	ATAATAAAAA	424620
TCCATATTAA	AATTAAATCC	CTCAATTCAT	GATTCCCTCA	ACTCCAGAAT	CAAAATAAAA	424680
AACATTGCTC	TTTAAAAAAT	AAGAAAATCC	TTTTCCGTTT	ATTTTGCTAT	CATTAAATCT	424740
AATTAATACT	AGCTCATTTG	GGGGGGATTG	CAACTTCTTG	TCTTTATTCT	TCCATAAAAG	424800
CCTATTTGAA	TTAAGCAAAT	AATAATTATT	TTTATCTTCT	ATTTTAAATT	CTACAGAATC	424860
TCTCATATCC	AAATCCTTTG	TAATATAAGA	ACCTTCCAAA	TTATTAAACT	TCCCTGAAAT	424920
TTCATTATCT	AGGGAATGAT	ATAAAAACCT	TCCATTCTCT	GCCTTATAAA	TTTATAGTC	424980
ATTGAAATAA	CTAAAGCTTA	AAGAATTTAA	AACGGTTTGC	TCTTTATTGT	ATACAACATC	425040
ATAATACTTG	ATTCCTAATA	TTTGTATTGA	AGGAACTTTT	TTGGCCACAT	CAGATCTACT	425100
AGAATACTCA	TCATAATCAA	AAGTACAAGC	AAAAACAAA	AACAACAAAC	AAAGTCTAAG	425160
TATTTTCATA	AATATTTTTC	ACAAGACTAA	AAATTTTTC	TATTTCAATT	GACAATCTAT	425220
AAAACATAAC	AACACAACAT	TAAAACTTT	ATCAAATAAA	ATTTATTTAC	ATAACCAATT	425280
ATAATGTAAA	ACACAAAATC	AAGGTAAAAA	CAC'TGCTCTT	AAGAACAATC	TTCTATACAA	425340
GAATTCTCCT	AAAATGCAAA	AATTCAAACA	AAAGTACAAA	AATTGCTCTT	ATTTCAGAAT	425400
AACATAAGGG	TAATTTACAA	CTTATTCCTT	TTAAGAGATA	GACTTATAAA	AATTAACAAT	425460
AATAATGCTC	ACATTCATCA	TCTCTTTTAT	AGTTTAAAAT	TTCATTGTCT	TTAAACCAAA	425520
TTGGTATTTT	GCGCATCGCA	TCTGCCTCAT	TTGCAGATGC	ATGAATCACA	TTGTAAATTG	425580
AAAAACCTTT	TTCATTTGAA	TACTTAAAAC	TATGATAAGA	AAAATCTCCC	CGTATTGTTC	425640
CAGGAATAGC	CAATTTTGGC	TCAGTAGCAC	CACAAAGCTT	CCTCACAACC	TCAATGCTTT	425700
CAACCCCTTC	AACAACAAAT	GTAAAAACAG	GGGAATTTGA	AATAAATTTA	ATTAAAGAAT	425760

TCCAAACAGC	CTCACTATGT	CTAAAGACAA	TATCATCATA	TAAATAATGT	TTTTTTGCCA	425820
AACTCTCATC	AACAATAAGC	ATTTTAGCAG	CTACCATCTT	TAAACCTACT	CTTTCAAATC	425880
TAGAAACTAC	ATCGCCAATT	AAACCTCTCC	TAACCTCCATC	TGGCTTAACA	ATACATAAAG	425940
TTTTTTGCAA	TAACATTGAC	ATAAATCCTC	CTAAAATTTA	GGATATATAT	TTAAAAATAA	426000
TTAAATAAAT	AAAAATACTT	ATTCAATACA	AAAATTATAT	CTGATTAATT	ACATTTATAT	426060
GGAATAATAC	AAATTATAAA	GCACTTAACA	TTGTATTGAA	AAATCAAAAT	ATAACTTTTA	426120
CAAAATTAAA	AACTACATTC	CAAAAGGAAG	AACTCCCATG	GTTTTTAATT	TTATCTCTTC	426180
TTTAACCTTA	GAGACAGCAT	CATTTAAAGC	AGATTTAATC	ATTTGTTCAA	AAGCATCATT	426240
GTCTAAATCA	TCAAAAAATT	CCTTATTGAT	TGAAACTTTT	TTAACATTAA	ATTGCGCCATC	426300
CATCTCAATA	GTAACAATAT	TGCTACCTGC	TTTACCACAA	ACCGTAATTT	TAGAAATTTT	426360
CTTTTAAATA	TTGTCAATAT	TATTCTTAAC	GCTAGACATA	TTTTTCAAAA	AATCTAACGG	426420
ATTTACTGCC	ATATTTTTAT	CCCTCCAGAA	CTTCACTTGC	TCCAAAAATA	TTTTTTACAG	426480
TTTCTAGTTT	TTCAAAATCC	TTTTCAAGGT	TTTTTAAATT	TTTCTGAAAC	ACAATGCTTA	426540
AATTGGGGAA	TTCTTTGTAA	AATTCAGATC	TTATCTCACC	TTTATAATTT	TGAAGCTCAT	426600
TATATTCAAA	CTCACTAAAC	ACCTTATAAT	AAAGAACATT	GTCATCAATA	GCAACCTCTC	426660
CCGAATGAAC	TAAAGTTTGA	ACATATCTTG	AAACAATATA	AATAAATTTA	TCTCTTATAT	426720
CAATAAAATC	ATTTGAATTA	CTCGCATTAT	CATCTTCAAT	AAAAATCTCA	TCAATCTCGT	426780
CAATACTATT	GGTCTCTAAA	ATATTTTTAT	CAATTTTTGT	TGATAAATTT	TCATCACGAT	426840
CAGCCTCCTC	TTTTTCTAAA	GATTTGATTT	CGGGAAATTC	ACATTTTAAA	CTAGATTTTG	426900
ATGGAATAAA	AGCCAAATCA	TCTTCGCTCT	TATTATTTGA	TAAACATCA	AAATGTTTG	426960
AATCTGTAGC	AATATTTTCT	AACAGATTGT	CTTCAAGATT	TTGAATTTGC	TTTATTAAAA	427020
CATGATTTGG	AACATAACTT	TTAAGTCTTA	AAATTTTAAT	AAAATTAATC	TCAAGCTCAT	427080
ATCTTGGAAT	AACCGAAAAT	TGCAAAATCCC	TGTAAGTTTC	AAGCAAAACA	ACAATAATTC	427140
TTTCAAGATA	GTTCAAATCA	AACTCAATTA	ATTTCTTTCT	CAAATCCTCA	GATTTAATTC	427200
CAATAAACTC	AAAATTTTTA	ATACCTATCT	TTAAAAATAA	TGCCTCTCTA	AAAAATTCGA	427260
TTGAATCTAA	AAGAAATTGC	TCATAAGACA	CTCCAGATAA	AAAAATAGAA	TCAAGAACAC	427320
AAATTAACCTC	TTTCACATCT	TCACCAAGAA	TGCTAACTGA	CAACTTTTCT	AAAAATTCAT	427380
CATTGGTTAA	GCCCATCTTG	GATCTTATTT	GATCTAATTT	AATGTTAGAA	TCAGTAAAAG	427440
AAACTATCTG	ATCAAAAAGA	GTATAAGCAT	CTCTTACGCT	ACCACTACTT	TTATATGCAA	427500

TCCATTTTAA	AGCTTCATCT	TCATATTTAA	TATCATCCTC	TAAACAAACT	TTCTTAAGCA	427560
TATTGTAAAT	CTTATCTAAA	GATAAAAGTT	TAAAACTAAA	ATGTTGACAT	CTGCTTTTTTA	427620
TTGTCTCTGG	AAGCTTGTGT	GA CTCTGTAG	TGGCAAAAAT	AAAAACAATA	TAATTTGGAG	427680
GCTCTTCAAT	TGTCTTTAAA	AGAGCATTAA	AAGCAGAATT	GGAAAGCATA	TGAACTTCGT	427740
CAATAATATA	TATTCTATAT	TTAGAAATTG	CAGGAGGAAA	CATTATCTCT	TCTTTAATTT	427800
GCCTAATATC	TTGAACCGAA	GTGTTTGAGG	CACCATCAAT	TTCAACAACA	TCAAGGCTGC	427860
TATCATTCTC	AATAGATTTA	CAATTGCTGC	ACTCCCCACA	TGGCATAACT	GTTGGACCAT	427920
TCCTGCAATT	TAAGCATCTG	GCAAAAGCCC	TGGCTGATGA	AGTTTTACCA	ACGCCTCTTG	427980
GCCCTGAAAA	GATATAAGCA	TTAGCTATTT	TATTTTTCTC	TATAGAATGC	TTTAGAGTTT	428040
CAACAACAAA	GTCTTGCCCT	TCAAGAGAGT	TGAAATCTCT	GGGGCGTTTC	TTAAGAGCAG	428100
TGCCTCTTGA	AGACGCCATT	AACTTTTTTAC	CTCCCTATGC	TTTAATAAGT	AAAATATTAG	428160
TAAATATATA	CTATACAACA	TATTTATATC	TCAGAGCTAT	TACTTTAAAA	GAATTTTATG	428220
AAACATAAAA	AATATAATAA	AATTGAAAGT	TACAAAAAGA	CAAATCCATA	TCTTAACATA	428280
AAGCAAAACA	TTGCATTTGG	GTTCAAAATT	AAACCTAAGA	CTTACGTACT	CATCAAAAAA	428340
ATCGCTTACC	GCTGCTACCT	TCCAGTCCTG	ACGGGATTCA	GCAATACTTG	ATAGTACGGG	428400
TCCTAGGAAT	CGGAGAGAAT	GGGATTCGAA	CCCATGATAC	ATTTTACTGT	ATACACGCTT	428460
TCCAAGCGTG	CGCCTTAAGC	CACTCGGCCA	TCTCTCCAAA	CTAACAAACT	TTTCGTGTCC	428520
AAGAGGACTT	GAACCTCCGA	CCTTAAGAAT	CGCAATCTAA	CGCTCTATCC	AACTGAGCTA	428580
TGGACACAAA	TAATTAGTTT	TTATTGTAAT	AAAAATTACT	ATTTATTACA	ATAAAAAACAT	428640
TCAATAGAAA	ATGGAGAAAT	TGTGAAAAC	AGAATAATCA	TTTTTCTTTC	AATATTATCT	428700
ATTCTATCAT	GCTCTAAATC	AGTCTCAAGT	AAAGTTAATT	CCGAATTTGA	AATTAAAACT	428760
AAAAATATCA	AAGAAAATGA	AATACTGCAA	AACAATAATA	TTCTCCATAT	AGATGCAAAA	428820
ATTCCTTTTA	TGGAATATGC	AACTTTTGAA	TTTGAAAATC	TTATAAAAAA	ATGGAAAAAA	428880
GACATCGAAA	ATAAAATATC	AAACCCCGAA	AACTCAAAAA	ATGAATATTT	TTATTTTTTCC	428940
AATTTTACAA	TATTTAAAAA	TGAAAATATT	GGCATTACAT	CTATTTTATA	CAAAGAATCT	429000
TTCAGAGAAA	AAGAATCAAG	CACTTTCTTG	AAATATTATT	CTTTAAACCT	AAAAGGAAAC	429060
AAAAAAATAG	AAATTTCAGA	AATAATATCA	AAAGATCAGC	TAGACTCTCT	AATAAACGTA	429120
TTAAAAGAAC	AGCTAAATAG	TAGAATTAAA	GATTTTTATG	TTAAAGGAAA	ACACAGTCAA	429180
AAAGAATTGG	AAAAAAAATT	CACAACAATC	TTTCCAAGAT	ATAAATATTA	TTTTAAAAAT	429240
AACCAAATTA	TAGTTTTTTT	TAATCCATTC	TCAAAATGATT	GTAATGGCTG	CGATAAAATT	429300

GAGTTTCAAT TCCCCATACA TGAAAACACA GAAAATGAAT ATCAACCAAA CAAAAACCTT 429360
CACTCTCAGT CTTAATCTTA ATACTTAAAA TTAAATGATA ATTACGGAGA GGGTGAGATT 429420
CGAACTCACG GTAGGCTTAC ACCTACAACG GTTTTCAAGA CCGTAGCATT AAACCACTCT 429480
GCCACCTCTC CAGAGTTAAA ACAAATTTTA ATAAATAAAA TACACGCTGT CAATATTTAA 429540
ATAATTACGG AGAGAATGGG ATTCGAACCC ATGGTCCCCT TTTAAAAGGA CAACTTCTTA 429600
GCAGGAAGCC CCATTCGGCC ACTCTGGCAT CTCTCCTATA ACATTAATAC ATATTATCTT 429660
AGAGATATTA TTATTGTCAA CCAAATAAAT TATAAATTAT TAGTAATTTA TTCTAAACTC 429720
TTTATAAGCT TCTATTAAAT TTTGAAAaTC CCAATAGAA ATGTCAATTT CGGGCAAAAT 429780
ACATTCTTCA TGCAAGATTT CTTGAACCAT TTTTTCCTCA TTGTTGCTAA ATTTTAATTC 429840
AATGCACTCA TCTTTAATTC TCCAAATATA CGTATTTACT CTTATATTGT GATCAAAAAC 429900
AAAAATAGGA TCTCTCAAAT TTAAAGAATT GTCAATAAAA AATAAATACT CTAAATACCA 429960
ATTTACTCTT AAAGATACTG CAAATTCTTC AAGCAGAGTT TCAATTAACA TATCCTCGCT 430020
GGACTCAAGC AATTTTAAAA ATTTTGAATA AGGCTCTGGA TTAAGCTCAC AAAGTTTTTT 430080
CATATAAAAA TAGGCATCCT CAAGATCACG ATTTCTAAGA AAAAATAAGG TTGCATATAA 430140
ATATATCAAA TCTAAGTTAG AATAATCATT AACCATTCTC TCAATAGACT TTTTAGGAGA 430200
AAATTTTAAA AGCTCAACTG TTGCAATATG CATATTGTAG ATCGTATAAA TATTAGGAAA 430260
ATTTAAAATA GCTTTAACAT AAGATGTTGT GGCTTGAGTC ATGTTGCCTA TTTTATGAAA 430320
AATAGTTGCC CTATTGTGCC AAATATATTT AGAATAATGA GAGTCTGTTA AAAATTTCTC 430380
AGAAAGCCTA ATTGCTCTGC TTATTTCCCC AATAGAATAA AAATAATACA TTAAATAATT 430440
AACAACAAGA GCAAGATTGG CATCAAAAAA AATTTTATCT ACTTTTAAAA AGCTTGCTGC 430500
TTGAAGAGAT GCACTATTTT TTAAATCCA AATATTAAGC TTAAGTAGAG AATTGTTTTG 430560
ATCCAAATCT CTAGCCTCAA AAAATAATTT TAAAGCCTCG TCTTTGTTAT CCAACATTTT 430620
GAATAAGACA GCACTATTGT TTAAAGCTTG TACAAAATCA GATTTTGTCT CTTTAGCTTT 430680
TAAAAAACAA CTTAAAGCAA GTTTATATTC TTTTAAATTA AAATAAAAAA CACCTAAATT 430740
ATAATTCTCA AAAGGACCTA AATCATCTTT ATTTTTTTCA ATTTTGCCAT AATCTATAAG 430800
TTTAACTAAA AAATTATATT CGCTCAAAAC AACAGGATAA GTATTTAAAA CATATAAAG 430860
AGCCTTATAA TCCTTTTTCT TGAAATAAAT AAGCGCTTTA AGTGCAAGAG AATCAAAATT 430920
CTCATCAAAA ACATCTAAAT TATCAAGAGA GCTTTTAAAA TCACCATTTT TATAAAAATT 430980
TAAAGCCTTC TCAAAACTAA AGTTATTCAT ATTTTTTAAA AATCTCCATA GGCCTTACAG 431040

AAATTCCTT TGAAAAAGAA GTCTTATTAA CACTTTTATC CAAATTGTAA GCGGCAATAC 431100
TAATATAGTA AAGTCTTCCG TCTTCAAGTC CTGTAATCTT AAAAGAAGTT TGATTTCCAA 431160
CATCAATAGG AGAAGTTAAA ACACCGCCGC CGGTTTTTCC ATGATAATTA CCAGAAACAA 431220
CACCAATATA AATGTAATAC CCCTCAACAC TGCTATTAAC AACAGGAATC CATTCAATAA 431280
AAACTTCTCT GGAACCTGGA ATAACTTTTG TTATCACAGG AGGAAATGGA GCTGCTTCAG 431340
GAACGTAAGT AATTGACATA CTATAAGAG AAGGACTACT TACAGAATCT CCACTAGGAT 431400
AAAATTCAAC TTTTATTTGA ATATATTTTG ATATCTTTGA ATCTGGAAAA TCTTTTTTAG 431460
GATCAAAATG AATCCATGCC CCAGTTAAAT TTTTTTTAAT ATTCCCATGA CTATCTGTAT 431520
CATAAAATAC CTTATTATCT AATCTGTAAT AATAACAAT CTCTGTATCC TTAGGAACAT 431580
TAGAATCAAC ATCAAAGGAT AACACTTGAG AATAATATTT AGAAAGCTTA ATAGGGCTCT 431640
GTAATAATGT ATCCCATATT CTTTGAGAAA AAAGCACTAC TAACCTCTTC AAAGCTTTTA 431700
TGTATTTCCA AATTCTCAAC CGCACCAGTA AAATAAGTTC CTAAGGTAAA ATCAATAAAA 431760
TTACCAATAC TTAATAAATA TCCTGATCCT TCCTTCTTAT CATCTGTTAT ATATTCTATT 431820
GCCTGAGGTT TAGAATCTAT CAAATATTCA AGTATGCCGT CCTTTTGCCT ATATCTTAAA 431880
GTATGCAAAT GCCATTTCTT TGGAATAAAA TCATCATTAC TTTTCATTCT AATTTTGATA 431940
GGATTTTTAT TGTCTTTTAA AAATACATTG TTTAAAACCC AAACAAAATT TCCCTCATCG 432000
CTTTCTAATC TAATAGACTG ATCTACCCAC GAATTATTAA TCTTTTTATA ACCATCCCAA 432060
CTAAAAATA TTTCTCCTGT AACAGACGTT GTTCGATATA CCCAAAACCTT AATAGTAAAA 432120
TCAGACACAG TATTGCCTGA AAAAAAGAAC GCTTTCTTTG TAAGTGCTT AAACCTAACA 432180
GGATTTTGAT TTGAATAAAA AATTAAAGAG CCATTAGAAA CATTACGAAA TTCATTTGAA 432240
ACTCTCAAAC TTTTGGCACT AACTAAATAA TTTGAAGATG TGTCTTTTAA TTTATTATCC 432300
CTTCCTATTT CTAAGCGCAA ATCAATATTA TTCAAATCTA AAACAGCTTT ATATCTATCC 432360
AAATAAATAC CAAGCAAACC CCTCATATCC CTTTCAAAG TAACATTGCT AAAATCTTGA 432420
ATAAATTTAA AATTTTTTTT CGAATCAAGT ATCAACTTCA ATTCTTGAGA TAACAGAGTA 432480
GAAAAGCACA AAAAAGrTAG CAAGAGCATT AAAATTAATC TCATTTTTGA CCTTTTATTT 432540
GTTATTACCC ATATTTTTTAA ATACCTCAAA ACATAAAACA AACTGCCTTA TGATACAATA 432600
TTATATCATA AGATGATTTT TAAAATCTAA AAAGTGCCTA ACATTATGAA AGAGAACCCTA 432660
ACAAATTTAT TCGAAAAAGT AATAAAATTA CCAACCACAA GCGGTTGCTA TAAGATGCTA 432720
AATGAAAATA AAAAAATACT CTATATTGGA AAAGCAAAAA ATCTAAGATC AAGAGTAAAA 432780
AGTTATTTTT TAGAAAAAAA TAGTCACAAA ATCAAAATAT TAATGAAAAA TGTAATATCA 432840

ATAGAAGTTA TTACAACAAA TAGCGAATAC GAAGCATTGC TTCTAGAGTG CAATCTAATT 432900
AAAACCCACA AACCTGATTA CAATGTAAAA TTAAAAGATG GAAAAGGTTA CCCCATGGTG 432960
AGAATAACCC ATGAAAAATA TCCAAGAATT TTCAAACCA GAAAAATAAT TAATGACAAA 433020
AGCGAATATT TTGGACCATT TACCAATGTA AAAAAATTAG ATCAAGTACT AGATTTTATT 433080
AACAAAACAT TTAAGATTAG AAAGTGTAAG AAAAAATCCA ATGCTCCTtG CCTATAtTAC 433140
CAAtATGGGAC AGTGCCtTG AGTATGCTAC AAGGAAAACC TTGAAAAAGA ATATCAAAAA 433200
GAGCTAGATA AGGCAAAATC CATACTAAAT GGAAATATAT CCGAAATATC AAGTCAAATT 433260
GATATCAAAT TAAACATGC CATACAAAAA GAAGATTTTG AAACCGCTAT CAAATTAAAA 433320
GAAATTAGAA ATTCTTTAAT AGAAATTAAT CAAATCCAAA TCGTTACAAA AACCAATAAT 433380
TTAAACATAG ATTATGTCCA TGTCATCCA GGAGAAAATG TAAATACAAT AATAGTATTA 433440
AAATATAGAA ATGGAAAATT AGTTGAAAGA GATGCAAACT TTGATGAGAG TATATGCAAA 433500
GAAAATGAGC TGATTTTACA ATTTTGTGATT CAATATTACA CATCTATTAA TATGATAGTA 433560
CCAGACAAAA TTCATATTTT TCTCAAAGAT ATCGACACTA AAAATGTTGA AAAACTAATA 433620
AATGAAATTA AAAATACAAA AACAGAAATT ATTTACAAAG AAACAGAAGA AATTTTAAAA 433680
ATAATGGAAA TGGCCATATC TAATGCTGAA TTATCTTTAA GAGAATATGA GAATAAAAGC 433740
ACCAAAGCAC TTGAAAGTTT GAAAATTGTT TTAGAAATGG ACAAACCTCC CAAAATAATT 433800
GAAGGATTTG ACATTGCTCA TCTTAAAGGT CAAGAAACAG TAGCTTCTAT GGTACTTTT 433860
AAAATGGGAA TGCCTTTTAA AGAAAACACT AGGCTTTTACA AACTAAATTC ACTATTAAAA 433920
GGAGAAATTG ACGACTTTAA GGCAATAAAA GAAGTAATAT CAAGAAGATA TTCAGAAATA 433980
ATTAATAACA ACTTAGAACT ACCGAATTTA ATTTTAATTG ACGGGGGCAA AGGACAATTA 434040
AATGCCGCTC TTTCTATCTT AAAGGGCTTA AAAATAGAAA ACAAAGTTAA AGTCTGCTCG 434100
TTGGCAAAAA AACAAGAAAC AATATTCTTA ACAACTAACA AAAAAGGAAT AAATCTACCC 434160
CAAGGACATC CTGCTCTTAG AATACTGCAA AATGTAAGAG ACGAAGCACA CAGAAAGGCC 434220
AACGGATTTA ACAAAAAAAG AAGAGAAAAA ATAACCCTAT TGTATACAAA AATACACGGA 434280
ATTGGAGAAA AAACAGCCCA AAAAAATATTA AAATCAATTG GAACCTATAA AGATATATTG 434340
CCTTTAAGTG AAAACGAAAT TTCAGAAAAA ATAAAAGTAA ACGTGCAACT TGCAAAAAGA 434400
ATAAAAGAAT TTGCAATAAA AGAGAACTCC ATAAAAATA ATAATCAAGA TAAATAAATT 434460
TTAAACTAGA TTATTATTTA TTAATATTTT TTAAAATAAA AACTATTTT AAATTCCAGG 434520
CGATAAAACC AAAAAAAGAT CATTAATAAG CTTATTTCTA GACTGTATAT TTAAAACATC 434580

TCCTAAAAGC TCTATTTTAT AACTTTCAGA AGAACTCTTA ACTACTCTAA AAAAATGAAC 434640
AACTTCAGTG TAATCAAAAT CATCCAACCTC TCCAATAACT TCATTTATTA AATTGTCAAA 434700
TATTTTTTTTA CGCTCTTTTT TTTCTAAATT TTTAATATTT AAAGATCTCC CTTCAATTTT 434760
ATTTAATTTA GCCAAAAATT TTTCTATACC GTTTTGAAAG TTAATATTTT TAATAACAAC 434820
TTCAAATTCA AAGCCCTTAG AAATATTTTT TCTACCTATT ATCTCATATC TTAGATTATT 434880
AAAAACAAA GGATAAAAAA TGAAATCATC CTTTGCCTGA GATTTCACC CACGAATTTT 434940
TGCCTTCAGA TCATCATCAC TTGGAATATT TAAATAATTA AAAAATATTT CAGGACTGCT 435000
TTGAAAATTT TTAATAGAAT CAAAAAATC TATTAAACA TTTTCAGCCA ATCTAGATTC 435060
AGATCTACAA GACAAAAAAC AAAATAATAA AATCCAACCT AATTTTTGCT TCATACATTA 435120
AAAATTAAAT TTTGATTCTG TAGAATAATG CATTAAAAA TTATTATTAA GCTTTAAAT 435180
TGAGAATATT AAAAATATG ACAAATTTTG ATGAATATTT TTAGAATAAA TTCTCAAATA 435240
TAAATCAAAC TTATATAAAA TTTTCAAAC AATTTTAATT TCTGGAATTG AATAATTTTT 435300
AATTCCTACT CTATAAATTT TATTTAATGA AAAAAGATT TTATTTTTAT TCAATGCACT 435360
CTGCAAGCTC CCATATGCAT TATAATCTAT TTGCACCTTT AATAATCTTT TAAATTGCCA 435420
AATAAGACTC ATTAAATAT TAAGCAAATC TTCTCCCTGA TCCAAAATAG ACTTAATCTT 435480
GATCAAAGAC TGAGTCATAT CTTTTCTCAA AATTGAATTA AATAAGGAAA AGGTGTTCTC 435540
AAAGCGAATA AAATAATCC AAGAAGCTAT ATCTTCCTCC TCAATGGTAT TATCTTGGC 435600
AAAAAGCGCA AAAGAATCTA TATAAATTT CAAAATTTTA GTATCTGAAT TTAACATTAA 435660
AAGCATTAAA TTTATTGCAG AATCTGTAAT TTTAATATTA AGATTAAAAA AATTTCTTTT 435720
TACAAATGTA AATTTATCAT CATCAGGAAT CTCATAAAAA ACTTTTTTTA TAACTTAAG 435780
CTTATTCTTA AAATCAATGT TACATGTATT GCTATTGGAA AAAAAATAA CAGTTTATT 435840
GTTAGACTTT AAGATTGAAT TACACACTAG CTCTAAATCT TTTCTGCTT TTTAAAGTTC 435900
AGACTCATAA ACAATAAAAA TTTCTTTTTT TGAAAAAAA GAATTGAAA ATAATTTCTC 435960
AGCAAATCCT ACAGCTGAGA GTTCTGACAA AAAAATTTTA GTAAGTAAA CTTGGAATT 436020
AAAAGCATCC ATTTTAATTA AAAGCTCTT TAAATAGGCT TCTTTTAAAC CTTGCTCATT 436080
ACCCAACAAT AAATAAACCG CTTGCATTAA AGTAAATTAT AATCCAAGTA GCAATATAT 436140
TATACTTAAG CTAGGAGGAG AATATGAAAG TCGCAATATT TACAGATACA TATATCCCAG 436200
AAAAAATGG AGTAGCAACA TCAATAAAC AAATTAAAGA GGGATTTGAA AAAAATGGCT 436260
ATGAGGTTTA CATATTTTGC CCAAATCCA AAAAATCTTT AAACGAAAA AACGTTTACA 436320
GATGCTCATC TATTCAAATA AATAAAAAAC TTGATGCTGT AATAGCTTTT CCCAATAAAA 436380

GAAAAATATC CAAAATAATA CAAAGCTATA AACCAGACAT CATTCATACT CACTCTGAAT 436440
TTTCTATGGG AAAAATTGGA AAACAAATTG CATTAAAAACA CAACATACCA ATAGTTCATA 436500
CAAGCCATAC AATGTGGGAT TATTATTTGC ATTACTTAGG AATTTTAAAA TATTTTATCA 436560
AACCCGACAA AATGATGCGA AAACATTATA ATAAAAATAA ACATTTTATT TACCCATCAA 436620
GTAAAGCAAA AGAGAGATAT TTCCAACTTT CAAATAATTC TTCyAACTAT AAAATAATTC 436680
CAAATGGGGT TGATAGAAAG CTTTTTATAA AAACCTAAG CAAAGAAAAA AAAGATGAAA 436740
TTTTGAAAAA GCACAATATA AAGCAAACAG ACAAATAAT AATATTTGTT GGAAGAATAA 436800
ATAAGAAAAA AAATATAAAT TTATTAGTAA CACACTTAAA AGATCTTTTA ATGCAAAACA 436860
ATAATTATAA GCTTATACTT ATTGGTAAAG GAAGTGAAGA AAAGGAAATA AAAAATTTTA 436920
GCATCAAAACA TGGGCTTGAA AAACAAATAT TGCTAATAGG AACAATTCCA TGGGAAGAAA 436980
TATACTATTA CTACAAAATT TCTGATATCT TTGCTAGCCT ATCAAAAAGC GAAGTATATC 437040
CAATGACAGT AATAGAAGCA TTAACCGCGG GAATACCTGC TATTTTAATA AATGATTATA 437100
TATATAAAGA CGTAATAAAA GAGGGGATAA ACGGATTCTT AATAAAAAAA TATGAAAAC 437160
TATCTCGGTA CATAGACAAA GTAATAAAAG ATGATGAAAT ACTAAAAAA TTTAAAGAAA 437220
ATGCAAAAAA ACACTCCACT AAATTTTCAA GCTATTTTTT CACAAAAAA ATTA AAAACT 437280
ATTACTCAGA AATTATTGCA AGAAAAATC ATTAATACAG CTTATCAAAA GGCACAAAAC 437340
AAATTGGAAC CTTAATTTTC ATATCCAATA AAACATTTTG AATAGACTCA CCAACAAAAT 437400
ATTGAAAATC CCAAAAAACC TCTGTATTAA CAAAAAATCG AACTTGCAAA ACTATATAAT 437460
AAGGAGTGTA TTTTTTAACA ATAAGAGTAG GAGCACAAAG CTCAACATTA AATTTCTTAT 437520
TATTGAAAAT CATTAAATCC TCTATTTTAT CCTTTAATAA ACCAATATTC GTATCATAGG 437580
GAACTTGAAA AGAAAACACA ACTCTTCTTC TAGTACATGA CGAAAAATTA ACAACAAAAT 437640
TGGATGTAAG CTTACTGTTT GGAATTTTAA TAATTTCTTT GTTAAATGTT TCAAGTGTAG 437700
TAAAAAAAAT TTGGACATCT GCAACCAAAC CTTCAACATC TCCACATTGA ATATGATCTC 437760
CACACTTAAA AAACCTAGAA TTCAAAACAA TAAATCCACT AACAAAATTA GATAGAATAT 437820
TCTGAGCAGC AAGCCCAATG GCAAGCCCTA ATGATCCAAA TACAGCAATA ATAGATGTTG 437880
TAGGCACCCC AAGATATGGC AATATTATTA AAACAATAAC AAAGTCTGTT AATATTTTAA 437940
AAAAAGATTT TAAAAAGTTA AAAACTGTAA CTTCTAACTT TTCCTCTAAT CTGGACTTTT 438000
CTAAAGTTTT AAATAAAATT TTTCCCATTT TACTAACTAT TAACTTTAAA AAATACCATA 438060
GCACTATAGC AATCGAAACT TTTAGACCAT AACCTACCAC GCCCTCAATA ATATAATTAA 438120

ATAATCTTG	AAATATAAAA	AACTCCTTAA	ACAAATTAAA	CTTTCCTTCC	GGGCTTTACA	438180
TAAATTAATT	GAATTATAGC	ACAAAAACA	AACAAGCCTT	CCAATAAAAA	CCCTAATTAA	438240
AACAATGACT	CAATATTTTA	AAGACACAAT	AAAGCATATT	TTCATTACTG	CCGCTCAACA	438300
ACAAAATGAA	CATTACAACA	ATATTTGTGA	TAAAATTAGT	ATCCAAAGGT	TTTTACTAAA	438360
TTTGACAAAA	CAAATGTATA	AAAAGAAACA	AAAAAAAATA	TATGAAATTC	TGGACTTGTT	438420
TTTACTTGTC	TTTAAAACAA	CAACACTTAC	AATTGGCGGA	GGATTAATAA	TTATATCTGA	438480
GCTTAAAAAA	ATATTTGTTA	AAAAAGAAA	AATAATATCT	GAGGACGATT	TTAACAAAAT	438540
ACTAGCAACA	TCAAATGTTA	TTCCTGGAGT	TACAGCGATT	AATTTTGTGT	TCCTAGTAGG	438600
AAGAAAATTT	GGAGGTTTTC	CATGCGCACT	TTTGCTCGTT	GTTGCAGGAA	TTTTGCCTTC	438660
CATTATTGCA	ATAATAATGG	TTTTCCTTTA	TCTAAAATTA	GTACCAGATA	GCATACATGT	438720
TAAAAAATTT	CTCGAAGGTG	CAAAAATATC	TTCAATTATC	ATAATGATAA	CCGTTGTTTT	438780
AAAATTTTCC	AAAAAATGC	TAAATGATTC	TATAATAAAA	TGGACAATAT	GTTTTCTTGT	438840
AATTTTGTGA	ATTTTAAAT	TAAAAATAAA	AATATCATAC	ATATTGTTAA	TTTTCTTTTT	438900
AGTATACACA	TTTAAATATA	TAACAATAAA	AAAAATATTA	ACTAAATAGA	AAAAGGATAT	438960
CGGTTGATTT	TAATAAATTT	ATTCATTACA	TTCTTAAAAA	TCGGATTATT	AAATTTGCGA	439020
GGCGGTAATG	GAATTGCAGC	AATAATAAAC	AACGAAATAA	TTAATAATAA	ACATTGGATA	439080
ACAAAAGAAG	AATTTGTCAA	TATGATTACA	ATATCAAGAA	TAACCCCTGG	GCCTATTGCA	439140
ACAAACATAG	CAACATACGT	TGGAATGAAA	ACTGCAGGAA	TTGCGGGAGC	AATAATTGCT	439200
ACAGTAGCAT	TAATAACAGC	CCCAATAATA	ATAATGATTA	TAATCCTCCT	AATACTACAT	439260
AAAATCGGCT	TTTTAAATTA	TTGCCTAGAA	AATCTAAAAC	CTATTATTGT	TGCGCTGTGG	439320
ATAATTACAA	TAATCATTTT	GCTTGAAAAT	ACATATTTAA	AAATAGAAAA	CAACAAAACA	439380
GACTTTTGA	AACTCTGGC	TATTGTAGGA	ATTAATTTTT	TTATTTTATT	TTTTTATAAT	439440
AAAATAAGTC	CAGCATTAGT	AATTATACTT	AGTGGATTTT	TTTATACATT	AATATAAATA	439500
TGATTAAACA	AAAATTAAAA	ATATCTCAAA	ATTTAAACTC	AATTCAAATA	CAAACAATAA	439560
AAATATTAAG	CCTTAACCAA	AAAGAATTAA	CAAAGCTTAT	ACTAGAAGAA	AGCGAAAATA	439620
ATGAATGTCT	AGAAATAAAC	TCAAATAAAA	TATTTTTTGA	AACATTGAAA	ACATATAGGT	439680
TTAAAAAAGT	TTTTTATAAA	GAAGATGATA	TGATAAAAAA	TCAACACGAC	ATAGCTCTTG	439740
AAAAAACACA	AACAAATACT	TCTTTAAAAG	AACACCTTTT	ACTGCAATTA	AGAATTCAAA	439800
GAATAAATGA	AGATGAAATT	AAAATAGGCG	AAATACTCAT	AAACAATCTA	AACAGCAAAG	439860
GTTTTCATAT	AATAAACCCCT	TACGATCTTT	TTAAAAAGGA	AGAAAAAGAA	AAAGTAAAAA	439920

AAATAATTGA ACTTATTCAA AAATTTGATC CAATTGGAAT TTGTGTCCCC AACATAATAG 439980
AATCGTTAAT TTTGCAAGCA AAGCATCATA AATTAGAAAC TAATATTATT AAAATTCTTG 440040
AAAAAGCAGA GCTTCTTGAA AAAACTCAAA AAAAGTTAAA AGAGGAACTT AAAATAAGAA 440100
GCAAAGAATT TAACACGGCT TTAGAAATTA TCAGACAAAA ACTTAACCCC AACCCAACGC 440160
TCGAATTTAA AGACCCAAAC GACACTAATT TTTATGTTGA TCCAGATATA TTAATAATAA 440220
ATCACAATAA TAAATTTAAA ATTAAAATCA AAGAAGTTAA TATCTTTAAA AAAGAACTTA 440280
AAAGGACAAG TGAAAACCCC CAAAAACAAA AAAAAGCAAA GTGGTTAATC GAATCCCTAC 440340
GATATAGAGA CGAAATACTT GCAAAAATAG GAATAGCTAT ATATACATTG CAAAAAGAAT 440400
TTCTAAGAAG AGGATTTAAA AGCTTAAGGC CAATGAACTT GAGCATTTTA TCAGAAAAAA 440460
TTAGTGTATC AAAATCAACA ATATCAAGAG CAATAAAAAA TAAATACTTA AAATGCGAAT 440520
GGGGTACAAT ATTAATCAAA GAGCTTTTTA GCTCTGTTGG TGGAGCAAAA ACAAATGAAT 440580
TTTCAAAATT AAGCATCAAA ATAACAGTAA AAAAGTTATT AGAAGCAAAT AAAAAGATGT 440640
CAGACAAAGA GATTTCTGTT ATACTAAAGT CCAAAGGAAT CTCTATTTCT AGAAGAACAG 440700
TAAATAAATA CAGAAATGAA TTAAATCTG AGAAAGGGAG AACATATTAT GGAACCTAAA 440760
ATTCAAACGG TTAATTACAG CTTGAATGAG AATGAAAAAA ATTTTATTCT CAAAAAGCTA 440820
GAAAAATTTG ATACTCATAT CAAAAACAT ATTGATAATT TAAAAATTAC AATTAAAAAA 440880
GAACATGAAC TTTTAAATT AGACGCACAT ATTCACTTTA ATTGGGGGAA AATAATACAT 440940
ATAAGAGAAG ATGGGAAAT ACTTCTTAAT CTTATTGATA GTGCAATAGC AAGACTTTAC 441000
AAAACAGCAA CCAAAGAGAA AGAGAAAAAA AACAACAAAT AAGATAAGTA AAAAATGCAA 441060
GAAGTAGAAA TTGAGATAAT AAATAAAGAT GGAATACATT CAAGGTCGGC AAACATCATT 441120
GCTGAATTCG CAAATAAACA TTCTTCGTGC GACATAAAAA TAACAACAAA AGATGGCAGA 441180
AAAGCTGACG CAAAGTCCAC AATAGAAATT ATCATATTGG GTATAATATA CAAAGAAAAA 441240
ATAAAAAATA CAGTCGTTGG AAAAAAGAA AAAC TAGCAA TTAAAAATTT ATTAACTTG 441300
CTAAAAATA ATTTTCAAA AGAGCTTTAA AAATGAACAA AAAAATTTT TACATAACAA 441360
TACTGCTGCA CTTACCTAAT CTTCTATTTT CATACTCAAC AAAATACGAC ATTGAAGTAA 441420
AAATGTCGGC TTTTGTGATG AGTCTGGCAA TCATCGTAAT CTCATCTATT TCAATAGGCA 441480
ATCTAGTAGC TAAAATAGGA ATTCCAAAAG TAATAGGGCA AATAACAGCG GGAATAATTC 441540
TAAGTCCGAA TGCCTTTGGA AAAATTCAAA TACCTTTATT ATTCCCATG GGAATAACTC 441600
AAATTGGAGA AAATTATTTA ATAAATGAAA AAATATTTGC AATCTCTACC ATAGCTTCAA 441660

TAATATTGCT	TTTCACAGCA	GGACTTGAAA	CTGACTTAAA	ATTGTTTATC	AAATTTTTGC	441720
CACGCGGAGG	AATTATTGGA	ATAACAGAGG	TTGTGGGAAC	CTTCACAAGT	TTTGTACTAA	441780
TGGCAAGCAT	AATTTTTAAC	GTTCCCCTAA	TAAGCCCAAC	CTCACTTTTT	ATTGGAATAA	441840
TTGGAACCCC	AACATCAGCA	GGAATCGCAG	CAAGCATACT	CTCGGCAAAG	AAAAAAATGA	441900
GTACCTCAGA	AGGAGTGACA	ATAATCTCAA	CTTCAATTAT	TGATGATGTG	CTTTCAATGC	441960
TTATGCTTAC	AAGTGTAATA	ACTATATCAA	GATCTATATC	AGATCTTGAT	ATAGCAAGCT	442020
CAATAAAAGC	TATAGTTCAA	AACATAGTAA	TTTGGCTATG	CTTAACTTTC	TCTTTAATAT	442080
ATATATCAGA	AACACTCTCA	AGACTGTTGA	AAAAATTAAA	CAGTGTCAAC	TTAGCAACCG	442140
TAATAACGCT	CTCTCTAGCC	CTTACTATTG	CAAGCATTTT	CCAAAATTTA	GGAATGTCTT	442200
TTGTTGTTGG	GGCTTATGTA	TTTGGACTTG	CTATGTCAAA	AACAGACATT	GTATACGTAA	442260
TTCAAGACAA	ACTAACAATC	TTTGAAAGAT	TCTTTATCCC	GATCTTTTTT	ACATCAATCG	442320
GACTTATGTC	AGATATTAAT	GAAATACTTT	CAAAGGAAGT	TCTTATTTTA	GGATTAGCAA	442380
TTAGCGCAAT	AGCAATAATT	ACTAAAAGTA	TATTTTGCTT	TATCCCAGCA	CTCTTTTTAG	442440
GATTTAATAA	ACTTGGAGCC	TTAAAAATTG	CAACCGGAAT	GGTTCCAAGA	GGAGAAGTTT	442500
CACTTATTAT	GGCAAATGTA	GCATTATCTT	CAGGATTTAT	TAGCCAAAAA	ATATTTGGAA	442560
TCATAATAAT	AATGGTGTTT	TTGCCAACAA	TCATTGCAAC	ACCCATAATA	AACTTTTTAT	442620
TTAAAAATAA	TAAAAGTGGA	CTTAAAAAAG	AACTCCCAAT	AGATCAAAAT	ACACACATAT	442680
GCGTATCATT	TGAATATGAT	AATTTAGCCA	AAATCTTAT	ATGGGACTTT	AAAAATGAGT	442740
TAAGAAAAGA	AGGATTTTTT	ACACAACAAA	TTAAAAATGA	TTCTTCACAA	TATATTAATG	442800
CAAGAAAAAA	CAATATATCC	TTCTCAATAA	AACGAGAAGG	TAGCAAAATC	ACATTTGAAT	442860
GCCCAAATAA	TCATTTAATT	ATAATACAAG	ATCTTTTTAG	AGAAACAATC	TTAAACCTAG	442920
AAAAAATAAC	CAAAGAAGTT	GAAACAGTCT	CTTTAAGAGC	AAAAAACTA	GATTACTCAA	442980
TAAATTACGA	TAAATCCTT	AGTAATATCA	ACCTAAATAA	AAGAATAAAA	AAGGAAAACA	443040
TTATTCTAGA	ATTAAAATCA	AGCAATAAGG	CTGATGTAAT	AAGAGAGCTT	CTAAGCGTAA	443100
TAAACATTGA	AATTGATAAA	GAAAGAATAT	TCCAAGATTT	AATGGAAAGA	GAAAAGTTAA	443160
TTACTACTGC	ACTAAAAGAA	GGCTTTGCCA	TTCCCCATTT	AAAAACAAAT	TTAATATCAA	443220
AAATACATAT	TGCAATAGGA	ATAAGCCATG	AGGGAATTGA	CTTTAATGCT	CTTGACAAGA	443280
ACTTAAGTCA	TGTTTTTATA	TTAATACTGT	GCCCAGCAAA	AGATTACGTT	AGCTACCCTA	443340
GAATTTTAGC	ATCTGTTGTG	GGCAAAGTTG	ATCTGTACAA	AAAAGAAATT	TTAAATGCAA	443400
AAACAGATAA	AGAAATTTAT	AATATAATAG	TGAGCTAAGT	TATGTTTAAA	GTTATCAAAT	443460

GTAATGAATT GAATGAAAAA TTGATAGACA AAAAAGTTGA AATAAATGCT TGGGTAAAAA 443520
AAATTAGACA CCACGAAAAA TTTATCTTTC TAAATATAAG AGACAGATAT GAAAAAGCTC 443580
AAGTTCTGGT AAATGAAGAA AAGCTTCTAA AGATCGCAGA AAAAATAAAA CTTGAATATT 443640
GCATTAAAT TCAAGGACTG TTGATCAAAA GACCCCCCAA CATGATAAAT GCAAATATGA 443700
AAACAGGACA TTTTGAAATA TTGGCAAAAA ACATTGAAAT TATCTCAAAG TGCAATGAAT 443760
TGCCATTTAT GATAGAAGAT GACAATAATG CCAAGTGAAA ACTCAAAACT TGAATACAGA 443820
TACTTAGATT TAAGAAGAGA TTCCTTGAAA AATAAAATTA TTTTAAGATG TCAGGCTACT 443880
CATCTTATTA GAAATTTTTT AATAAAAAGA AAATTTTTAG AGCTAGAAAC TCCAACTTTT 443940
GTAAAATCAA CGCCAGAAGG TGCAAGAGAT TTTGTAATCC CATCAAGGAT TCACAAAGGA 444000
TCTTTTTATG CACTACCTCA ATCTCCACAA CTTTACAAAC AACTCATAAT GATAGCAGGA 444060
TTTGACAAAT ACTTTCAAAT AGCCCGCTGC TATAGAGACG AAGATTCAAG AGGGGACAGA 444120
CAACCAGAGT TCACCCAGCT CGATCTTGAA ATGAGCTTTG TCAAAAAGA AAATATTTTT 444180
AAATTAATAG AAAATATGCT TTTTTTAATA TTCAAAAATT GCATCAATAT TAACCTACCT 444240
AAAAAATTCA AAAAAATAAC ATACAAAAG GCAATGAACA AATATGGAAG CGACAAACCA 444300
GATACTAGAT TTGAACTTGA ATTACAAGAT ATAAGTCGTA ATCTAAAAA TTCAGAATTT 444360
AATATATTCA AAGATACTCT AAAAAACAAA GGTTCATTA AAATTTTAAT AGTAAAAGAT 444420
AAAGCTGACA AGTTTTCAAG AGCAAAAATA AACAATTTAG AAGAAATTGC AAAGCTTTAC 444480
AAAACACAAG GGCTTTATTT TACAAAAATT GAAAACAATA AATTTTCCGG GGGAATTGCA 444540
AAATTTTTTAA AAACAGAAGA ACAGGAATTA ATAAAAACCT ATTCTTTAGA AAATAATGAC 444600
ATAATTTTCT TTACAGCTAA TAATAACTGG GAAACTGCAT GTAAAGCAAT GGGTCAAATT 444660
AGAATAAAAA TTGCAAATGA TCTTGACTA ATAGATGAAA ATAAATTTGA ATTTCTATGG 444720
GTCTATGATT TTCCACTATT TGAATATGAC GAAAATACAA AAACCTATTC ACCAGCTCAC 444780
CACATGTTCT CGCTTCCCAA AAAGCAATAT ATTGCTAATT TAGAAAAAAA TCCAAAAAAA 444840
ACTATAGGTG AAATTTACGA TCTTGTTTTA AATGGCGTAG AACTTGGCTC AGGTTCATTT 444900
AGAATACATA ACAAAGAGCT TCAACAAAGA ATTTTCAAAA TAATAGGATT TCAAAAAGAA 444960
AAATCAGAAG ATAGATTTGG ATTTTTTCTA AAAGCATTAG AATATGGAGC TCCTAATCAT 445020
GGTGGCATTG CTATTGGCAT TGATAGACTA ATAATGTTGA TGACAAAATC AACTTCAATA 445080
AAAGATGTAA TACTGTTTCC TAAAAATTCT TTTGCAGCAA GCCCTCTTGA TAATTCCCCC 445140
TCTAAAATCT CAAATGAACA ACTCAAAGAA CTGGGAATTA ATATTGTTGA TGGTGACAAT 445200

TAATCCATAA	TGCAAGCTCT	GCCATATACC	TTTAAAATTA	TAAAAATCAG	CTACTCAACA	445260
TTCCTTGGAA	TTTTTCAAGA	TACTGCTATT	CTTTCAAGAA	ATTAAGTCTC	AAAATCTAAA	445320
ACAAAATGCT	TTTTTAAAAT	TTAAAAAAAT	CTTATTAATT	AATTACTTTT	TCAATCAAAA	445380
CAGTCTCATA	AACACAGCAT	TTAATAATAA	TTTTAAAAAT	AAATTAATCT	ATTATTCAGG	445440
TTTTGAAAAA	ATAAACAAAA	AAATACCCGA	TAAATAGTAA	AAACTATAT	CAAACAATCA	445500
ATAATTTTAT	AAATATCTAA	AATATAATTA	GAATAATAAA	AAAGCCGCTC	AAAAAGCAGC	445560
TTGCAAATAA	AAATTAGTGA	ATTTTTATTT	AATTTCTATT	AATATTATTA	AGATTTTTTGC	445620
ATGCAATCTT	CACACGGTCT	TTCATAGAAA	CTTCAGCTTC	TCTTAACCAA	ACCCTTGGAT	445680
CATAAAATTT	CTTATTTGGA	ATATCAATAT	CCTTGCCATC	TCCTAATTGA	CCTTGCAAAC	445740
GACTTTCATT	TTTTTTGTAA	TAATTTAAAA	CACCCTCCCA	GGCAGCCCAC	TGTGTATCTG	445800
TGTCAATATT	CATCTTTACA	ACGCCATAAG	AAAGCGCCTC	ATTAATCTCA	TCAATTGTAG	445860
ATCCAGACCC	TCCATGAAAA	ACATAAGAAA	CTGGCTTAGC	CATATTTACT	CCTGTTTTTG	445920
ATATGACATA	ATCTTGACCA	TCTTTTAAAA	CTTTTGGAGT	AAGCTTAACA	TTCCCCGGTT	445980
TATATACCCC	ATGAACATTT	CCAAAAGCTG	CTGCAATCTG	AAAATTTGGG	CTAACTTTTA	446040
AAAGTTCTGA	ATATCCATAA	TAAATATCCT	CAGGAGTAGA	AAATAGTTCA	TGCAAAGCTC	446100
TATCTGAATT	GTCAACTCCA	TCCTCTTCCC	CACCCGTAAT	TCCAAGCTCT	ATTTCCAAAA	446160
ACATTTCAAT	TTTGTCCATT	CTTTCTAAGA	ATTTTTTTAGA	AATTTCAATA	TTTTCTTTAA	446220
TAGGTTCTTC	TGATAAATCT	AACATATGTG	AAGAAAATAA	TGGTTTTTTTG	TGCTGACTAT	446280
AGTATTTCTC	TCCATATTCT	AAAAGGCCTT	CAACCCAAGG	AAGCAAATTT	TTAGCACAGT	446340
GATCAGTATG	AAGAACAACA	GGAACACCAT	AATGCTCTGC	CATTAAATGA	ACATGCATAG	446400
CACCAGAAAT	AGCTCCAAC	ATTGAAACTC	CTTGTGGTTT	TTCCATCTTT	AATCCTTTTC	446460
CAGAAATAAA	AGCAGATCCA	CTATTAGAAA	ATTGTATCAT	AATAGGAGAA	TTAATTTCTT	446520
TTGCTGCCTC	CAAAACTGCA	TTAATAGAAT	TTGTTTCCTAT	ACAATTAATA	GAAGGAATAG	446580
CAAATCCTTC	CTTTTTACAT	ATTTTCATATA	AAAAATGTAG	TTCTTTCCCA	TAAACTACAC	446640
CTGGTTTAAT	CTTATCTAAA	ACACCCATTT	ATATCACTCC	TTTCCATTTT	ATTTTTTCTT	446700
TTATCAAATG	CCTATAATAA	ATTATACACC	TAAGAAGTTG	AATTGAATTT	AAATCAAAAA	446760
ATAAATAATT	ATTAAATCAA	AACCAAACAT	AAAATTTATT	AAAAATTTAT	TATTTTGCAT	446820
AAAAAAGTTT	AAAATCAAGT	CTTCTTGGTA	GACTCTAGCA	TTTTATACCA	CTGTGAAAAT	446880
TCTTTTATTC	CTTCTTTAAT	AGAAACTTTA	GCCTCATACC	CAACATCATT	TTTAAGCTTT	446940
AAAATATCAC	AACAACCTTC	TACAACATCT	GCTTTTTTGCA	TAGGCATATA	ATTTTTTAAG	447000

GCCTTTTTAT CAAAATTTGC TTCAAGCTCG CTAATAAAAT CTAGCAGTTT AGTTGCGTGT 447060
CCAGTTCCTA TATTATATAT TCTGTAAGGA AAAGAAGAAG TTGATGAATT TGGATTTTTA 447120
ACGTCAAAAT TACAATCACT CTTAGCCGGA TTTTTCAAAA CTTTGTA AAC ACCGTCTGCA 447180
ATGTCACCCA CATATGTAAA ATCTCTAGCC ATATTCCCAT TATTAAAAAT ATTAATAGCC 447240
TTGCCATTTT TAATTCCATC TGAAAATAAA TATAAAGCCA TATCGGGTCT TCCATAAGTC 447300
CCATAAACTG TGAAAAATCT AAGCCCTGTT GTGGGAATAT TAAAAGATGC ACTATAAGCA 447360
TGCGCCATCA TCTCATTAGA TTTTTTACTA GCTGCATATA AATTTAAAGG GTGATCCGTA 447420
ATAGAATCTT CACTAGACGG CATATTTTCA TTTATGCCAT AAACCGATGA CGTTGATGCA 447480
TAAACAAAAT GCTCGATGTT TTCTTTATAA ACTCTACATA CATCCAAAAC ATTAAAAAAC 447540
CCAACAATAT TTATTGAAAC ATAGCTATCA GGATTTTCAA GACTATCTCT AATGCCCGCT 447600
TGAGCAGCCA AATGGCAAAC ATGTGTAAAC TTATGATCTT TAAAAAGTTC TAGCAGTTTA 447660
TCCTTATTTA GTATATCAAG ATAAGCAAAA GATAAATTAT TATATTTTTC ACTCTTAATA 447720
ATCTTATGCG TTTTAACATC CTTAGAACAA AACCTTAAAG CTTCTAACCT TTCATGCTTA 447780
AATTTGAGTT CATAATAATC ATTTAATACG TCTATTCCCA AAACCTCATG CCCTTTTTC 447840
ACAAGCTTTT TAGCTACATG AAATCCAATA AACCTTGCAA TTCCGGTTAA AAAAATCTTC 447900
ATACTATTAT TCCTCTTTAA AATTCAATAC AAAGCAAGCC CATTAATCTA TTTTTTAAAA 447960
CCAATATCTC TTTTCTGATA ACCACGAGAA TTGTTGATAC CATACTATT ATTTCTAACA 448020
TAAGAGACTC TTATTCTTTT TATATTTCCA TCTCCCTCAC TTTGAGTTTT TATGTCAC TA 448080
TAACGATTTA AAGTTGTATG AACAAATCCTT CTTTCAAAAG GATTCATTGA TGGCAACAAA 448140
ATAGAGCGCC TGGTTCTTTT GACTTTATGA AAAGAATTTA TTGCTAAATT AATAAACCTA 448200
GATTTAAACC GTTCTCTATA ATCTCCAATA TCCAATATAA CCCTATTAAA AGCCCCATTT 448260
TCACCAATAA GCTTAGAGGC ATAAACATTT GTTAAAAGCT GCAAAGAATC TAAATTTT TA 448320
CCCTCTCGTC CAATCAAAAT ATTTGGACTA TCTGTTTCAA TAGAAATCTT AACATATCCC 448380
CCTTCTTTGG GCTCTATTGT CAAATGTACA GAATATCCCA TTTTAATTAG CATTTCTTTT 448440
ACAAATTCTA AAATTTTATC ACAAATTTCA TCACCAATTT TAATTTCAAA ATCGTCTTTT 448500
TTAACCTCCT TTGCATGAGG AGAAACCCGT ATTTTAATCA TTTCTTTCTT AAATAAAAAT 448560
CCAACCCTTT CTTTATCTAA AATTTCTACA TCAAACCTGC CTTCTTTTAA TTCTAGATCT 448620
CTCATTGCTT TCTTTATTGC TTCTTGCTCG GTTTTTCCGT AAAATTCATA GCTCATATTA 448680
TCCCCCTTT AAGACAAATG CATCTTTATA TAGTATTGCT GCAAAATAGT AAAAATATTT 448740

GTTGTAATCC	AATATATTAA	AAGCCCTGAT	GGCATATTGT	AAAGTATGAA	AAAAAACATA	448800
ATAGGCATTC	CAAAATATAA	AAACTTCTGC	TGCGCCCCAA	GATTTTTTTAA	ATCCATATTA	448860
GAACTAACAA	TTGTAGATCC	CAATTGAGTA	AACATCATAA	TAAAAGGCAA	AATTCTAATA	448920
TCGGTCCAAG	AAACAAAATA	AAGCTTATAT	CCAAAATGAT	ATACACTGTC	ACCGATAGAT	448980
AAATCATCAA	TCCATCCTGG	AATAAAACTA	GCTCCTCTTA	ATAAAAATAA	ATTATTTACA	449040
AGTGAATAAA	GAGCAAAAAA	TATAGGAAGC	TGCAAAATTA	CAGGAAGACA	CCCCCAAGA	449100
GGATTAACTC	CTTCTTCTTT	ATAAAGCCTT	CCCATCTCTT	CATTTAACTT	TTTAGGATCA	449160
TGCTTAAACT	TTGCTTGAAG	CTCTTTCATT	TTAGGTTGAA	GCTTGGAAG	yTCCGCAGTA	449220
GCTCTAAATC	CCTTAAATGT	CAAAGGAAAG	ATAAGTATTC	TAACAACAAT	TGTCAAAAAA	449280
ATAATTGAAA	GCCCCCAATT	AGGTATAACA	TCATAAAAAA	CTTGCATTAC	CATTTGCATA	449340
GGAACCTGAA	TCAAATACCA	AAAACCTCTT	TCCACTGACA	TTCCAAAAAA	AATATCAAAT	449400
AAACCAAAGG	TATTGTCATC	TCTCTTGTC	AAAACGTCTA	AATATCTATT	ATCCTTAGGT	449460
CCAGCGTAAA	TAAAAAACTC	ATCGCTAATA	TTTTTTTTTAT	TTCTAACATT	ATTAATAATA	449520
AACGATTTAA	GAGTTCCTCT	TTCCTTCTTA	AATTCAACCT	CCATATTTTC	TTTgGAACT	449580
AACACCCCAA	AATACTTAGT	ACTAGAACCA	ATCCATCTGG	GATTGTTAAT	CCTTAGACCA	449640
TCTTTACCAT	ATTTAAGCTT	ATTATCATAA	TAAATTATTT	GAGACAAATA	ATTATTATAT	449700
TGTAGCTTTG	CTTTATCACT	CAACCTTTCA	ATCTCAGAAC	TAAAAATAAT	TTTATAAGAA	449760
TCAAAATCAA	ATAAGTTATA	ATCCTCAAGA	CCATTTACAG	TAACCTTGAA	TTGCATTAAG	449820
TACTCATCTT	TTTTCGAAAA	TGTATACTTC	TTTACATATT	CATAAGTTTT	ACCATTATTT	449880
TTAAATAAAG	CTTTAAATTC	ATGATTAAAA	TCATCTATCT	TTTTATACAA	AAACAAATCA	449940
TCTACAAAAT	AGTCAAAACT	AATGTCAAAA	AAAGTTTCAT	TTTTGCGATC	AATATTAATC	450000
AAATCTGTAG	GATTTTTTTT	CAAATTTAAA	TGATTTTTTA	GCTTTAATGA	AACCAAATTT	450060
CCTTTAAATG	TAGAAAAAGT	AGCAACATAT	ATCCCTGTCT	CTACAATAAT	ATCTTGAGAT	450120
TTATTAATCA	AATTAAAGCT	ATTACTCTTA	ACTGAAGACA	TCTCATTATC	ATCAAACTT	450180
TTGTTTAAAT	CAAACTGCAC	TTCCTTATCA	GAAGACTTAG	AACTTAAAT	GTTTGAAGAA	450240
AAAATATCAT	TAATAAGCAT	GAAAAGACCT	ATTAAAAATA	AAGACAAATA	AACTGTTCTT	450300
AAAATTCTTC	TACTTTGATT	CACCTATGCC	CCTTTCACAC	CTTAAACCA	AACCTTTCAT	450360
GAGAGATTCA	ATGCTAAAT	AAGTCAAAGT	TAACCTACCA	TAAGAACTA	CAAAAATAAT	450420
ATCTAAAGCA	ATCCCTTCTA	ACAATTCTAA	TCTTTTTCTA	AAAGCTTCTT	TAAAAAGTCT	450480
TCTAATGCGA	TTCCTTTTAA	CAGATCCCCT	AAAGCCTTTA	GAAAAGGTAA	CAAGAATTCT	450540

AGAATAAACC AAATGATTG ATTTATAGAA CATTTTAAGA TTAAGATTGC TAAATCTAAT 450600
CAGCTTGCCT TCTTTGAAAA TTTTTTGAAT TTCTATTTTT GATTTTAAAC TAATATTTCT 450660
TTTTCTCATC AGAAACAGTT AATTTTCATTC TTCCTTTTGC CCTTCGCCTT GAAAGAATAA 450720
GTCTTCCGCC TTTAGTTTTT ATTCTAGCTC TAAACCCAAA TTTTCTATTT CTTTAAACAC 450780
GACTGGGTTG ATAAGTTCTT TTCAAAACGC TCCTCCATTA AAAACAATTT TATGCTGCCA 450840
AGCTACAAAT TAAACACTAA CATGGTATAG CATATAAATG CAATTGTCAA TAATAATTAC 450900
CTTACCAAAA CCTTTATATC TATTATTTTA ATACCTGTTA ATTCTTTTAC TGAATTTATT 450960
ATCTTCGACT TATTGATTGC TATACTACAC AAAATACTTG AATTGCTTAC CTCAAGAAAA 451020
AGGATCTGCT CATTTTTTAAA ATCTAAAAAC TTTACATCAT CTGATAAAGC CTCAAATATC 451080
TGATTCCATT TATCGGCAAT CAATAATTTT GAACTTATTT TTTTATTAAC AAGCAAATTG 451140
GATTCTAAAT AATCCTTAAG AACATTGCCT ATTTTTTTTAA AAGCAGAATC ATTCATATCA 451200
ATTTTTTATA CCACAATGCA AAAACAATA TTGAATAAAC CTAGAAAAGC TTATTTTAAAT 451260
ATTCAAAATA GCATTAATAA CTCACTTTAA CCCAAAGACA TCGGCATTAT CAAGTGCCTA 451320
AAATTAAAAT TTTCAGGTTT GCTCAATTTT AATACATTGC CCGAATTAAA TTGTATTTCT 451380
ATCTTTGAAG TTTCAAAAAC ACTAATAGCT TCAACAAAAT ATGAAATATT AATAGCCATA 451440
ACCTCATCTG CTCCGTCATA CAGATAATTT GGATCTTTAA TGAAAAATTC ACCTTTTCTT 451500
CCAGTAATCA AATCTTCTCC AAGAAGTTTT AATTGTAAC TCAAGAAAAGT TAAAACCAAC 451560
TTTCTTGATT TATCAACATA TAAATTGACT CTTGCAAGTC TATCTTTTAA AATGCCTAGC 451620
GAACTAAAG ATTTATTTTT CTGTTCTTTA GGTATAATGC TTTTATAATC CGGATAATTA 451680
CCATTAATTA AGCTACAAGC TATTTTATAA TTATCAAATT CAACATAAAA TTTTATATCC 451740
GAAACTTTA TTTTAACCAT ACCTTCTCCC GACATAAGAT GTTTTAAGAA ATTAAATATT 451800
TTTACAGGAA CTATAAAATT CACATCTTCT TCAACTATGA CTTCTGTTTT ACAAATAGAC 451860
ATTCTGTGAC CATTAGTAGA AACAAGTAGT AATTTAGAAT CTTTATCTTT TGAAAAATAC 451920
ACACCATTTA ATACATTCTT AGATTCATCA AGATGTGCTG AAAAAGCTAT TCTATTTATT 451980
ACTTTTTTAA AAGATTTTTG TTTTATTTCA ATTCCAAAAG TATAATCTTC ATTAACCATA 452040
TCATAATTGT AATTTTCTAT TTCTTCGTAT GAAAAAGTGG GCTCTTTTAA ATGATCTTCA 452100
TATTCCTCTT TCTCATCATT TAACTCTCCC ATAATTTCTA ATTTACTATT ATTTTCATTA 452160
AAAATATTT TGATTTTCTT ATAAAACTG AATGCTTTTA CTGCATCATA AAAATTTGAA 452220
GCATTAATTA ATACCTTAAA ATCTGTTTCT GAAACAATTG AAATTGTGCT TTCAAAAAAT 452280

ATATTTCTGT CTGTTGATTT GATTATGAGA TTAGATTTTT TACTTCTAT TAACAATGCA 452340
CTCCAAATAT CATTCAATTT TCTGTTTAAAT ATTATCCCT TTGCTTTTTC TATCTCATTC 452400
ATAATTTGAT TTGTTTCGCA AATAAAAAAT GTGTTGTGTA GCATGATGCC TCCTTATATA 452460
TTCTATTACA TTTTATCTTA ATAAGATTTT GTGGATTTTG TATTTTTATT TTTTATAGAT 452520
ATATAGTAGT AATAGTAGTA AGCTACTGTT TGATTGTTTA ATTGTATTTA ATACTATATG 452580
ATGCAAGTAA ATATCTTGTT AAATTGTAGG TTGTTTTTTT GTTGTATTTT TGATAAATTA 452640
TTTGGTTCAA TTGTTTAAAA TAATTTTGA TTCTTCAATT AAGTTTAATT TTTTTTTATT 452700
TTGTTCATAA GTTCTGTGAT TAAATTGTTA ATTTCTTTGT CATTATTTCT GTCTCTATCT 452760
ATTTTATTTA TCGAATAAAG CACTGTTGAA TGGGTTTTCC CTCCAATAAT TTTTCCAATT 452820
TCAACTGTTG ATAGCTCTGT AAAATTTCTC AAAAGGTACG CATAAATATG TCTAGCTTTT 452880
GTTATCTCTG GTTTTTTACT ATGCCCCCA ATATCTTTGT GTGTGATTTT TAGCTCTCTT 452940
AAGAGTATTT TTTTTATATT TTCGATATTA ATTTTATTGT TTGGCTCATT GGTTGTTTCT 453000
TTTTCGTAAA TTATTATTTT TTTGATTATT TTTTCAACAA TTTCAATGTC AATTTCTATA 453060
TTGTCTAAAT CTATATATGC TTTTAGTTTT GTTACAGCAG CTTCAAGGTC TCTTACGTTG 453120
GTTGTAACTT TTTGAGCAAC CAGATTTAGT ATATTTTTAG GGACATTTAT GCCATCTTCT 453180
TCTGCTTTTT TTTCGACAAT AGCTGCTCTG AGTCAAAAAT TGGGCTTTGA TATATCAACA 453240
TTTAATCCCC TTGTGAATCT GCTTTTTAAT CGATCTGTAA AATTTGTAAG TTCAGAAGGA 453300
GATCGGTCAC ATGTGAATAC TAGTTGTTTA TTGTCTTCAT AAAGGGCATT AAATGTGTGA 453360
AAAAGCTCTT CTTGTATACC TTCTTTTTTT TGTAAGTCGT GGATATCGTC TATAAGTAGC 453420
ATGTCTAAGT ATCTGTATTT TTTTTTAAAT TTTTTTGTTT CGTGTGTCTT TATGCTTTCT 453480
ACAAATTCAT TAAAAAATT TTCAGCAGTA ACATATAATA TTTTAAGGTT ATGATGTAAT 453540
TCTTCTGTTT TGTTTCCTAT GCTTTGAAGC AAATGTGTTT TTCCAAGTCC AACTCCACCA 453600
TAAATTAAAC ACGGATTATA TTTTTTCCCA GGATTTTTTG AGATTGACAA GCTGGCATTG 453660
TAAGCAAGTT TATTATTTGG CCCGATGATA AAATTTTCAA ATGTATATCT TTTTTTAAGA 453720
AAGGGGTTTT TAAATTTTGT GGGCTCTTCT TCTTCTTTTT TGATATACAT TTTTATACGA 453780
TCTTGAATAT TTTGGATTGC TTCTTTGGAA GTTGTTTTTT CTTTGAGCTT GTCGAACTTT 453840
GAAAAAGTTT CGTTAAGAGC CGGGTTTTTA GTTCTTGTTT TGTTAGAATG AGTTTTGGGT 453900
GGTTGATTTG TAAATACAAT GACTATGTTA TTGTAGCCAT TTTTATAAG GATTTCTTTA 453960
ATTTTTTTTG TAAATCTTTT TTCTATTTGA TTTTATGAA ATAAATTTGG AGTAGATATT 454020
TTAATATTGT CACCTATTGA TTCTAAAAAG CACAAATTTT CAAACCAAAC ATAAAAATCT 454080

TCTTCTGATA GTTCTTTTTT TATTTCTGTT AAAATCAAGC TCCATATATT TTTTGATTTT 454140
TCCATTTTTT TGTCTTGTT GGTTTTAGCA CTATACTTTT AACATTATAT AGTATAATGT 454200
TAAATTAGGA TTCTATCTAA ATTGTTTGTT AATTTTTTAAA AGTTTTTGGT ATTCCTATG 454260
TAATAGATAT TATTTTTTTTT TTAATGTAGA ATTTATCTGT GTCTAGATTT TAATTAAATG 454320
AATGGAAGGT TTATGAATTA TGTTGCTAGT AACATTCAGG TCTTAAAAGG ACTTGAGGCT 454380
GTTAGGAAAA GGCCTGGCAT GTATATAGGC TCAGTTTCTA TTAATGGATT GCACCATTG 454440
GTTTATGAGG TGTTGACAA TAGCATTGAT GAGGCTTTAG CTGGGTTTTG TGATAGAATA 454500
GATGTTATTA TCAATTTAGA TAATACTATA ACTGTAATTG ATAATGGGAG AGGTATTCCT 454560
ACCGATATTC ATGAAGAGGA GGGTATTAGT GCCCTTGAAC TTGTTTTAAC AAAATTACAT 454620
TCTGGTGGA AGTTTAATAA AGGCACGTAT AAAGTTTCTG GGGGACTTCA TGGCGTTGGA 454680
ATTTTCGGTTG TAAATGCTCT ATCTTCGTTT TTAGAGGTTT ATGTTAATAG AGATGGAAAA 454740
ATTTTTAGGC AAACCTTTTTC AAAAGGTATT CCGACTTCTA AAGTAGAAGT TGTGGGGGAA 454800
TCTTCTGTTA CGGGGACTAA GGTACTTTT TTGGCGGATT CTGAAATTTT TGAACTTTA 454860
GATTATAATT TCGATGTTCT TGAAAAAAGG CTTAAAGAGC TTGCTTTTTT AAACGATAAA 454920
ATATACATTT CAATTGAAGA TAAAAGAATT GGTAAAGAAA AATCTTCAAA ATTTTATTTT 454980
GAGGGTGGGA TAAATCTTT TGTAATTAT TTAACATAG ACAGCAAAGC TTTTCAATCA 455040
GAACCTTATT ATATTGATGG TTTTATTAAT GATGTTATTG TTAATGTGGG GCTTAAATGG 455100
ACTGAAAGCT ATTCTGACAA CATTCTTTCT TTTGTTAATA ACATTAATAC AAGAGAAGGG 455160
GGAACCTATG TTATGGGATT TAGAAGTGA CTTACTAAGG CCATGAATGA AGCTTTTAAA 455220
AATTCAAAAA TAAGTAAAA AGATATTCCA AATCTTACAG GAGATGATTT TAAAGAGGGG 455280
CTTACAGCTG TTATTTCTGT CAAAGTACCA GAACCTCAAT TTGAAGGTCA AACAAAAAGT 455340
AAGCTTGGA ATTCTGAGT AAGAAAAATA GTTGAAGTTG TTGTATATGA ACATTTATTG 455400
GAAATTATTA ATTTAAATCC TTTAGAGATA GACACTATTC TTGGAAAAGC AATAAAAGCT 455460
GCTCGTGCTC GTGAAGCTGC AAGAAAAGCA AGAGAATCAG AAAGAAAAAA AAATGCATTT 455520
GAAAGCTTGG CATTGCCTGG AAAATTGGCT GATTGTACTT CTAAAAATCC TTTGGAAAGA 455580
GAAATCTATA TTGTAGAAGG TGATTCTGCT GGAGGAAGTG CTAAATGGG TAGAAATAGA 455640
TTTTTTCAGG CCATTTTGCC ACTGTGGGGG AAAATGCTTA ATGTTGAGAA AACAGAGAA 455700
GATAAGGTTA TCACCAATGA TAAGCTTATT CCCATAATTG CATCTCTTGG TGCAGGAGTT 455760
GGTAAACTT TTGATATTAC AAAACTTCGT TATCACAAGA TCATTATTAT GGCAGATGCC 455820

GATGTTGATG GATCTCATAT TAGAACTTTG CTTTCTAGCTT TTTTCTTTAG ATATATGAGA 455880
GATTTAATTG AAAATGGATA TATATATATA GCCATGCCTC CTCTTTATAA AATAAAGTAT 455940
GACAATCGTA TTTATTATTT TTATGAAGAG AAAGAAAAAG AAAAATTTTT AGATTCTATT 456000
GAAACTAAAA ATCGCAATAG TATTTCTCTT CAGAGATATA AAGGGCTTGG GGAGATGAAT 456060
CCAACGCAGC TTTGGGAAAC AACTATGGAT CCTGCTAGAA GAAAAATGAG ATTGATGAAT 456120
ATAGATGATG CTATTGAAGC TGAAAAAATT TTTGTTACTC TTATGGGAGA TTTAGTTGAG 456180
CCCAGAAAAG AATTTATTGA ACAGAATGCA CTTAATGTAA TTAATCTTGA TGTGTAATTG 456240
GAGCGTTAAT GGCAGTTGGA GAAAATAAAG AACAAATATT AAATGTTAGG ATAGAAGATG 456300
AAATAAAAAC TTCTTATTTA AATTATGCAA TGTCAGTTAT TGTTTCTAGA GCTCTTCCAG 456360
ACGTAAGAGA TGGTCTTAAA CCAGTTCACA GGAGAATACT TTATTCTATG TATGAGATGG 456420
GACTTCGTTT TGATAAGGCT TTTAAAAAAG CTGGTAGAAT AGTGGGAGAT GTTCTTGGA 456480
AATATCATCC TCATGGAGAT CAATCAATTT ATGATGCTCT TGTAAGACTT GCTCAGGATT 456540
TTTCGCTTAG ATATCCCGTA ATACGGGGAC AGGGAAATTT TGGATCTATT GACGGAGATC 456600
CCCCCGCTGC TATGAGATAT ACTGAAGCTA AAATGGAAAA AATAACTGAA TATATTGTTA 456660
AGGATATAGA CAAAGAGACT GTTAATTTTA AGTCTAATTA TGACGATTCT TTAAGTGAGC 456720
CTGAGATTAT GCCGTCATCA TTTCCATTTT TTTTGGTAAA TGGCTCTAGT GGAATTGCTG 456780
TTGGAATGGC TACTAATATG GCACCTCATA ATTTAAGAGA AATTGTGAT GCCATTGTTT 456840
ACATGCTAGA TAATGAGAAT GCTTCTATAT TTGATTTGCT TAAAATAGTT AAAGGGCCTG 456900
ATTTCCCAAC TTTTGGAGAG ATTGTTTATA ATGATAATTT AATTAAAGCA TACAAAACG 456960
GCAAGGGAAG TGTTGTTATT AGGGCAAGAT ATCATATTGA AGAAAGAGCA GAAGATAGAA 457020
ATGCTATAAT TGTTACAGAA ATACCTTATA CGGTAAATAA ATCTGCACTT CTTATGAAAG 457080
TTGCGCTTTT AGCAAAAGAA GAAAAGCTAG AAGGACTTTT AGATATAAGA GATGAATCTG 457140
ATCGAGAAGG TATTAGGATA GTTCTTGAAG TTAAAAGAGG ATTTGATCCT CATGTTATTA 457200
TGAATTTGCT TTATGAATAT ACTGAATTTA AAAAGCATTT TAGTATAAAT AATTTAGCCC 457260
TTGTTAATGG TATTTCCAAA CAGTTAAATT TAGAAGAATT GTTATTTGAA TTTATTGAGC 457320
ATAGAAAAAA TATTATCGAA AGACGTATTG AATTGACTT GAGAAAGGCA AAAGAGAAAG 457380
CACATGTTCT TGAGGGATTA AATATTGCTT TAAATAATAT AGATGAGGTT ATTAAGATTA 457440
TTAAATCATC TAAATTAGCA AAAGATGCAA GGGAGAGGCT TGTTTCGAAT TTTGGTCTTT 457500
CAGAGATTCA GGCCAATTCA GTTCTTGATA TGAGGTTACA AAAACTTACA GCCCTTGAGA 457560
TTTTTAAGCT TGAAGAGGAG CTTAATATAC TGTTAAGCTT AATAAAAGAT TATGAAGATA 457620

TTCTCTTGAA TCCAGTAAGG ATTATTAATA TTATAAGAGA AGAAACTATT AATTTAGGTT 457680
TGAAATTTGG CGATGAACGT CGAACTAAAA TAATTTATGA TGAGGAGGTT TTAAAAACTA 457740
GTATGTCGGA TTTAATGCAA AAAGAAAATA TTGTTGTTAT GCTTACAAAG AAAGGTTTCC 457800
TTAAAAGACT TTCACAAAAT GAGTATAAAT TGCAAGGTAC GGGAGGAAAA GGACTAAGTT 457860
CGTTTGATCT AAATGATGGA GATGAGATTG TTATTGCTTT GTGTGTCAAT ACTCATGATT 457920
ATTTATTTAT GATTTCAAAT GAAGGAAAGC TTTATTTAAT CAATGCTTAT GAAATAAAG 457980
ATTCTTCAAG AGCTTCAAAA GGTCAGAATA TTAGTGAGCT TATTAATTTA GGAGATCAAG 458040
AAGAAATATT AACTATTAAG AATAGTAAAG ATTTAACTGA TGATGCTTAT TTATTGCTTA 458100
CAACTGCAAG TGGAAAGATA GCTAGATTCTG AATCTACAGA TTTTAAAGCA GTAAAGTCAC 458160
GAGGTGTTAT TGTATTAAA CTGAATGATA AAGATTTTGT TACAAGTGCA GAGATTGTTT 458220
TTAAGGATGA AAAAGTAATT TGTCTTTCTA AAAAGGGTAG TGCATTTATA TTTAATTCAA 458280
GGGATGTTAG GCTTACTAAT AGAGGTACCC AAGGTGTTTG TGAATGAAA TTAAAAGAAG 458340
GTGATTTGTT TGTAAAGTT TTATCGGTTA AAGAAAATCC TTATCTTTTG ATTGTTTCTG 458400
AAAAATGGGTA TGGAAAAAGG TTAAACATGT CTAAATATC TGAGCTTAAA AGAGGAGCCA 458460
CTGGTTATAC TAGTTATAAA AAATCTGATA AAAAAGCGGG TAGTGTTGTT GATGCTATAG 458520
CAGTTTCAGA GGATGATGAA ATCTTGCTTG TAAGTAAACG TTCAAAGCT TTAAGAACAG 458580
TAGCTGGAAA AGTATCTGAA CAAGGCAAAG ATGCTAGAGG AATTCAAGTA TTATTTCTTG 458640
ATAATGACAG CTTGGTTTCT GTTTCAAAAT TTATTAAATA AAGAATTGGT TTTTCTTGTT 458700
TAAGAATGTT CCACGTGGAA CATTCCTTTT TTTTATTCTT AAATTGTAAT TCAATATTAT 458760
AACCTGGTAA AATTTTGTGT TGTAGGAGGT TTTGACAATA TGGATGGAGT TTTTAAAATG 458820
ATAGATATTC ATCTTTTAGA TATTGATAAT GATCAGCCAA GGAAATCTGT TAGTCTTGTT 458880
GAATTAGAAG AGCTAAGCAT TTCTATAAAA GAAAATGGAA TTTTGCAACC TTTAATTGTT 458940
TGTAAGCAA ATGATAGATA TAAAATAATA GTAGGAGAAA GAAGGTTTAG GGCTGCTAAA 459000
CTTATTCAGT TGACAAATAT TCCTGTCATA GAGGTTGACA TAAAAGAATC CTGTAAAGAT 459060
TTTATGCCCT TGGTTGAAAA TATTCAAAGA GAAAATTTTA CTCCTGTTGA AGAGGCTTAT 459120
GCCTATAAAA ATATAATGAA TAAATATTCG TTAAC TCAA AGGATTTATC TGAAAAAATT 459180
GGTAAAAGCA GGACCTATAT TTCAAATTTA GTTAGAATTT TAGATCTTGA GCAAGAAATA 459240
TTAAATGCAA TACATAGAAA AGAAATTTCT TTTGGGCATG CTAAAGTTAT TTTATCCTTA 459300
AAAGACAGGC AAGACAGGTA TAATCTTTAT TTAATTATAC TTAAAAAAA ATTTTCTGTA 459360

AGGGATGCAG AAAAATATGT TAAAAATTTT TCCAAATCCA TAGTAAAAAA AAGAGAGCTA 459420
GAACAAGATC CTTTTTTAAA TAATATAAAA GAATTTCTAT TTGATAAAAT CCAAACAAAA 459480
ATAGATATCA AAGGGAATCA AAATAAAGGC AAAATAGAGA TAGAGTATTT TACTGCTGGC 459540
GATTTAAAAA GGATTGTTTC CCTTTTTGGT CATAGTAGCT AAATTATTTT TATAATTTAA 459600
AGATTGTAAA ATATTTTATG AGAATTTTAA TTTTTTAGGC ATTTGTCACA ATGCATAAAT 459660
TTTTTAAGCT TATTTTAAAA TTGTTTAGTT TTTATAAAGA AATATTGGGC TTAAAAGAA 459720
GGGCAAAGTT TATATTTTGT TATTTGTAGT TAAATTTAAA AGTAAAAAAA TAATATTTAA 459780
AAAATGAACA ATAAGAATAT ATTTTATATA TTCTTATTAG TGCAGCTGTA AATTTAAATA 459840
GAATTATTTT TAATATATTT TATTTTTTTC TTTATTTCCA AAATAGAATT AAAAAATAAT 459900
TTTAAGTTTT CTGTCTTAA TTTGTTAAAT TCGATATTTT TAAATCTTT TATATTTTTT 459960
AATATAAAAT CTAATACTTC TTTTATGTCA TTTTCATATT TTTCGTTTTT CTTAAGTAAT 460020
GGTTTGCGCG TATCCTTTAA ATCAAACTT TTTTATAAAA CAATTTTAAA TTCTTTTAAA 460080
GAATTTATTT TTCCATTTAG AACTTCGGTT TTTAAAATAG GGGGACAAGA TTTTTTAGAT 460140
ATTTTCATATG ATAATGATAA AGGTAATTTT TCTATAGTGA GCTGCTTGTC GGAATTTTCG 460200
ACAAGCAGAT TGTATCTTGA TATTAAGGCG TAAACCTTGT CTTTTTTAAA TCCCATACTT 460260
TTGAACCACT GATAAAAAAG CCCGTTATAT TGATTGTTTC CTTTTAATTT GTCTTGAGCG 460320
TCTTTAAGTA TCTTTCCAAT TTTTGTATAA GTGTTGTTGA AAATATTGAA AATTTTCATAT 460380
TGCTTTTTTT TTAaaaaATC AGAAATATCT TTATCTAGCT TATTGTAGTC AAAGTTTTTT 460440
CTTTCAATCG AAATAATTC TTTTTTTTCA GTATTTTCTG AATTATTTGA AGATGTTTCT 460500
AATTTTTTAC CCATTAGAAA CATTAAGTT TCTAAATGT CAGACATAGC TATTCCTTAA 460560
TTTTGTTTAT TATCTCTTT GAGAGCTCTA AAAATCTTT TGCAGCATTG CTTTCCTTGT 460620
CATATTCATA TACAGGCATT TTTGCTTCTT GAGATTTTGA GATAGTTATA TTTTCCCTTA 460680
TTTTTGATTT TAAAAGCTTT TCTTTAAAAA CTTTTTTTAG CGAGCTTACA TATTTTCTT 460740
TACTTTTGTT CCTTATGTCG TATTTATTTA TAAAAACACC CGCAATCTCT AAATTTTTAT 460800
TTATTTGCTT TACAGTAGTT ATTGTATCTA TTAGTTGATT TATGCCTTCA AATGCAAAAA 460860
ATTCCGTTTC AATTGGTATT AACAAGTAAT TGCTTGCAAT AAGTGCATTT ATAGTTAATA 460920
TTGAAAGTGT AGGGGGGCAG TCGATAATAA TAAAATCATA TTTGTCTTTT TCATACAGTG 460980
TTAATGCATT TTTTAAAAAA TTTTCTCTTG AAAGTTCATT TATTAATTCT TTTTCAAGCA 461040
AAGCTAATTT AATGCTAGAA GGAATTATGT CTAATCCAAA ATGATTTAAA GGTTTGACCT 461100
TTATTTTTTT GTTAATAAGT TCATAGCTTG ATTTTTCGGC TATATGCTTT GAGGTATTTG 461160

TGCCGCTAGT AGAGTTTCCT TGCGAATCAA TATCTATTAG AAGAATTTTT TTATTAAGCA 461220
GGGTCATTGA ATAAGAAATA TTAATGGCGG TTGTGGTTTT TCCTACGCCT CCTTTTTGAT 461280
TGATTACAGA TATTATTTTC ATATAAATTT CTCTTTTTAT TTGGTTTTGT TTTTATATTT 461340
TAAACATAA ATGATAAAAA TAATAATATT TTAAATTAGT TTTTAAATAT TTGATTATTT 461400
GACATGCATA TTATTCTTTA TTAACTTTA AGATTTCTTG AATTAAGCCA TTTTCTATAA 461460
AAAATTCCGA TATTTTTTGT TTATTTTTTG TTTTGAATTT AATTGAAGTG TTTATTTTGT 461520
TTGAAAAGTT TGAATCTATT ATTTCTATTT CAAGTTTATT TTTCATTTTT AATAATGAAT 461580
TGTATTGGTT GTAAGTTAAA TTTAAGCTTA AAATTTCTAA TTCCTCTTTT TCCATTATAG 461640
ATGTATTATT AATAACTTCT TTGGCAGACT TGTAATACGC TTTGATTAAT CCCCCTCTAC 461700
CAAGTAAAGT GCCTCCAAA TATCGCAATG TGATTATTAA AGTATCGGTT AAATTGTTAT 461760
GTATTATGGC ATCCAATGTG GGCTTTCCAG CTGTAAATT AGGTTCTCGA TCATCACTCA 461820
TTCCATTTAG AAATGAGTTT TTGTTCCGA TTCTAAATCC ATAAACCACA TGCGTAGCAT 461880
TTTTAAATTT TATTTTGTAT TTTTAAATAG TTTTATTTAT ATCGTCTTTT TTTTCAATAT 461940
TAAAAATATA TGAAACAAAG ATGGATTTCT TTATTTCAAT TTTAGAATTA CTATTGTTTT 462000
TTGGCACAAA CATCATATAA CGTAAGTATA CTATCTTTTT AGATATTGCA GTATTTATTG 462060
TTTATGTATA TTATTAATAG TGTTTGTTTT TATTATTGAT TTTTATAAAT ATCCAGAAAA 462120
GAGGTAAAA TGATATCAGG CTTGAATCCA ACATTAAGGT TGTTTAAAGA TCATAAAATA 462180
CTTTATTCTA ATATGGAAAG AGGATTGAAG CCTCTTTTAG AAGTAGATAA TTTTATCAAT 462240
AAGTATATCC AGAATAAAGA AGGACTTGAA ATTTATGATA AAGTTGTGGG CAAGGCAGCA 462300
GCCGTTATTA TTTATAATAT AGGGCTTCAA AATGTTCAAG CTGGGGTGT TTCTCAACCC 462360
GCAAAGGATT TTTTAGAAAG CAGAGGAATT AAAGTGGCTT ATAAAAAATT GGTAGAAAAA 462420
ATAAATGACA GGGCAGAAAG CTTGATTGAA AGCTTAGAAA ATCCGAAGA GGTTTATAAG 462480
TATATGATTA AAAGAGGTAT TATAGTTAAT AATTTATAAA TTATGAAAAT AGTTGAGCCA 462540
TATGTTAGCT AACTATGTGA TTTTGAGTAT ACAGTGATAA TTAGGGCTAT GTTGTATATT 462600
AATATTATTA AATTTCCCCA ATTTAGGTAA AAATTGCTTT TGTCATAGTT AAAGATCCAA 462660
ATTCCAACAT AAACACCTAA AAATCCTCCT ATAGAAGATG TAAACATGAT TAAATTGGGT 462720
TCAATTGTAT GTTGATTAAT TTTGCTTTGA TTTTCTTTAA CATTAGGCTG TTCGGTAAAT 462780
TTGCTGTCAA TAAAAATCAT GGCAAAACCT GCAAGAGTAA TGCATAAAAA ATAGATCATA 462840
AATATTTTTC TAATTAATGC AAACATAAAT TTTCCCTTTC TTTTAACTTT TTAATCATT 462900

ATACTTAATG ATATAACTAA ATGTAATACA AAAGCAAGTA TTTTGATAGA CATATAAAAT 462960
ATGGCTTATG TCTTATTCTT GTATTGTA AGTAAAGGT TTTGGATTTT TATCATTAAG 463020
AAAAATGTTT TTAATATATT TTATTTATTT TTAGTTTGG AGGAATTAAA AGGGCCTGTG 463080
TTATATATTG TTGGTACGCC AATAGGCAAT TTAGAAGATA TTACTTATAG AGCAATTGAT 463140
GTTTTAAAT CGGTAAATGT TATCTTTGCG GAAGATACGA GAGTAACTAG CAACTTTTG 463200
TCTCGATATA AAATTAATAA AAAAATGATT TCTTGTAATG CCGTAACAGA AAACAAGAAG 463260
ATAAGCTTGC TATTGGATTA TTTGGCAAAA GGAAATTCTG TTGCTTTTGT TAGCGATGCT 463320
GGTACTCCGG GGCTTAGTGA TCCGGGTAGC TTATTAGTTG CTGCTGCTTT TAGAGAGGGA 463380
TACAAAGTTT GTCCAATTCC TGGAGTAAGT TCTTTTAATA CAATTGTAAG TGTTAATCCT 463440
TTTAGAGATA AATCAGTGTT TTTTGAGGGA TTTTGCCTA ACAAAGGCCT TAAAAGATTT 463500
AAAAGAATTG CTGAGCTATA TAAAAGGGGA GATGCTTTTG TTCTGCTTGA ATCTGGTCAT 463560
AGAATTTTGA AATTGCTTGT TGAAATTTCT TCTGTAGTT TAGATGCGAA GGTCTTATT 463620
GGTCGCGAGA TGACAAAAAT TTATGAAGAA TATCAAATTG GCAAACCTTT AGAATTAAAA 463680
AAATATTTTG AATCGAGTAA GGATAAGGTT AAAGGAGAGT TTACTATTCT AGTCAGCAGA 463740
AGTCGTTTAT AATAAATGTT TTCTACTTGG ATTTTAAAT TTATTTATTC TTGATTTTGC 463800
TCGATTGATT TATTGTGTTA TACTTGAATT TTGATAGGGG TTTTATGAA GATTTATTTA 463860
GCCTCTCCAT TTTTAAAGGA AGAGGAAATT AACTAAGGG ATGAGGTTTT GAAATTTCTT 463920
GAAGAGTTTA ATTTAGAAGT ATTTTCTCCA GAGCATCATG CTGTCAAAAA GATGGGATTG 463980
CTTGAAAAGG TTGATTATAA GTTTGCAAAT AGAGATATAA GGGAGAAGAT AAGAGAAGTA 464040
GATTTAAAAG AGCTAGTTAG TAGCGATATT GTTTAGCCT TGGTTAATTA TGTGATTCT 464100
GGCACGGCTT ATGAGAGAGG ATTCGCCTTT GCCAAGAAAA TACCAAGTAT AGATTTTTTTT 464160
AAAGATAAAC AAGATTCTGA TTTTATAAT TTAATGTATA GCGACTGTGC TGCTGCTTTT 464220
TCCAATTACA AGGATCTTAG GGAAGGAATT TTAACCTTTA AAGAACTGTG GATTAAGTTT 464280
AAAGGAGATA ATGAAAATTT CAGAACCTTT TTTGATTATT TAAAAGCTAA ATTGGGAAAT 464340
AAATTAAAAA AAATTTTAC AACTTTGCCT GCTAATGAAA AGTGTGGCTG TTAATGCTTT 464400
TATCACTGTT TATTAATAAA ATTTATTTT TTACATTTTA TATTAATAAA AATAATGCAA 464460
AGGTATTGAC AATATGATTC TTATTTTGTT AAAGTATTAA AGGTTGAAAT GATTATTGGA 464520
AGATGAGAGA AGGGAAGAGT TAAGTAAGGT TAAAAGCCAA AAGAATAAAC AAAACCTGTT 464580
AATTTTTTTA AATAAAAAA TAAAATAACG AAGAGTTTGA TCCTGGCTTA GAACTAACGC 464640
TGGCAGTGCG TCTTAAGCAT GCAAGTCAAA CGGGATGTAG CAATACATTC AGTGGCGAAC 464700

GGGTGAGTAA CGCGTGGATG ATCTACCTAT GAGATGGGGA TAACTATTAG AAATAGTAGC 464760
TAATACCGAA TAAGGTCAGT TAATTTGTTA ATTGATGAAA GGAAGCCTTT AAAGCTTCGC 464820
TTGTAGATGA GTCTGCGTCT TATTAGCTAG TTGGTAGGGT AAATGCCTAC CAAGGCAATG 464880
ATAAGTAACC GGCCTGAGAG GGTGAACGGT CACACTGGAA CTGAGATACG GTCCAGACTC 464940
CTACGGGAGG CAGCAGCTAA GAATCTTCCG CAATGGGCGA AAGCCTGACG GAGCGACACT 465000
GCGTGAATGA AGAAGGTCGA AAGATTGTAA AATTCTTTTA TAAATGAGGA ATAAGCTTTG 465060
TAGGAAATGA CAAAGTGATG ACGTTAATTT ATGAATAAGC CCCGGCTAAT TACGTGCCAG 465120
CAGCCGCGGT AATACGTAAG GGGCGAGCGT TGTTCGGGAT TATTGGGCGT AAAGGGTGAG 465180
TAGGCGGATA TATAAGTCTA TGCATAAAAT ACCACAGCTC AACTGTGGAC CTATGTTGGA 465240
AACTATATGT CTAGAGTCTG ATAGAGGAAG TTAGAATTTT TGGTGTAAGG GTGGAATCTG 465300
TTGATATCAG AAAGAATACC GGAGGCGAAG GCGAACTTCT GGGTCAAGAC TGACGCTGAG 465360
TCACGAAAGC GTAGGGAGCA AACAGGATTA GATACCCTGG TAGTCTACGC TGTAACGAT 465420
GCACACTTGG TGTTAACATA AAGTTAGTAC CGAAGCTAAC GTGTTAAGTG TGCCGCCTGG 465480
GGAGTATGCT CGCAAGAGTG AAACCTCAAAG GAATTGACGG GGGCCCGCAC AAGCGGTGGA 465540
GCATGTGGTT TAATTCGATG ATACGCGAGG AACCTTACCA GGGCTTGACA TATATAGGAT 465600
ATAGTTAGAG ATAATTATTC CCCGTTTGGG GTCTATATAC AGGTGCTGCA TGGTTGTCGT 465660
CAGCTCGTGC TGTGAGGTGT TGGGTTAAGT CCCGCAACGA GCGCAACCCT TGTTATCTGT 465720
TACCAGCATG TAATGGTGAG GACTCAGATA AGACTGCCGG TGATAAGTCG GAGGAAGGTG 465780
AGGATGACGT CAAATCATCA TGGCCCTTAT GTCCTGGGCT ACACACGTGC TACAATGGCC 465840
TGTACAAAGC GAAGCGAAAC AGTGATGTGA AGCAAAACGC ATAAAGCAGG TCTCAGTCCG 465900
GATTGAAGTC TGAAACTCGA CTTTCATGAAG TTGGAATCGC TAGTAATCGT ATATCAGAAT 465960
GATACGGTGA ATACGTTCTC GGGCCTTGTA CACACCGCCC GTCACACCAC CCGAGTTGAG 466020
GATACCCGAA GCTATTATTC TAACCCGTAA GGGAGGAAGG TATTTAAGGT ATGTTTAGTG 466080
AGGGGGGTGA AGTCGTAACA AGGTAGCCGT ACTGGAAAGT GCGGCTGGAT CACCTCCTTT 466140
CTAAGAGAAA GATAAACTAA GGCTAATTCC ATTAACCTCT CCCTACwCTT TTCTTTTGAT 466200
AAGAGAGTTT TTAAAACCAG TGTTATTTAT GTAAGTTTAA GAGAAGTTTA TGTATTAAAT 466260
TATTGATATT AAATAGTTTT ATTAGGCTTA GACTTAATTT TAGGTCATTT TGGGGGTTTA 466320
GCTCAGTTGG CTAGAGCATC GGCTTTGCAA GCCGAGGGTC AAGGGTTCGA GTCCCTTAAC 466380
CTCCATTGGG CTTATGyCCT AAATTGTAAT TAAGTATGTT TTTAAGTAAC TTTGTTAAAG 466440

TAATTGTTGG AATGTGAAAC ACAAGAAGTT AAAATTTCTG GGTAAAGTTG AGATCTGTTG 466500
ATATTAAGAA AAATGTCTAG AAGCAAAAGC AAGCTTTCGA TAAACCCGA AGTTGTTTCG 466560
CTAAAGTGCA AGGATTAAAC AGGATTGTAT TTTTCAGCAG CCTATTTTAT AAACGATCTG 466620
CATTTAGTAA ATAGTTTTTA GTTAGGAAAT AATGTAGATT ACTAAGTGTG ATGTCTGAGA 466680
GAAGGACAAG TATTGTAGCG AGCTTAAATC CTTATTATCG TTGCCAGTAT TTAGTGGTAG 466740
GGATTCGGAT AAGATTGCCA GTTATAAGTT GGAGGAAGGC AAAGATTGCA TTAAATCGTT 466800
ATCGCTCTTA TGTTTTAGGT TACAAGTTTG CAACAATAAC TCAAAAAGC CAAGCAAAAT 466860
ACCATAAAGC AGATTTTCAGT TTGGATTTGC CCGACACTCA ATGGCATGAA GTTGTAATTG 466920
TTAGTAATCG TGTATACCTT AATATAGAAA TTGAATAAAT TTTTGTTTTT CTTATTAATT 466980
ATAGCTTAAA ACAGTATTGT CGTAATTAAA ACAATGGAAT ACATTGGGAC CAGGATGAGT 467040
TGAACATCCG ACCTCAGGTT TATCAGACCT GCGCTCTAAC CACCTGAGCT ATGATCCCTT 467100
AAGCATATCA ATTCTTTACA AATTTTATTT AAATCTTATG ATTTTGTCOA TATCTCTTAT 467160
ATCTTTTCAA GATGTAAGAG ATATTGCATA TAGTTTATAA TTTTATATAT ATTTGTCAAT 467220
ATTCGATATT TTGTATTTTA GATTAGCATT TTCATATAAG CTGATTTAAG TTGAACTAGt 467280
TCAACTTTTT AAATTTTTTT GATTAAAAAT CAAAAAATT TATTAATCAA CCAAGAATTT 467340
ATTTAAATA TGTATTTACT GGGTGATTAA ATGATTTTAG TTTTATTTT TATTCTAGGC 467400
AATATGTTTT CATATTTTAC ATGTGTGTTT TGGTAATAAT TTTTATTATT ATTTTGTTTT 467460
AAAATTGAGC TTATGGATCG ATATTTTTTT TTgCAAGATG CtACTACCGT TGCAAAGTTA 467520
TTGCTTGGTA ATTTGTTGAT CAGAAAGATC GACAAAGAGG AAATAGTTAC CAGAATTGTT 467580
GAAACGGAAG CTTATATGGG GATAACAGAT AGCGCTTGTC ATTCTTATGG CGGCAAGATA 467640
ACAAATCGCA CAAGTGCTAT GTATAGAATA GGAGGATATT CTTATGTGTA TATAATATAT 467700
GGTATGCATT ATATGTTTAA CGTTGTGACT GCAGATAAAA ATAATCCTCA AGCTGTTTTA 467760
ATCAGAAGTG TAGAGCCTAT TTCTCCACTA TTGGGAGAGA AGAGCATTCT TACTAATGGT 467820
CCTGGAAAaC TTACAAAATT TTTAAACATT GATTTAACTT TTAATAAAGT TGATCTTATT 467880
GGGAATAATG AGCTTTTTTT ACAAGAGGT TTGAATCTAG ATTTTAATAT AGTTTGTTCA 467940
AAAAGAATCA ATATTAATTA TGCACAAGAG AGTGATATAA ACAAGCTTG GAGGTTTTAT 468000
ATCAAAGATA ATAAATktGT TTCAAGGCGT TGATTTTCAT TTAATTATAT TTTTTTAAAT 468060
TTTTTTAAAA AAATATAATA TTATTAAATT TTATTATTa TGCTTTAAGA ATAATTTATT 468120
AAGAATAAAT TATTTGTGAT AGTATATCTT AAAGAGAGAT TATATATGAT CTAATTATAA 468180
AGATATAATG CTGGCTTTTG ACCTTGATGG CACTTTATTG AATAATAACC ATGAGATTGC 468240

CTTTTAACT CTTGAGGTTT TTTTGGCTTT GAAGrAAGAT TTAAAATAA TTATTGCAAC 468300
CGGTAGAAGA TTGAGTGAAG TAAAAAATAT AAGGAGCCAA TAAAAGAAA TTrGTATTAA 468360
TGAAAATTAT CTTGTAACGG CGAATGGGGC TGAAGTGTTT TTssAAGAAA ATTTAATTTT 468420
aGATACGCAA TGAATTATGA CyTAGCAAAA GAAATTCTCA AGATAmATAC AGATAATGTT 468480
GATGTTAATC TTTATACTTT TGACACTTGG TATTCTAATG CAGATGTTAA AAGTCCTATT 468540
ATGAAACATT TTATTAAAGA TTTGGGCTTA AATGTTATTA TTGGAGATTT GACCAACTA 468600
AACGTTgATT CTGTTTctAA GATTGTTTAT TATTGTGACG ATTTGGCAAT TCTTAATAAA 468660
CTTGACACTG AGATTAAAAG TAAAGATTTT CAGGACACAA GAGTGTTTTT TTCTTCTAAA 468720
GATTTATTAG AGGTtACCAA TATTAATGCT AATAAATATA ATGCTATTAA AAATATTGCT 468780
TTTCTTGAAA GCATTCCATT GTGTGATGTT TTAGCTTTTG GAGATAATAA TAATGATTAT 468840
GAAATGCTCA AAAATCTTGG TAAAGGGGTT TTAATGAAAA ATGCCAATGA ATTTCTTAAA 468900
ATTAATTTAG CAAAGAATGA AATAACAAGA TTTAGTAATA ATGAGGATGG CGTTGCTAGG 468960
TTTTTAAttg atTTTTTTAA GCTTAATATT AAATATTAAT AATTTGTATT TAAATGtTTA 469020
ATCCATTTGA TTTATTTTAA GCAGGATTTT CTATTtAAAA TATAAATTTT TTACTTATAr 469080
TGTATTTTTG AAAATTTATT TATTAAAATA TTGGAATAAG TATTGACATG GATTAAACAA 469140
AGATATATAT TATTTTATGT TGCATAACA AATTGGCAAA ATAGArATGG AAGATAAAAA 469200
TATGGTCAAA GTAATAAGAG TCTATGGTGA ATGCCTAGGA GCTTTAAGGC GAAGAAGGTC 469260
GTGGTAAGCT GCGAAAAGCT TGGGGGAGAA GCAAACATTT ATTGATCCCA AGATTACCGA 469320
ATGGAGTAAT CCAGCTAGCA AGATGCTAGC TATCTATTAT TTAAATAATA GAGGCGATAC 469380
CAGGGGaAGT GAACCATCTA AGTACCCTGA GGAAAAGAAA TCAArGAGAT TCCCTTAGTA 469440
GTGGCGAGCG AAAAGGGAGT AGCCCAAACT TTAAATGTGT CAAGCTGCAG AGCGTTGCAT 469500
TTATGGGGTT GTAGGACGTT TAGGCTTAGT CTGTAATAAG CAAAAAAGTT ACAAATATT 469560
TATATAGAAG AATAATCTGG AAAGTTTAA CAAAGAAGGT GATAGTCCTG TAATTTAAAT 469620
GTAAATATCT TTTTAAAATG TTCCTGAGTA GGACGAGGCA CGAGAAACCT TGTTTGAAGC 469680
TGGGGAGACC ACTCTCCAAG GCTAAATACT AGAAAGCTAC CGATAGAGAA GAGTACCGTG 469740
AGGGAAAGGT GAAAAGAACC CCGGGAGGGG AGTGAAATAG AACTGAAACC GTAGACTTAC 469800
AAGCAGTCAA AGCCGTAATT TATTGCGGTG ATGGCGTGCC TTTTGCATAA TGAACCTGCG 469860
AGTTATCATG TCTAGCAAGA TTAAAGCATA GAAGTGCTGG AGTCGAAGCG AAAGCGAGTC 469920
TTAAAAGGGC GATTTAGTTA GATGTGGTAG ACCCGAAGCC GAGTGATCTA TTTATGGCCA 469980

GGCTGAAGCT TGGGTAAAAC CAAGTGGAGG GCCGAACTCT AGTCTGTTTA AAAAGGCAGG 470040
GATGAGCTGT GAATAGGAGT GAAAGGCTAA ACAAACCTCGG AGATAGCTGG TTCTCCCCGA 470100
AATGGATTTA AGTTCAGCCT TATTTTAGTT TAATAGAGGT AGAGCACTAA TTGAGCTAGG 470160
GCCTGTCAAA GGGTACCAA CTCAGTTAAA CTCCGAATGC TATTAAATGA TGAATAGGAG 470220
TGAGACTATG GCGGATAAGG TTCATAGTCG AGAGGGAAAC AACCCAGACC AACAGCTAAG 470280
GTCTCAAAAA TGTGTTAAGT GGAAAAGGAG GTTTAGGTAC GTAAACAGCC AGGAGGTTGG 470340
CTTAGAAGCA GCCATACCTT TAAAGAGTGC GTAATAGCTC ACTGGTCGAG TACTTAAGCG 470400
CCGATAATGT AACGGGGCTA AACACATTAC CGAAGCTTTG GATCTTAACG AAAGTTAAGA 470460
TGGTAGGGGA GCGTTCTGTA AGCCAGAGAA GTTAAACTGG AAAGTTTGAT GGAGGTATCA 470520
GAAGTGAGAA TGCAGGTATG AGTAACGAAA AAATGGGTGA GATTCCCATT CGCCGAAAAC 470580
CTAAGGTTTC CTGGGTAAAG GTCGTCTTCC CAGGTTAGTC GGTCCCTAAG GCAAAGCTGA 470640
AAAGTGTAGT CGATGGGAAA CGGGTTAATA TTCCCGTACC TCTTATAGTT TCGATGGAGT 470700
GACGCATGAG GTTAACTACT GCTAGGCGAT GGTGTCTTA GTTTAAGCAT TAAGGTGATG 470760
ATCTTGATAG GAAAATCCGT TAAGAGAGCT AAGATGTGAT GATGAGTGCT ATTTAGGTAG 470820
CATGAAATGT AGGTAGTCAA GGTGCCAAGA AATAGCTTCT AAGGTTAGGC TATAAGGGAC 470880
CGTACCGCAA ACCGACACAG GTAGGTGGGA TGAAAATTCT AAGGCGCGCG AGAGAATCCA 470940
CGTTAAGGAA CTCTGCAAAA TACGTACGTA ACTTCGGGAT AAGTACGACC TAAGCAATTA 471000
GGTAGCATAA AAATGGTCCA AACGACTGTT TACCAAAAAC ACAGGTCTCT GCAAATCTGT 471060
AAAGAGAAGT ATAGGGACTG ACACCTGCCC GGTGCTGGAA GGTTAAGAGG AGATGTTAGT 471120
TTATGCGAAC GTTGAATTTA GCCCAGTAAA CGGCGGCCGT AACTATAACG GTCCTAAGGT 471180
AGCGAAATTC CTTGTCGGGT AAGTTCCGAC CCGCACGAAT GGTGTAACGA TTTGGACGCT 471240
GTCTCAACGT GGAGCTCGGT GAAATTGAAG TATCGGTGAA GATGCCGATT ACTTGTGGTT 471300
AGACGGAAAG ATCCGTGAAC CTTTTACTAT AGCTTGGTAT TGAGATTTGA TTAAATATGT 471360
GTAGGATAGG TGGGAGACTT TGAAGCTATC TCGTCAGGGG TAGTGGAGTC AATCTTGAAA 471420
TACCACCCTT GTTTAATTAG GTTTCTAACT TATAGAAATA TGAGGAGAGT GCCAGGTGGG 471480
TAGTTTGA CTGGGCGGTCG CCTCCTAAAG AGTAACGGAG GTGCGCAAAG GTTACCTTAG 471540
AGTGGTTGGA AATCACTCTG TAAGTGTAAG GGCATAAGGT AGCTTAACTG TAAGACTGAC 471600
AAGTCGAACA GATACGAAAG TAGGTCTTAG TGATCTGGCG GTGGCAAGTG GAAGCGCCGT 471660
CACTTAACGA ATAAAAGGTA CTCCGGGGAT AACAGGCTTA TCCTTCCCAA GAGTTCACAT 471720
CGACGGAAGG GTTTGGCACC TCGATGTCGG CTCATCGCAT CCTAGGGCTG GAGCAGGTCC 471780

TAAGGGTATG GCTGTTCGCC ATTTAAAGCG GTACGCGAGC TGGGTTTCAGA ACGTCGTGAG 471840
ACAGTTTGGT CCCTATCTGC CACAAGCGTT GGATATTTGA GAGGAGCTAT CTTTAGTACG 471900
AGAGGACCGA GATGGACGAA CCTCTAGTGT ACCAGTTATC CTGCCAAGGG TAAGTGCTGG 471960
GTAGCTACGT TCGGAAAGGA TAACCGCTGA AAGCATCTAA GTGGGAAGCC TTCCTCAAGA 472020
TGAGATATCC TTTAAGGGTC CTGGAAGAAT ACCAGGTTGA TAGGTTAGAA GTGTAAGTAT 472080
AGCAATATAT TAAGCTGACT AATACTAATT ACCCGTATCT TTGGCCATAT TTTTGTCTTC 472140
CTTGTAAGAA CCCTGGTGGT TAAAGAAAAG AGGAAACACC TGTATCATT CCGAACACAG 472200
AAGTTAAGCT CTTATTCGCT GATGGTACTG CGAGTTCGCG GGAGAGTAGG TTATTGCCAG 472260
GGTTTTTATT TTTATACTTT AAACCTTGAT TTTATTTTAA TGTTTTTTAA ATATTGGTGT 472320
TTTTGAATGG GTTGTTTAAA TAACATAAAA AATAAAATAT ATATTGACAT GCATTAAACA 472380
AAGATATATA TTATTTTATG TTGTATAAAT AAATTGGCAA AATAGAGATG GAAGATAAAA 472440
ATATGGTCAA AGTAATAAGA GTCTATGGTG AATGCCTAGG AGCTTTAAGG CGAAGAAGGT 472500
CGTGGTAAGC TGCGAAAAGC TTGGGGGAGA AGCAAACATT TATTGATCCC AAGATTACCG 472560
AATGGAGTAA TCCAGCTAGC AAGATGCTAG CTATCTATTA TTAAATAAT AGAGGCGATA 472620
CCAGGGGGAA GTGAACCATC TAAGTACCCT GAGGAAAAGA AATCAAGGAG ATTCCCTTAG 472680
TAGTGGCGAG CGAAAAGGGA GTAGCCCAA CTTTAAATGT GTCAAGCTGC AGAGCGTTGC 472740
ATTTATGGGG TTGTAGGACG TTTAGGCTTA GTCTGTAATA AGCAAAAAG TTACAAAATA 472800
TTTATATAGA AGAATAATCT GGAAAGTTTA ACCAAAGAAG GTGATAGTCC TGTAATTTAA 472860
ATGTAAATAT CTTTTTAAAA GTTCCCTGAG TAGGACGAGG CACGAGAAAC CTTGTTTGAA 472920
GCTGGGGAGA CCACTCTCCA AGGCTAAATA CTAGAAAGCT ACCGATAGAG AAGAGTACCG 472980
TGAGGGAAAG GTGAAAAGAA CCCCAGGAGG GGAGTGAAAT AGAACTGAAA CCGTAGACTT 473040
ACAAGCAGTC AAAGCCGTAA TTTATTGCGG TGATGGCGTG CCTTTTGCAT AATGAACCTG 473100
CGAGTTATCA TGTCTAGCAA GATTAAAGCA TAGAAGTGCT GGAGTCGAAG CGAAAGCGAG 473160
TCTTAAAAGG GCGATTTAGT TAGATGTGGT AGACCCGAAG CCGAGTGATC TATTTATGGC 473220
CAGGCTGAAG CTTGGGTAAA ACCAAGTGGA GGGCCGAAC CTAGTCTGTT TAAAAAGGCA 473280
GGGATGAGCT GTGAATAGGA GTGAAAGGCT AAACAACTC GGAGATAGCT GGTTCCTCCC 473340
GAAATGGATT TAAGTTCAGC CTTATTTTAG TTTAATAGAG GTAGAGCACT AATTGAGCTA 473400
GGGCCTGTCA AAGGGTACCA AACTCAGTTA AACTCCGAAT GCTATTAAAT GATGAATAGG 473460
AGTGAGACTA TGGGCGATAA GGTTCATAGT CGAGAGGGAA ACAACCCAGA CCAACAGCTA 473520

AGGTCTCAAA AATGTGTTAA GTGGAAAAGG AGGTTTAGGT ACGTAAACAG CCAGGAGGTT 473580
GGCTTAGAAG CAGCCATACC TTAAAGAGT GCGTAATAGC TCACTGGTCG AGTACTTAAG 473640
CGCCGATAAT GTAACGGGGC TAAACACATT ACCGAAGCTT TGGATCTTAA CGAAAGTTAA 473700
GATGGTAGGG GAGCGTTCCTG TAAGCCAGAG AAGTTAArCT GGAAAGTTTG ATGGAGGTAT 473760
CAGAAGTGAG AATGCAGGTA TGAGTAACGA AAAAATGGGT GAGATTCCCA TTCGCCGAAA 473820
ACCTAAGGTT TCCTGGGTAA AGGTCGTCTT CCCAGGGTTA GTCGGCCCCCT AAGGCAAAGC 473880
TGAAAAGTGT AGTCGATGGG AAACGGGTTA ATATTCCCGT ACCTCTTATA GTTTCGATGG 473940
AGTGACGCAT GAGGTAACT ACTGCTAGGC GATGGTTGTC CTAGTTTAAAG CATTAAGGCG 474000
ATGATCTTAA TAGGAAAATC CGTTAAGAGA GCTAAGATGT GATGATGAGT GCTATTTAGG 474060
TAGCATGAAA TGTAGGTAGT CAAGGTGCCA AGAAATAGCT TCTAAGGTTA GGCTATAAGG 474120
GACCGTACCG CAAACCGACA CAGGTAGGTG GGATGAAAAT TCTAAGGCGC GCGAGAGAAT 474180
CCACGTTAAG GAACTCTGCA AAATACGTAC GTAACCTTCGG GATAAGTACG ACCTAAGCAA 474240
TTAGGTAGCA TAAAAATGGT CCAAACGACT GTTTACCAA AACACAGGTC TCTGCAAATC 474300
TGTAAGAGA AGTATAGGGA CTGACACCTG CCCGGTGCTG GAAGGTAAAG AGGAGATGTT 474360
AGTTTATGCG AAGCATTGAA TTTAAGCCCC AGTAAACGGC GGCCGTAACCT ATAACGGTCC 474420
TAAGGTAGCG AAATTCCTTG TCGGGTAAGT TCCGACCCGC ACGAATGGTG TAACGATTTG 474480
GACGCTGTCT CAACGTGGAG CTCGGTGAAA TTGAAGTATC GGTGAAGATG CCGATTACTT 474540
TGGGTTAGAC GGAAAGACCC CGTGAACCTT TACTATAGCT TGGTATTGAG ATTTGATTAA 474600
ATATGTGTAG GATAGGTGGG AGACTTTGAA GCTATCTCGT CAGGGGTAGT GGAGTCAATC 474660
TTGAAATACC ACCCTTGTTT AATTAGGTTT CTAACCTATA GAAATATGAG GAGAGTGCCA 474720
GGTGGGTAGT TTGACTGGGG CGGTCGCCTC CTAAAGAGTA ACGGAGGTGC GCAAAGGTTA 474780
CCTTAGAGTG GTTGGAAATC ACTCTGTAAG TGTAAGGCA TAAGGTAGCT TAACTGTAAG 474840
ACTGACAAGT CGAACAGATA CGAAAGTAGG TCTTAGTGAT CTGGCGGTGG CAAGTGGAAG 474900
CGCCGTCCT TAACGAATAA AAGGTACTCC GGGGATAACA GGCTTATCCT TCCCAAGAGT 474960
TCACATCGAC GGAAGGGTTT GGCACCTCGA TGTCGGCTCA TCGCATCCTA GGGCTGGAGC 475020
AGGTCCTAAG GGTATGGCTG TTCGCCATTT AAAGCGGTAC GCGAGCTGGG TTCAGAACGT 475080
CGTGAGACAG TTTGGTCCCT ATCTGCCACA AGCGTTGGAT ATTTGAGAGG AGCTATCTTT 475140
AGTACGAGAG GACCGAGATG GACGAACCTC TAGTGTrCCA GTTATCCTGC CAAGGGTAAG 475200
TGCTGGGTAG CTACGTTCGG AAAGGATAAC CGCTGAAAGC ATCTAAGTGG GAAGCCTTCC 475260
TCAAGATGAG ATATCCTTTA AGGGTCCTGG AAGAATACCA GGTGATAGG TTAGAAGTGT 475320

AAGTATAGCA ATATATTAAG CTGACTAATA CTAATTACCC GTATCTTTGG CCATATTTTT 475380
GTCTTCCTTG TAAAAACCCT GGTGGTTAAA GAAAAGAGGA AACACCTGTT ATCATTCCGA 475440
ACACAGAAGT TAAGCTCTTA TTCGCTGATG GTACTGCGAG TTCGCGGGAG AGTAGGTTAT 475500
TGCCAGGGTT TTTGTTTTTA TACTTTAAAC CTTGAATTTA TTGTGTATAT TTATTTTTAC 475560
ACAGTGGTAA AACTGTTGTT TTTAATAAGG GAATTTTAAA ATAACATGAA AAAAGCAAAC 475620
TTTTTAAGTA CTAATTTTTT AATTTTACTT TTGGTTTGCT TTGTCAACGT CAATTTATTT 475680
TCTAAGGATA TTTTCAAGTT TAAGCTTGTA GATCAATTTT TTCCTTTTTA CTACAAGAAT 475740
AATAAGGAG AATATGAAGG ACTTATTTTT TCTATTTTAG ATAAATGGGC AAAAGATAAT 475800
AATGCTGATA TTATGGTTGA GCATATTGAT AATTTAAATG AAAGTGAAAT TGAAGACGAA 475860
GCAATATATT TAGGATTAAC TTATAATGTA AAATTAAATG ATTTTTTTTA TTTTAAAAGT 475920
GAGCTTGCTA GGAGTATTTT AATTTTATTT TTTAAAACT CTAATAAAAA ATATAAAAAAT 475980
ACCCATTCAA CATTTTTATC CAATTTTAAT ATAGGAGTTA TTAAAAATAC AATATATGAA 476040
GATATCTTAA GGTAAAAAAA CGTTAACACC ATTTTTTTGG CTGATAATTC TCAAGAGTTA 476100
GTATTGGCCT TAAAAACGA TAAAGTTGAT TATATATATG GTGATTGCAA GACTTTACAT 476160
TATATTGCAA ATAACTTTTT AAGTGAAGAT CTTGTGATTT TTACCGGGGA TGTTTTTTAT 476220
AGTATCAAAA ATAGAGTGGC TATTAGTAGA AATGCTCCTG AGATAGTAAA GAATTTGAAT 476280
TTAGATTTGT TTTCATATTT AATGAAAATG CCTGAGGAAC TTGTTTTTTC TTTTTTAGAT 476340
AGCAATGCTA AGGGAAGTTT TGTTGATGTT GGTTTATATA ATGATTATCC TCCTTTAAGT 476400
TTTATTAATT CACAGGGAAA ATTGTCTGGC ATTTTAGTGG ATTTGTGGAA TCTTCTCTCA 476460
AGACAACATA TCTTTAAACC TATTTTTAAG GGATTTTCCA AAGAGGATAT TAAGAAATCA 476520
TTAGATGGAA AATCAGTAGG TATTTTTGGA GGAATTATTA GCAATGATAG TGTGTTGGAA 476580
AATGTTAATT ATGTAGTAAG TAAGCCAATA TATCCTCTTA ATTTTAAATT TTATTCTAAA 476640
GACCTAAGCA ATGATGCTGG TCCAATAAAT TCTCAGTTTA TTGATTTTAA TTTTAATAAT 476700
ATTCAATTAA ATAAGAATAA AGATATTGTT AATAACTTTA TAGATATTGT TAATAATTCA 476760
TATGGGTTTA TAGAAAATTC AATAACAACA AAATATTTGT TAAAATTAAA TGGATATAAC 476820
GGTAGATTAA AATCTTACGA TTCGATTTTT AATAAAAATA GGTTTTTAGT ATTAGCCATT 476880
GATAATAGGA TTTATAAGGT TATTAAATAT ATTCTCAATT CTATATTTGA TGATATTTCA 476940
TTTGAATCTT TGCTTCAAAT AGATAAAAAAT TGTTGGATA AAGAAGAGAT TAATAGTTCT 477000
AGAATAAATA GTTATAAAAT TATGAATAAG GTTAAATTTA ATATAGAAGA AAAAATTTGG 477060

TTATCAAAAA ATAATAAATT AAATCTTGCT GTTAAAAATT GGTATCCAAT AGATTATGTT 477120
GAGGCAAATA ATTATAAAGG AATAAATCAA TTTTGTGCTG ATAAGATTAG AATGTTTTCA 477180
GGTTTGAGAT TTAACATAAT TAAAGTACAC AGCAGTTTAG ATCTTAAAAA ATTAATCAAA 477240
TCTGGAAAAA TCGATATGCT AAATACTAAT GCAACCGATT CAAATTTAGA TAATGTTTTTC 477300
AACATAAAAT TAAATTCTCG AATTCCACTT TATATTTTTT CAAATAAGAA AAGGGTGCTT 477360
CCATCTAGAT CTTTAGAAAA GTTTGCTATA CTGATTTTTT TATATAGTAA AAATTTGGCT 477420
TCTAATATTA AATCAAAGCT TATTCTGGTA AGCAGTTTTA ATGAAGCGTT GCTTCTTCTT 477480
TATAAGGGAA AGGTAGATGG GATTATTAGC GATGAGTATA CAGCTGCTGC TGTTTTTGAG 477540
GAATTAAATA TTGATGATGT TGAAAAAATT CCTACTTTTA GAGATTTGGC TTTTGATTG 477600
AGTCTTGCTA TTTATAATCA AGATTATATC TTGAAAGAAA TTATTCAAAA AGTTGTTATG 477660
CGTTCAAAATG TTGACAGTCA GATGTATTTA AATGATTGGA AATTTGATAT TTATTATAAA 477720
TCCAGAAGTA TCAGGTTTAA AAATTTCAAA TTTTGTAGTA TAACATTCAT TATATTTTAT 477780
TTTACTTTTT TAGGATTTGT AATTATATTT ATGTTTCAGAT TATCATTTGA GCAGAAAAGA 477840
AGATATTCTT TTGTGATGAA TGAAAAAAG ATTGCGGAAG CCGCTAATGC TGCTAAAACC 477900
ATTTTTATAG CCAATGTCAG TCATGATATT CGTACCCCTA TTAACGGAAT AATGGCGGCT 477960
ACTGAGCTTT TGGATACAAC TATTCTTACA GATGTTCAAA AAGATTATGT TAGGATGATA 478020
AATTATTCAT CTGATTCTTT GCTTTCTTTA ATTGATGATA TATTGTATTT GTCTAAAATA 478080
GATGTCAATG AATTATATGT TGAGAGTCAA GAGATTGATT TAGAGAGTGA AATGGAAATG 478140
GTTTTAAAAG CTTTTCAATC TCAATGTGCA AAGAAAAATA TTGATTTATT CTCTTATTCT 478200
AAATCTATTT TTAATAATTA TATAAAGGGT GATATTGTAA AAATTAAACA AGTTTTAATT 478260
AATTTAATAG GAAATGCTTT TAAGTTTACA GATGATGGTG TTATTGTTTT AAATTATGAA 478320
GAAGTATGTA GAACAAGAAC TGATGGTAAT AGGGTTTTGG TTACAGTTGA ATTTAAGGTA 478380
ATAGATACAG GCAAAGGGAT TGAAAAAGAA AATTTTTCTA AGATATTTGA AATATTTAAA 478440
CAAGAGGATG ATTCTTCTTC AAGGGTTCAT GAAGGTGCAG GATTGGGATT GTCAATATCT 478500
AGAGAGCTTA TAAGACTAAT GGGTGGTCTT GGTATTGCTG TTGATAGCAA GGTGGGAGAG 478560
GGTACAACCTT TTTCATTTAT GTTGCCCTTT TTATTGGGTA GTGAGCTTAA AAGTAAAAAA 478620
TTGTCAATCA ATAGATTTCA ATCAGTAAAT GGTGACAATA AAGTATTAAA TGTGCTTTTA 478680
AGTCAAAAAT CTATTAAAAT TTTTGAGCAC GTTTCGATTT TATTGGGATG CTCTTCTAAT 478740
GTGCGCTATG TAGCGTCTTT TGAGGATGCT TATAAAGTCT TCAAGAAATA CCCTTCTTAT 478800
AATTTTGTTT ATATAAATGT AAATAACGAT AATATTCAAG AGGGTATTCG ACTTGCCAAT 478860

AATATTGAAA GACTAAATTC TGATGTACAA ATTATTTTTT TATTTTATTA TTTAGATAAT 478920
AAAGCTCTAA AAAATTTAAA ATATGGTTAT GTTAAAAAGC CTTTAATGGG GCTTGGTATA 478980
TGCTCTATTC TTTATAAAAA AGAGTTTAAC CCAGAAATGG ATTTTGAGGA TTTGGTTCCA 479040
ATAGATAGTG CTTTAAGGAT AAAAGAGCCC ATTAATGTTT TAATAGCTGA AGATAATCAG 479100
GTAAATCAAA AAGTGTTGAA AGATATTCTT GTTGTTATAG GCATTAATGA AAATTTTATT 479160
GATGTTGTAG ATGATGGAGT AAAGGCTTTA AAATCTTTAA AAGATAAAAA ATATACTATC 479220
TCTTTTATTG ATATACGAAT GCCAAGATAT GATGGATTTT CGGTGGCTAA GGAAATTAGA 479280
AAATTTGAAA AGGCAAAGAA TTTAAAGCCT TGTGTTTTGG TTGCTGTAAC AGCGCATGCT 479340
TTGCAAGAGT ATAAAGACAA GTGTCTTGCA AGTGGTATGA ATGATTATAT CTCAAACCA 479400
ATACACATAA GTTCAATTAA AACTATATTA AAAAAATACT TACAGTTTGA AGTTGATGAT 479460
ATTGGGGAGA ATGAAAATTT GAATCAACTT GTTAAGTTTC CTAATTTAGA TGTTAATAGG 479520
GCTTTAAAAG AATTAAATCT TTCATATGTA TCATATTCTG AATTATGTAG AGGGCTTGTT 479580
GATTTTATCT CTATTAATAT TATTGATTTG GAAAAAGCTT TTGATGAGGA AGATTTGTCT 479640
TTAATTAAGG ATATATCTCA TTCAATATCT GGAGCTCTTT CTAATATGCG TAGCGAATTG 479700
TATAAAGATT TTCAAAAAAT TGAAACAAGT AAAGATTCAA TTTCTGAGTT GAAAAAATG 479760
TATTCTTTTG TAAAAGATGA TTTATTTCAA CTAATAAGCG ACATAAAGGA AAATATTTTG 479820
TTTGAGTCTG AGATTGTTAG TGAGAACAAG CTATATTTTA AAAATAATGA TCAATTTTGA 479880
AACCTTCTCA ACAAACCTTT AATTGGTATT AAGACTAGAA AGCCAAGAGA ATACAAAGAA 479940
ATTCTTGAGA GCATTAATAA ATATGTTTTA GACGATAATA TTCAGGTATT ATTTAGTGAT 480000
CTTCGCAGAA ATTTAAGATT ATATAGATTT GCTGAGAGCT CTAAGATTCT TGAAGAGATT 480060
ATTGAAATGC TTAATAATAA GAGATATTAG CAGTGGAAT GATAATTAAA GATAAAGCTT 480120
TTGAAGCAGA GAATCAGAAG CTTTTAATTG TGGATGATTC TCCCCACAAT TTAGATTTAT 480180
TGGTAAATAT ATTGCAAGGT GCTTACGAGA TTGAGGTTGC AACAAATGGA CTTGATGCTT 480240
TAAAGCAAGT TGAAAAAGAT AGTCCTGATC TTATACTTCT TGACATAGGT CTTCCAGATA 480300
TTAACGGTTA TGAGGTATGC AGAAAGCTAA AAAGCGATCC CGATACTAAA GAGATTCCTG 480360
TAATTTTCAT TAGTTCAAGA AGTTCCACAG ATGCTCAGCT TGAAGGATTT AACGTTGGTG 480420
GAGTAGATTA TATTTTAAAG CCTTTAATA GTCGAATAAT TGATGCTAGA GTTAAGACAC 480480
ATCTTGAATT AAAAAGGTTA AGAGATTATT TTAAAAGCTT GTCTAGAATT GATGGGCTTA 480540
CTCAAATTCC AAACAGAAGA TTTTTTATGG ATAAATTTTC TAAGTCGTGG ATGAAAGCTT 480600

TAGAAAAGTAA	AGAAATAATA	ATTGTTGGAA	TGTTAGATAT	TGATAATTTT	AAAAATTACA	480660
ATGATAATTA	TGGCCATACC	AATGGTGATG	AATGTCTTAA	ATTGATTGCT	AAAGCCTTAT	480720
ATAAGGTTTC	CTTAAAATAT	AAAATAGATG	TTGCTCGATA	TGGAGGGGAA	GAATTTATTT	480780
TTTTTTCTGT	CAACAAAAGT	CTAAATGAAA	TGGTTAGTAT	TATTAAAACA	ATGATTAATG	480840
ATATAAAACG	CTTAAGAATA	GTTTCATGAGC	ACAGTAGTGT	TTCTGGCATT	GTTACTGTTT	480900
CAATTGGGCT	TGCTCAAGAA	GTTCCATTATG	ATAACAATTT	TACCAATATC	ATAAGGCTTG	480960
CTGATCGCAA	GCTTTATGAG	GCTAAAGTTT	CTGGAAGAAA	TCAGTTTAGA	TATTAAATTT	481020
ATATTTAATA	GACTTTAGTA	TTTATAAGTT	ATAGACATTC	CAATAGAATC	GTAATAAAAA	481080
TAAGAATTGC	CAGTTGCTAT	TCTTTTTGAA	ATATCAGCCA	GTCCGGCTGT	GTTACTTGTTG	481140
TATGTGGGAT	TTGTAGATAA	TTTAAATTGA	AGGCCAAGTG	TTAAAGGTTT	GATAATTTCA	481200
AAATTAGCAA	CAATAGAAAT	GTTGTGATAA	AAAATATCAC	TTCCCCAGCC	TTTGTTTTTTC	481260
CAAGAGCTTA	TGTTTCTTTC	TTTGCCAATT	TGTGTTTTTTC	CTTCATAAAG	CAGGCCTATG	481320
GTGTTAAGAG	GTATTGGCAT	TTTGTAAGCC	AAAAGAGCGT	AAGGTTTTTAT	TAGCATGCCA	481380
TTTATATTTT	TACCATCATC	TGCTTTATAT	TTCCAAAGTT	GATCTTTTTT	TGCATGGGGA	481440
TTGATTAAGT	ATGTAAAATC	ATTTCCAATA	ACTGTAATAA	TGTGTGTCCA	TTCTCCTTGA	481500
AAAATAGCGT	TTAAGTCAAA	TTGGAATCGT	CCCCCGCTG	TTATTTCTGA	ATAAAATTCA	481560
ACAGCATTTG	AATATTTCCC	ATTTTCAATG	TGTACGCCTA	CTCCTTTAAA	TCCAAAAGCT	481620
TGCCAACCTA	TGCCAAGTTC	ATTTGATGCA	TATAAATTTA	AAAAGCAAT	AGGAGTAAAG	481680
CTTACTGTGC	TTTTAAATGA	GACAATTACA	GGAGACAATC	CGATATTTAA	ATCTATATCT	481740
ATACCATTAT	TTTTAAAAAA	TATAGAATTG	GGATTGTTTA	GGGCTTTAAA	ATTTTTATAG	481800
TAGCCCAAAT	ATGATATTAG	TTTTATTCCC	CCCCAATAAT	TGACTGGAAT	TTTTAAACTT	481860
GGGTCAATAT	TTTGGAAGTT	AGGATGTTTA	AAGCTTTGTG	AAAAGCCGCT	TCCATTTGTA	481920
CCCAGCTCGT	GGGGAGGATA	ATAAGCAGAT	TGAAAATTAA	AATAAAAATA	TTCATTATTA	481980
AATTCTAAGT	TCTGTTGATC	TTGGGAAAGA	ATTATTTTTG	CTTGCAAAAG	TAACAAACAA	482040
AAGCAAATTT	TTTTTATTAA	CATTTTATTT	AAAATACCTT	TTCCATTTAA	TTTTTTTTTTA	482100
ACATTATTTT	AATTATCTTT	TTTTTTATTT	CATCAATTTT	AACAGATGCA	TCAACATTGT	482160
TAAGTCTAGA	GCATTTTGAG	TAAAATTCTA	TTAGCGGTTT	TGTTTGTAAT	TTATATTCTT	482220
TGAGTCTTGT	TTTTAAGCAT	TCTTCTTTAT	CATCTTCTCG	TTGATAAAGA	TCTCCCCCAC	482280
AAACGTCGCA	AATACCATTT	TTTTTTGTTG	TTAGGGTATA	TATATTGAAA	ATATTATTGC	482340
AAGATTTGCA	AATTCTTCTT	CCCGAGAGTC	TTTTTATCAC	TAACCTTTCA	TCAATTAAAA	482400

AATTTATTAT TTTTACATTT GGCAAAAATT TGTCAAGAGC CTCGGCTTGA CAAATATTGC 482460
GCGGAAATCC ATCTAAAATA AAATCTTTGT TCTTTTAAAT AGCTTTAATT TTATCTTCTA 482520
CTATTTTGAT TGTAAATTAGG TCGGGGACCA GTTCTCCCCT TTCAACAATT TTTTTTATTT 482580
CTTGCCCAAG AGCCGTAGAA TTTAAAATAT TTTCTCTAAA TAAGTCTCCT GTTGAAATGT 482640
GTTGATATTT AAATTCATTA GAAATAATTT TTGAAATAGT CCCCTTTCCA GAACCCGGAG 482700
GACCTAAAAA TACAAGCCCC ATATATACTC CTGTTTAAAT ATTTGTTATT TTAAGGGTTT 482760
ATTTGAAAAC ATTTAATAAA AATTTAAGTC CTACGATTGT TCCAATTGTA GATCCAAGGT 482820
TTACAAAAAT CACTATTAAT AGAATTCTTG TAACTTTGTT TTTGAAATAT CCTTTTATTG 482880
TCGACAATTC TTCTTGTAAG TTTTCAAAGT CTTTGACTTT TGGTTTGTTT ATATAAGCTT 482940
CAACAAGCCC TGCTACCATA CCTGTTCCCTA TGAATGGTAT TAAGGAGAAT ATTGGAGAAC 483000
CTATAATAGC TGTTAAAATT GTTAAGGGAT GAGATTTTAA TAAAATCGAT GCGATGCCTG 483060
AAAAAATAGA GTTAGATATT ATCCAAAGCT TTAAATTTTT GTAAGCAAAA TCAAATCCTT 483120
TAAAGTAAAA AGAGCTTACT ATTAGTAAAA TGATTGAAAT TGCAATCAAG TAAGATAGCA 483180
CTTTGCTAAA TGAAAAATGT TTTTLAGGTA TTTTCTCGAG TTCTTCAACG TTTATTATTT 483240
TTTTATTTTG ACTTATTTCT TTAAAGTTC TCATTATTCC GCTTACATGG CCTGCACCCA 483300
CAATGGCAAG AATAATGCCC TCTCCTTCAA GTATTTTGTT TGTAATAAAT TCGTCTCTTT 483360
CGTCAATTAA AACTTTTTTT ACTTTGGGTA TTTCTTTGGA AAGTTCTTCC ATTATTTTTG 483420
AAAGAGCGTC CTGTTCTTTG AGTTTTTCAA TTTTCATCTTT TGTAATTTTT GCATCTGTTA 483480
GGGAAAAAAG GCTTGAGATT ATTTTGTGCT TTTCAAATAT TGGAATAGAT ATCCAAGCTC 483540
TTTTTAGTGT TGTTTCAATT TTTCTGTCAG CAAGAATTAG TGGAATATTG TGTTTTTTAG 483600
CTTTTAAAT AGCTGTTTTT ATTTCTTCAC CAGGTTTTAT TCCCTGTTCT TTTGCTAATT 483660
TTTTTTGAAA ATTACTAAGA ATTATGTTTA TTATGAGAAA GAAAGCTTTT CCTTGTTTTA 483720
ATGCTTTATC TATATCTAAG TTTCTCCATT TTTTCATTTT ATTGGTATTT AAGATCGAAT 483780
GATAGCGAGC TTCATCAAGT TCAACGGCAA TATAGTCTGG TTTTAAGATT TCTATTAAAT 483840
TTGCAGTATC TTCTGAGCTT TTTTTTGACA CGTGAGCAGT TCCAAGTATG TATATTGTTT 483900
TATTGTGTAT ATTAAATTTA CTTACATGAG AAAACAGTC TTCTGTTTCG GTGTTTTCTT 483960
TTTTATTGTC CAAAAATAT TCCTTGTTTA AAAAATTTA GCTATTAATT AGTATAGCTT 484020
TTAATAATTT TACCATATGG CTTAGTGGA CTATATAGTC TATATTGTTT TCCTTTATTG 484080
CTATTTTGG CATTCAAAA ACCATAGAAC TTTCTTTATC TTGCGCAATA GTTAGTCCTC 484140

CAGCTTTTTT	TATATCTCCA	ATTTCTCTTG	ATCCATCATT	TCCCATTCCA	GTCATTATTA	484200
TGGCAATTGC	TTTATCTTTT	GCAATCTCTG	CAATAGATTG	AAATAATACC	CCAATAGATG	484260
GTTTGTGACC	ATTTATATGT	TTACCATCGA	GGGTTTTTAT	TTGATAGTTA	CCATCGATTT	484320
TTTTGATTTT	TGTATGATAT	CCGCCCAGAC	TAATGTATGC	ATATCCTTGC	TTTAATATTT	484380
CGTTATTGGT	GGTTTCTTTT	ACGCTTATTT	TACATAGATT	ATTAAGATTT	TTGGCAAATT	484440
CTTCTGTAAA	TCCTTTAGGC	ATATGTTGAA	CAATTATTAT	TGGCGGAAAG	CTTTCAGGTA	484500
TTTCTGGTAA	TATTGATTTT	AAGGCTACAG	GCCCCCCCCG	TGATACTCCA	ATTGGCTATT	484560
ATGTCAAATT	TTCTCAGTTT	AAGTTTTTTT	ATTTCTTTTT	CATTTAATGT	TTTTTCTTTT	484620
GCATGTTCTT	CAAGTTGATT	TAATGAAGAA	ATGTCATTTT	TGTGATTTAA	AATAAAATTA	484680
GCTCTTTCGT	AGTTTTTTGT	TTTCATGTCC	TTATTGCAGG	CAATTTTATT	TTTTATAGAT	484740
ATCGATCCAT	AGGCCAAAAG	AGAATTAATA	ATTTGTTCTT	TTTTGATTTT	ATGTGATTTT	484800
TTGTTTTTAG	ATACTAATAT	AAGATCATCG	GCGCCCTTTG	AAGCAGCAAT	ATTTATTAGG	484860
TTTTGATTTG	AAGATGTGAC	GACAATTGGT	ATTGTTTTGT	TTAAACTGTT	TTTTTCCTCC	484920
AAAAATAGAA	TATCTTTAAT	ATTGTTCTCT	TCTAAATTCA	TTAATATTAC	TCGGGGTTTA	484980
TGTTTTTTAA	GTTTATTTGT	TGCAAATTTG	CTGTTAGAAG	CAGTTGCAAT	GACTTGGAGT	485040
TTTGGAGATG	AATTGATAAG	GTCTGATATA	AGTTTTCTCT	TTACAGCAAA	GTATTCTATG	485100
ATAAGTACAG	AAATTTTTGT	TTCCACCGTT	ACTTTTTTCC	CATTTTATTC	TTGTTAAATT	485160
ATAACTTATA	TTTATTTTGT	GATTTGAATT	TTTCTTTTTG	ACAGCCAGTA	TCTTTTTTTT	485220
CATATATTAT	TGCCCCAAGT	GTTTTTAAAA	ATTTAAAAGG	AAGGTTGAGC	CCAAAAAGTG	485280
ATTCTGAGTG	TCCTATAAAT	AAATAGCTGT	TTTTAGACAT	ATTGTTGTAA	AATTTTTTAA	485340
GTACTTTTAT	TTTTGATTTT	TCATCAAAGT	ATATTAAAAC	ATTTCTACAA	AAAACAACAT	485400
CAATTTCCGA	AAAATTACTT	TCAAAGTTTA	AGTTATGATA	ATCAAATCTT	ATGTGATTTT	485460
TAATTTCAAT	TTTAATTTTA	TATCCGTTTG	AATGAGAATA	TATGTAGTGT	CGGTATTCTT	485520
TAGGAATATT	TTACATTTTA	TTTGATGAGT	AATATCCTTC	CTTTGCTATC	ATCAAAGATT	485580
TTAAGCTTAA	ATCAGAAGCA	ATAATAACAA	AATCTATTTT	TTTTGGAAGC	TTTGATTTGA	485640
GTACAAATGC	TAATGAATAA	GGCTCTTCTC	CTGTTGAACA	TCCCGCAGAC	CAGATGATAA	485700
TCCTATTTTT	TTTTTCTATG	TTTTTAATAT	TAATTAAATT	CGGAATTACA	AATTTTTCAA	485760
AAGTTTGAAA	ATGTAGCGAA	TTTCTAAAAA	ATCTTGTTAA	ATTTGTTGTG	ACCAAATCTA	485820
AGAAATATTC	TTTTTTTAAT	TTTTCACTAA	TTATTAAATT	ATAAAGTTGT	GATGGGTTTT	485880
CAAGAGCAAG	AGCTCGTACT	GCATCATTCA	CTCTGCTTTG	AAGAACAAAT	TTATTTTTTTT	485940

CATCAAAACG	AATTCCACTG	TTGTTATATA	TAAAATCACA	AAATTTTAAA	AATAGTTTAT	486000
CTTCAATTTT	TAGCATTTTT	GGGAACCTGC	TTAATTCTTC	TCTTTATAAA	TAAGTATTGC	486060
CTATTTATAA	TAAATCTCTT	AGGTAAGAAT	ATTTTTTTTG	AAAAAAAATT	GTAAAATTAA	486120
TATAAGTAAT	TTTATTATAA	GACATAGGTT	TATAAAAAGG	TTTTTGTTTA	TTTAAATTTA	486180
TTTGCAAGCA	TAAATGAGGA	ATTTAATGAG	TGTTGGAAAA	AATGTTTTC	AATGTCGATT	486240
TAATATGCAT	TTTAAAAAGA	TCAAATGATG	TTTGATGAGT	TTAAAAGAAC	AATCTTAGA	486300
GAAGATATTA	AGTATGAAAT	TTTTAGAAAA	TTTTTTCATA	TTTTTAGCTT	AATAGTTTTA	486360
GTTTTTTATA	GAATAAATTT	TTGGATAGGG	CTTTTTTCTA	ATATACTTTT	TATGATTTTA	486420
TACTTAAGTT	CTGAAATTTT	TAGAATTACT	GAAAAAATA	TACTTTTCTT	TAAAAACATT	486480
TCAAACATAA	TATTAAAATC	AAGAAAAATA	TTGCCCAATA	GAGTATCTTT	TTCTCCTGTC	486540
TTTTTGTTTT	TAGGTATATT	GATATCATAT	TGTTTATCTA	TGCATCCTTT	TAATTATATT	486600
GGAATATTTT	CGGTATGTCT	TGGTGATGGA	TTTGCAAGTC	TTATTGGAAA	GTTAATTCCT	486660
TCTTTTAAGC	TTGTAAATGG	TAAAACGATT	TCTGGCAGTC	TTGTTGTATT	TTGTGTTACT	486720
TTTTTTTCAT	ATTATTATTT	TTTTCCTTAT	TTGACAGTAG	CTTTAATTCT	TGGGATTTTA	486780
GCAGTATTGG	TAGAGCTTTT	TGATGCTGCT	AATTATGACA	ATTTATTTTT	ACCGCTTGTT	486840
GTTTCAGCTT	CGTCCTATTT	TTTAACTTCT	TTTTTTTTATA	GCCAGTAAAA	GAAAATTTTC	486900
CCTGATTTTT	TTAAGTAGAT	TGGTATACCA	ATTGAGATTG	GGAGAAAGGC	ATAAGGCATT	486960
TTTAGCAAAT	TCAAGTAAAT	TCCACTTAAT	ATTAAAAGCA	TTGAAACAAA	AAGGAAAAAA	487020
TAGTCAAAGC	TTTTTTTTCT	TAAAAAGGCT	ACTATAAAGT	TTGTTAAAT	AAGTAGCAAG	487080
AATGCATCTA	TGTAAAATTT	TGTATTTTCT	ATTTTAAGAA	TTCCGTGGTT	TTGGCTATTT	487140
TCGTACGAAT	TAATAGGCAT	TGTGTAAC	TATATGCAGG	CAAAGATCAA	AATAATGTAA	487200
ATTGTATAAT	GTATTGATTT	TATTTTGAAA	TCGCATATAT	ATAAACTGAG	AAAAAATAAA	487260
TTTAATAATG	AAAAAGTGTT	TACAAAAAGG	ATAAATTTTG	TAAACAAATA	ATAACTTGAA	487320
TTTAGATTGT	TTTTTAAAAA	AAAATCTTCA	GAGATTAAAA	TAGGGTCTAA	TGTATATGAG	487380
CTAATAAAGC	AATAGAAAAA	TATAAATTGT	ATATTGTTGG	TTCTTTTGTA	GTAAATGTAT	487440
GACCACAGCG	AGCCTATGAT	CCCAGCAATA	AAGATGGTTA	ATTTATTAA	CAATATTATA	487500
AAATTATTAT	TGTAAATTTT	TAGAATATAA	TTTTGATAGT	TTTCATTATA	TTTTATTTTA	487560
TAGGAGAAAG	TCAGTATAAC	TATTGTTGCC	AAAATAAAAA	TTATAAAAAG	AAAGAGATTG	487620
ATAGAAGCGT	TTAACTTTGC	AAATATTGAT	TTCATTTAAA	TTCCAAGAA	TGCGTGTTTT	487680

TTATTTTTTT	AATATTTTTT	TTAATTTTTG	AATCAAGTTT	TTCAAAAAAA	TCTATCTTTG	487740
TTTTTTTTTC	AATTAAGTCA	ACGCTAACAA	CATAATTTTC	CAAATCCAAG	TCTTTTGCTT	487800
TTTCATTTGG	GATAATAAAA	GAGATTATGT	CATAATAATT	GTTATTATTA	ATTGCCAGTA	487860
CTATTTTATA	AAAATTTTTA	GGTATCAAAA	TTTTGTTTTT	ACCAATAAAT	CCTTTATTTT	487920
CTGTTAAAAT	CCCAGCGCTA	ATAATATATA	TATATCCTTT	TGAGATTGCC	CATTCTCTTA	487980
CTAATTTTTC	AAGTTTTAGC	CAAATTCCAG	AATTAAATTC	GCTTTTTTTGA	GGTGACATAT	488040
TTGATAAAAA	ATATGTATCT	TTCATTGCAT	TTTCAGAAAA	AGACATATCT	GCAGAACTTA	488100
CTATGTGTCC	TCTGTCATAA	CCGCTTTTAA	AGTAATCTTC	AAGTTTTGGA	AAAGCGCCCT	488160
TAATGTTGGT	GTCTTCAAAG	AATTTGGTAC	TTCTTTTAAT	TTTTTTTGAT	TTTAACAAAG	488220
TTAATGCTAG	TTCTACCATT	TCTCTTTTAA	GCGGATAAGC	AGCCCATTCA	GATTGTCTTG	488280
CGCTTTCAGC	ATATCCTAAG	GTATAGTGTT	TTTTGCTTAT	TATTTGAGTA	GTAAGATATC	488340
CTTTTGGTAT	TAATTGGGCT	TCTTTTATTG	GAATAGATTT	TGTAATGTCA	GTGTATTATT	488400
TCTATTATTT	CTAAATAGTC	ATAAATTTGT	GTTTAATTTG	TTTTAGGGCT	TTTGGATTTA	488460
ATGAAAAAAA	TAAAAATCCT	GTTAGGCATA	AAATATAGCA	GTAAAGAAAA	AATTTCGACC	488520
TTTTTTTTCAT	GTTTCCATCT	CGTTTTTGTC	CTTAAAATTA	TATCTAATAG	TAAAAATAAA	488580
AGAAATGTTA	AATGTATCTA	AAAATAAAAA	ATCAATTTTA	AAGTCTAACC	CCATTAAAGG	488640
AATTGCCTTT	TTAGAAGAAA	TTTCAATAAA	CATATAAGGC	TCTATTACAT	AAGGCAATTT	488700
TTCGTAAAAT	CGAATGTCTT	CTATAAAGTT	TGTAGATAGG	TAAAAACGAC	CACCTATGCC	488760
AATGGTGGCG	GAAAAATATT	TTGTTTTTTT	AATTAAGTTT	GCAATGTGCC	AGTTTATTCC	488820
TCCTCCAATA	TAAGATTTAA	AGTATTGCAT	TTTTTTGGGG	ATATTAAGGC	TTTCCCTTGT	488880
TAATATCATA	GCAACGATTA	AAAAATCAAA	AGTATTATTA	GAGAATGTAT	AATAAGGTCT	488940
AAAGATAAGG	TGTTTAATAT	TTGAATTTAG	AAAAATCCA	ACTCCAATCC	CAATTCCTGT	489000
TGAATATATG	AACCCTCTTT	CTGGGCTAAA	AAAATTAGAG	ATTTGTTTGG	GTTGATCATT	489060
TTTTTCATTA	GTATTGCCTT	CTTCATTTGC	AAGTGCATTT	AAATTGGAAA	TGATAAGCAA	489120
TGTTAAGAAA	ATACAAGTGT	TTGGAGTTTT	TTTCATAAAC	TGATTATTTT	AAATAATATA	489180
AAAATTGTTT	TACCTTTTCA	ATATTGCGAT	ATGTATTTAG	ATAAAATTTT	CCTGTTTAGT	489240
TTAAAAAATA	TTTTTTATAT	TAGGTGGCTG	TGGTATGCTA	TTTTTATTGT	ATATTATACA	489300
ATATGTTTAA	TTACTAGGAG	ACCACAGTTA	TGTTTTTTAA	TTTTTTGAAA	AAAGATCTTG	489360
TATTTGTTTT	GCCAGAAGTA	AATTCAAAAA	AAGATGTAAT	TGATTTTTTA	ATTGAAAAAA	489420
TCAATGATAA	GGGATATATA	GATAATAAAA	AAGAGTTTCT	TCAAGGAATT	CTTGATAGAG	489480

AAAAGATAGG TGACACTTCT TGGGAAAATG GGGTTGCAAT TCCTCATT TT ATAGGAGATG 489540
TTGTTAAGAC TAGTTTTATT TCATTGCTTT ACATTAAAGG TTCTGGGGTT AAGTGGTCTG 489600
AAGAAAACCC CCCTGTTAAT TTAATATTTT TGATTGTAT GTCAAAAAA CAACAAGGTA 489660
ATGAACACCT TAAGGCGATT GCTTTTATAG CTAACTATT TGAAGATGAT GCTTTTCAAA 489720
ATGCTTTACG CGGGTTTGT ACTACTGATG ACATTTATTA TTATATTGAA AATGTTCAAA 489780
GAAAGGCTAA AGAAGAGGTT TTTGGAGCTA CAAAAGCAGA AAAAATAGTG GCCGTAAGT 489840
CTTGTCCTGT TGGAGTTGCT CATACGTATA TTGCAGCTAA GAAAATTGAA AATGAAGCTA 489900
AAAAGCAGGG TTATAGCATT AGAGTAGAAA CTCAAGGATC TATTGGTATT GAAAATGCCT 489960
TAACAGAAGA GGAAATTAAG AATGCGTCCG TTGTAATACT TGCTGTTGAT AAGGATATTG 490020
ATGAAAAGAG ATTTGAAGGT AAGAGAGTTT ATAAAGTTTC AACTGTAAAA GCGATAAACA 490080
ATACAGAAAA TATTATTAAG GAATCTTTTA ATGCTCCGGT ATTTAAAAGC AAAGACTCCG 490140
GTACTAATAG TGATACTAAA GCTTCGGTTG CAACAGGCAA AGGTAGTTTT TATAAATATT 490200
TAATGAGTGG GGTATCTCCA ATGATTCCTG TTGTTGCAAG TGGAGGAATT TTAATTGCTC 490260
TTAGCATTGC TTTTGTGGG ATTGGACCTG ATGGGCCTAA TTTTGCTGAG CATCCATTTT 490320
ATAAGCAGAT TGCAGATATT GGTTCTATAG CTTTTGGGAT GATGTTGCCC GTGCTTGCTG 490380
GTTTTATTGC AATGGCAATT GCTGATAAGC CTGGTCTTAC CCCCAGTCTT GTTGGTGGAG 490440
TAATGTCTGG GAATGTAAAA GCAGGTTTCT TGGGCGCAAT ATTTGCGGGC TTTCTTGCA 490500
GTTATGTTGC AAGGTTTTTA GCAAGAAGAT CTGTTCTGA GTGGTTAAGA CCTGTAATGC 490560
CTATATTTGT AATTCCGCTA ATAAGCACCA TTATTGTCGG CTTTTTTATG CTGTATTTTG 490620
GTGTTTATAT TGGAAAATTT ATGGGGGTGC TTGAGAGTGG GCTTAAATCT TTACAGAGTA 490680
ATTCGGAAAC TTTTGGCGTG TTGGGTAAAA TTTTCTTAGG CTTAGTACTA GGTTCATGA 490740
TTACTGTTGA TATGGGCGGA CCTTTTAATA AAGTGGCATT TCTTTTTGGT GTAGGGCTAA 490800
TTCCTCAAGT GCCAGAAATA ATGGGAATGG TAGCAGCAGC AATCCTGTT CTCCTATGG 490860
CTATGGGGCT TGCAACCTTT TTAGCACCTA AATTGTTTGA AAATGAAGAA AAAGAATCTG 490920
GTAAAATAGC CTTTTTAATT TCATTTATTG GTATTAGCGA AGGAGCTATT CTTTTTGCTG 490980
CTAGTGATCC CGGACGGGTA ATCCCTTCGA TAGTGGTAGG GGGAGCTGTA TCAAGCATT 491040
TTGCCGCTTT TTTAGGCGTT GCTAATCATG CTCCACACGG AGGACCAATA GTACTTCCTG 491100
TTATTGATAA TAAATTTGGG TTTATTATTG CAATTGCTGT TGGAGTTGCG GTTGCAACAG 491160
CTTTGGTAAT TTTTTTGAAA TCTTTAAAAT TAAAGGAATC TGAATGAATA ATGAAGATAA 491220

TATTTTTTTTA ATGAAAAATA ATATTAAAGA ATATGATTGG GCGGAATTA ATTTTATTC 491280
CAATCTTTTG GGTGATAAGA TTGATGGAAA GCCCAAGGCT GAAATGTGGC TTGGAGCACA 491340
CAAGACATTT TCTAGTAAGA TTTTGTATAA AAATGAATAT GTGCTTTTAA GCGATTTTTT 491400
AGAAGATCAT AAAGAGCTTT TAGGCTGTAA TGACGAATTT CCTTTTTTGC TTAAGGTATT 491460
GTCTGCAAAT AAGCCCCTGT CTATTCAAAT TCATCCTTCT AAAGATATTG CCTTAAAAGG 491520
GTATGAATCA GAGAATAATA AAGGGATAGA CATTAATGAT CCCAAAAGGA CATACAAAGA 491580
CAAAAACCCC AAAATTGAAC TTATTTATGC TCTTAGTGAT TTTTATGCTC TTAAAGGCTT 491640
TTTACCCTTA GATGAGATTA AAAAAATTTA TGAAATTCTG GAATTAAATT TCGACTTTCA 491700
ATCACATAAA GATTTTGTAA AGACTATTTT TGATTTACAA ATGTATGAAC TTGAGAAGAT 491760
TATTGAAAAA ATTTTAAAAA ATTTGGATCT TATTGATAAT TTTAGGGGCT ATTGGTTTAA 491820
TGAAATTTAC AATATTTATG GTATAGATGT GGGCCTTTTG GTATTTTATG GTATGAATAT 491880
TTTAAACTA AAACCAGGAG AAGTTGTTTA TACAAATAGT CAGGAGGTGC ATGCATATCT 491940
TAAGGGAGAT TGCATTGAGC TTATGACCAA TTCCGACAAT GTTATTAGGG CTGGGCTTAC 492000
TACAAAGTAT ATTGATAAAG ACGAGATGTT AAGAGTTGGT CAATTTGAGG AAGGAAAGTT 492060
ATCATTTTTA AATCCCGATT TTCAAGATAA TTTTAGCGTA TTTAGACTTC CAAATACTAA 492120
TTTGAAATTG ATTCAAAAAA AAATAAATGA GAACATTTGT ATTAATAGAA ATAGTGCAAT 492180
GGTCTTGCTA GTTTTAAATG GGTGCGTGAG TATAAATAAA TCCTTAAATC TTAAGAAAGG 492240
TGAGAGCATA TTTATAGGTA AAAAAGCAGA AAACCTGTTT ATTGATGGGG ACGGCGAAGC 492300
TTTTATTGCT GGTTTTAATT AAAATTAAGC TTGCTTATGC GAGCTTAATT TTAATTACCA 492360
ATTTAATTAT TTGGTTAATT AAATGCAAAT TTTATGAATC CAAATCCAA AAAATTGAAT 492420
TTAATTCCTT CAAATAAAAT GCTTGGTTTT GTTAGTAATA TTGTTGGCCC TACTGCAGGA 492480
TAAATTTTGA ATCCTATGGA TAAATTTTTT GCAAAATTAT ATTCCATTAT AAAAGGAATT 492540
CTTATAACAG CGCCTATTCT CTCATAATCA GTTCTTCTT CTTCATTAGG GGTATAAGG 492600
GATGTTTTTG ACCAATCCGC ACCTATTCCA ATGCCGCCGC CAATTTTCAT ATATTGTCCA 492660
ATTTGCTTTT TAAAAATAAC GTCTATTCCA CCATTTAGAT AATTTTCAA ATTGTTTGAC 492720
TTAAGGCCAA TAAACCTCC ATATCCAAAA TCAATATTTA TATAAGGAAT TGTAATCATA 492780
ATATTTGCAA TAGGATCTCC TATTCCAATG CCCATTGAAA ATAAGTCATA ATTTTCTTT 492840
TCTTTTATTT CTTTAAGCTT TGCGATACAG GTGGTTGAAT CTTCTTCCTT GCTGCATCTG 492900
ACCATATAAT TGTCAGATGC AAAAGAAAGG TGTGCCATAC CTAATACTAA TGTTAAAATG 492960
TATATTTTTT TAAAAATTTT TATCATTTAT TCTCCACTAT ATATATATTT TTATAAGCC 493020

TGTGCCTAAG AAATTAAATC TAGCTCCTTC AAATGACATT GGGCTGCCAA GTAGCATAGT 493080
TGTTCCAATA GTAGCAACAG CTTTAAATCC AATCACAATA TTTTAAAGAA AGCTGTACTC 493140
TATTACCAA GGCAATCTTA TCACAACCCC TATTCTATTT TGAAGAGAAG CTACTTGTTG 493200
TGCTTCATTT TCTTCCTCTT CTTCAAGTTT TTCATTTGAT TTTTCAGGAC TTCCTTTTGA 493260
CCAATCTGCA CCTATTCCAA TGCCTCCAGA AATCATAGTG TTTTGTGTA TTTCATCTTT 493320
AAATAGAAGA TCTACACCCA TCACAACATA GGGCAAGAAA TTGTTGGGTT TAAGCCCTAC 493380
GAATCCTCCG TACCCAAGGT CTATGTCTAC ATATGGAACA GATATTGTAA TGTTTGCAAG 493440
TGGATATCCA ACTCCAAAAC CTATGCCAAA TAAACGGCGC ACAGACTCTT CTTTTGCAAG 493500
AAGTTTATCA AAATCAAAGT CATCTTCAGT CATACTTTTG CTTTTGGATT GTGCAGCTAA 493560
TAAACCCGTT GTTAATATAA GTATTATTGT TGCTAATAGC ATTCTCATTG AAATTCTCCT 493620
TTTTTATTTT CAATTTTAGA AATTATTTTT ACAATATTTT TAATAAAGCA TAAAAAATTA 493680
AAAATATTGA TATTTATTTG CTTATTTTGA TAGCAAACT TTATTGTTGA ATTTTTTATC 493740
GCTTTGTTTA TCAAGGTTTT GGTTATCAAA AAATTTTTAA TCACAAATAC AGCTATTATT 493800
ATACTACTTG ACTGTATATT GATGTTAATC TTGTTTGTTT GTAAAGGATT TTTGGGAAGA 493860
TATTTTTGTT TTGATTTTTT GGCCTTTGAA AAAAATATAA ATTTATGAAT TTGCAATAAA 493920
TAAGTTTTTT TGCAATGTTT TATTATAAAA CTATGGCAAA AAAACTTTAT TTGCCTCAAG 493980
CTTTTGAAG CTAACCTTAG GCCATTAAAT CTTTTTTTCA AAAATTTATC CCAAAAATTT 494040
AAATATTAAG TTTTAAATCT ATAAACAAAT AGTATATCAA AGTTTGAAT TTGAAATGCT 494100
GTTTTGATAT TATTTTAAGT AAGGCTAAAT TAATTATAAA TAAGATTTAG TAGATAATTT 494160
ATTGTTATTA AACTTATACA AAGCTTATGA TTAAACTATA TATCGTTTTT TTTTATTTTT 494220
TTTCTTTTCT GTTGGGGTTT CCAGAAAATA TTTTTTTTAA AAATTTAGGA TTTTCTAATA 494280
ATGATCGGTA TTTTATGTTT GCGAATATG GTTTTGAAAA TGGATATTAT TACTCTGCTG 494340
CATACTTTGT TGATGTTGTT AAAAATAATT TTGCAAACTC TGGAGTACAT TCTAAGACTT 494400
TTAAAGAGCA CATTGGGTAT TCAGACAGTT ATGATAAAAG TCTTTATGAG CTTTTAAAGA 494460
TGATTAATTT TAAAGTTAAA GAATTTAAAA TTAATCATTT AAGAAGAGGG CGTGAAATTT 494520
ATTTTTATGT AAAAAGTGAA ATTCCAGAAA CAGATTTTTT AAATTTTGTT GATTTTAAAA 494580
CAGAAACGA ATATCAAGTT TTTGTAAATA AGGATATTAA TTCCAAGAA CTTTCTTCTT 494640
CTTTTAATAT TTTTTTATCT GTCAGATATT GTAATTCAAC TCTAGAAAAG CATTTGACTG 494700
TTGGAAGAGG AAATTATTAT AGAAAGAATG TTATTGATTA CAGAATAAGA GAGATTGTTT 494760

TATTTCCAAA	TGAAGATGGA	ATTGTTTTTG	TTTTGGAAAA	AATCATGTTA	AATTCTTATG	494820
GAAATAGGTA	TAAACGGTTT	ATGGTTGAAG	TTAAAAATA	TTGAATATAA	TTATTTAGTT	494880
TTTTAAAGAA	GTGAAATGCT	TTATTGAGGA	TAATTTATGA	GTGATTTTAT	AGCATCAAAA	494940
GAAGATGATT	ATTCTAAATG	GTATTTAGAT	ATAGTCCAGA	AAGCAAACT	TGCTGATTAC	495000
AGTCCTGTAA	AAGGATGTAT	GGTAATTATG	CCTTATGGGT	ATTCTATTTG	GAGTAAAATT	495060
CAGAGTATAC	TTGATAAAAA	ATTTAAAGAG	ACGGGACACG	AGAATGCATA	TTTCCCTATG	495120
CTTATTCCTT	ATAGTTTTTT	AGAAAGAGAA	AAGGATCATA	TTGATGGATT	TTACCCGAG	495180
TTTGCTATTA	TTAAGGATGC	TGGTGGAGAG	AGTTTGGCAG	AGCCTTTGGT	TTTAAGGCCT	495240
ACCTCTGAGA	CAATTATTTG	GAATATGTAT	AGTAAGTGA	TTAAGTCTTA	CAGAGATCTT	495300
CCTCTTAAAA	TTAATCAATG	GGCAAATGTT	GTTTCGTTGGG	AAAAGAGAAC	AAGGCCTTTT	495360
TTGCGCACTA	CCGAATTTCT	ATGGCAAGAA	GGACATACTG	CTCATGCTAC	CGAAGAGGAG	495420
GCATTAGAAG	AACTTTTACT	TATTTTAGAT	GTATATAAAA	GATTCATAGA	AGACTATTTG	495480
GCCATTCCGG	TGTTTTGTGG	TAAAAAATCT	GAAAAGGAAA	AATTTGCGGG	GGCTGTTTCT	495540
ACTTATTCAA	TTGAGGCATT	AATGCAAGAT	AAAAAAGCGC	TTCAAGCCGC	TACATCCCAT	495600
TATTTAGGTT	TAAATTTTGC	AAAGGCATTT	GATGTAAAAT	TTCAAGACAA	AGATGGCAAG	495660
ATGCGGCATG	TATTTGCTAG	TAGCTGGGGT	GTTTCTACCA	GATTGATTGG	TGCTTTGATT	495720
ATGGTTCATT	CTGATGAGAA	AGGTTTAGTT	TTGCCGCCTC	GCATTGCTCC	AATAGAAATT	495780
ATTGTTATTC	CTATTTTTTA	AAAAGAAGAT	GAGATTAATA	AAAAAATTTT	AGATTATTCT	495840
GATTGTGTTG	TGGATGCTTT	AAAAAAAGCA	GAATTTAGGG	TTGAAATTGA	TAAGGACGTT	495900
AGAAGTTCTC	CGGGATTTAG	ATTTTCATCT	GCCGAGTTTA	AAGGAATTCC	AATACGCCTT	495960
GAAGTGGGGA	TAAATGATGT	CCTTTTAAAT	TCCGTTACTA	TTTCAAGAAG	AGATAAAGAC	496020
AGAAAATTTA	AGTATCAAAT	ATCACTTGAT	TCTCTTATAA	GCAAGGTAA	GGTAGAGCTT	496080
GATTTGATGC	AAAAAGATTT	ATTTCAAAGA	GCATTAAATT	TTAGGATCTT	GAATACTAAG	496140
GAGATTTTTA	GAAGCAGTAA	GGATAGTTAT	GAGACATTCA	AAGCCTATGT	GAATGATTAT	496200
TCTGGATTTG	TGCTTTCTTG	TTGGTGTGGC	AGTTTGAATT	GTGAAAATAT	TATTA AAAAT	496260
GAAACTAAAG	CCACAATAAG	ATGTATCCCC	GATGATTTTA	AGGCCAGAGA	TTTAACAGGC	496320
ATGACTTGTA	TTTATTGTTC	ATCTAAAGCT	AAATATTTTG	TTTTATTGTC	CAAATCCTAT	496380
TAATTTGTTT	AGCTTTAATT	AATTTTTTCT	TGATCTTTTA	ATTCTTTGAA	GTTTATTATA	496440
TGAATGATTG	CAATGTTAAA	AGCAAAGTCG	ATTAGTAAAG	CCAAAGAGAT	TAATATCGGC	496500
AGCATTGGTG	TTATGTTTGA	AACATTTAGC	TCTATTCCTT	TTGTATATGT	AGAGCAAAGC	496560

ATTGTAATTA TATAAATTAA ACTATTTGGT ATATGAGGAA ATGCAAAGAC AAAAACAAAT	496620
GATAAAGTGC TCATATAGCT TATTTCATAA ATAGAAATGG GTAAGCTAGA ATATGATTTT	496680
AAAATTATAA AAAATGATAT TACTGAAACA AAAATAGTGC CAAATTTAGA TACAAAATTT	496740
ATTAAAGGTA TGTTTATAAT TATGGATTTT TTTATATTTA TTCTTTCGTT TTTAATATCT	496800
TCTATTAATA TCACATAAGG GGAATAAGAA TCTTTTGCAA GTCCTGAAAA TATTATGTTT	496860
TGAAATGATA CAAAAATGCC TTTATATATC ATTTTAAAAC TTTTGTGTTA TCTATAACTA	496920
ATTGTTGGCA ATATTACGAA TAAAATTATA ATTGTCCATG CAAAAAGAA TGTTATGCTG	496980
TTTGTATAAT TTGGGTAATC TTTGAAGTTT TTTAAGTTTG CAGCGTAATT TGCTGTTATA	497040
AAAATGATCC CTATATTTAA TATGTTTACA ATAAACCCAT TTGCATGGTA AAAAAGATTG	497100
GATGCGCTTA GCATCAGTTC TCTAGCTATT CTGCCTTTTT GTTTTGCATA ATAAAACTT	497160
GTGCCTATTA TTATTGAAAT CATGTAAATG CTTAGTAGAT TTGGATTGCT AGATGTAAAT	497220
ATTTTGAAAA TATTTTTTTG AAAGAATGTT TCTAGTAAAG CTCTTTTTTC AAAAAACAT	497280
GTATTTTGTA TTGTTTTTTC TAGTATTGGA ATTCTTTGCG GAAGATATAT TGTTGCAGCT	497340
ATTATTGATA CAGCAACTCC AGATAGGTTA GTTAAAATTC CATAATAAAT TGTTTTACCA	497400
AAAAGCTTTT TAAAGTTTTT ATTTTCAATA ATATTTTCAA TTCCTAATGG AATTGAAAAT	497460
ATTAAAAAGG GAATAAGAGA TAAGTATGAT AATCTTATAA AAGCATGTGA TAAGGAGCTA	497520
TAAATTCCAA GAGGGAAAAA CAATCCTAAA AAGATTCCAA TAGGCAAAGT GAAAAAAAAA	497580
TTGATTTTTA TATTCATATG ACTTCTCCTT TCAGAGATTT AAGGTACACT GTGTATAATA	497640
AATAGTACTA AATTTTTTTG TAAATATAAA CTTTAGAGTT ACAATTGTAC TTGTGTCGCT	497700
ATATTGCTTG TGGGTGTTTT TGGGGGTAGT TTGTATAAGT ATCCTGATTC TGTAGATACA	497760
GATTTAAATT CGAGATTGCC AAATATTTTA ACTTTAGAGG AGCATGATAA GCAATTTTTT	497820
ACTAAAGATT TTTATAAAAA TCTTATTTCA AGCAGTAAAG AAATTGGCTT TAAGCTTCAT	497880
AAAGTTTTGG TAGATTATTT AAATCCGCAG TCAGAAGAGG TTGATAGGGT TTTAAAAATAT	497940
AATCAAGTGA TTAACATTTA TTGGTCTTTT CTCAGATCAA TTGCAAAAAA CATTTCAAAA	498000
TTGACCATGG AGCAGAAAAT TTTATTTAGA TTTGCCGCAC TTATTCCAAA TGCACTTGGA	498060
TCTGAAATTC AGCTATTAAT TTCAAAACT ATTTGGGACA ATCATTATAA TGAGTCTTTT	498120
ATTTATTTTG ATGAATGGCT TTATGGGGTT AATAATTTTA AGCTTAGTAG ATTAGCAACC	498180
GATTTGCCAA CGGATAATTT TAAAGAAGAA GATATGAAA AAGTTTTACT TAATAAGAAA	498240
GAAAACTTT TGGCAAATAT TGATTTTGCA AAAAGTAGCC TTAAGAGAAC TGATAAGATC	498300

AGAAAAGAGG	CTCTTAGTAA	GTTAAGAAGC	ATGTTTGAAT	TTTTATTTTC	AAATAATAGT	498360
CAAAGCGATT	TAACTTATAT	GA CTGAATAC	GGAGTGCAGA	GTTCTTATCC	TAATTCGATT	498420
TTAAAGCCTT	TAAATTTTGC	TAGTAATTAT	GTTGATGATC	TTATTAAATC	AAATCGGGAT	498480
ATTAATGTTT	TTATTAATAA	AATTGAAGAT	ACTAACAGAG	AGCTTTTTTGA	AATTCAAAAT	498540
AAAATGAATA	ATATTGGGAT	GTCTACTGAA	TCAACTATTG	CACATGATGA	AGTTGAAGTT	498600
ATCAGAAGCG	CCAATAAACT	TGCGATAGGG	CCAAGAGGCA	ATCATTTTCC	TATTCTTTTG	498660
AAAAATAATG	TAGTTGCTAA	CCCTCAATTT	TTTGGAAGTA	GAGAAAGAAT	TATGCAGCTT	498720
GTTTGGGAAA	TCGAAGATAT	TCAGCCTAGA	CTTTTTCAAA	AAGCGTATAG	AGGAGATTTG	498780
CTCAGAGTAG	TTCTTTATTT	TATATTAATA	CCTTCTTATG	GTGATAAAGG	AATTTGTTGG	498840
GAATCAATTG	ATGTTAAAAA	CAGAGCAAAT	GGTAGGGGTA	AAATATTAAT	ACCTATGTAT	498900
GCTAAAAACT	TAAGAAAGGC	GGTTATTTTG	GGTATTGGTG	ATTTTGTTTG	GGAACTTGCA	498960
AAAGAGCAAG	CTTCTTTTAG	GTGGATGGAA	ACAGGAATTA	CAGGCCAATA	TTACGATTAT	499020
TATGTTAAAT	TTATTAAAAA	GGGAAATGTT	AAAAAATTTT	TTTTAGAAGA	TTATTTTCTT	499080
TGGATAGAAA	AAGAAAGTAA	AGGAATTCAA	AACTTGAGA	AATTAGTACG	CGGAATAATG	499140
TGGAGGAATT	TACCCTTTTC	TAAAAATTTA	AAAGAGACGC	TTGCTAAAAA	ATCTTTTATA	499200
TACAAGGATC	TTATTGATAA	AGATAAAAAAT	ATCCAAGCAT	CTGATGGGTA	TTGAATTTAT	499260
TTTCTATTTT	ACTAAAATTC	GA ACTATTTT	TTTGTTTTTA	AGCTTTTTTAA	GTTTTTTTTT	499320
GAAATGTGCG	TCAATGTAAA	TTTTTTTCTT	TTCCAGAGAT	TTAATTAGTT	TTATATTTTC	499380
TGTTTCTATT	GCGGCTTGCA	TTGGTGTTTT	TCTATTTTTA	AGTGTGAAAC	TTAAATCAGC	499440
TCCGCTTTCT	TTTAAAAATT	CAAATATTTT	TTGTTATTA	GTATATATTG	CCCAAAATAT	499500
TGGAGAATAA	CCTGTATCAT	CTATTTGATT	AAGGCTTATT	CCGTAATCTA	TCAATATTTT	499560
TGTGATTTCA	AATTCATTGT	TTATTATTGA	AATTGAAATT	GGAGATATTT	TATATTTAAA	499620
GTTTATTTCT	GCTCCAAGAT	TTAGTGCAAT	TAAAATCCCT	TTTTTATTGT	TGAAAAAAAC	499680
AGATATTATA	AAAAGCTCAT	TTTTGATTTT	TTCTAAACTT	TGTAAGATTT	CTTTGTCATT	499740
TATATTTATT	GAATTTATAA	ATTCATTTAA	AGTGTCTTTA	TCTTTTTTGAT	ATTCTTTGCT	499800
ATTGAAAATA	TATAAATTTT	TTTGCAATTC	TTTTACTATT	GAAGTACTTG	TATTAGTATT	499860
TATTGAGTTT	AAATTCATTA	TTGTTTGCAA	TAACAGTAAA	AGCATAATGA	ATTCTTTTTT	499920
CATGTTTTGT	GAGTTTTGTA	TTCTTTTAAT	AAAGTGTTTA	ATTTTAGACG	ATTGCTTTTT	499980
AAATAGGTAT	TAAATTAACA	TTTATTATAG	GTCATTATAA	GATTATTTTT	CAACGTTTTT	500040
GTGGTCATAA	TTGTCAGTTA	TGAAATGATT	TTTACTATTT	TTTTATATTG	GAGTTTTATG	500100

CTAAATTTTA AATTTAGGCT TTAGTTTTGT TGTTTTAATA TTTTACATT GGTGTTAATG	500160
TAAAATGTGG TGATGTTAAG TTAGTATTTA TAAAAATTTT GACAACTTTT TAAATTGAGG	500220
TGTGCATTTT ATTATGTGTA GTTTATATTG TAAAATACTC TTATGAATCT ATTGGTCAAA	500280
ATTGCTAAAT TTATTTTGAT TTTGTTTTTA TTTACTTCTT GCAACCAAAA GCAAAGCGAG	500340
ATTCAAAATC TTACACATCT TTTAAAATCT TCTAATAAAA ATAGATTAGA TAAATTTCTT	500400
ATTATTGATA GAGTTGTAA CATATATATT GCAAATAAAA ATTATGAAGA TGCTTTAGAA	500460
ATTGTAAATA ATGGAATTAT TGATGATGAA TCTAGAGAAT ATTATCCTTT GTATCTTTAT	500520
TTAATGGGCA ATATTTATGA TTCCATGGGA GAAGATTTTG TAGCTTTTAA TATTTACAAG	500580
CGTGTGTGTG ATAATTTTGA TGATTATGTT TATGAAAACC ATTCAATGAA AACAAGGGTT	500640
GCTAAAAAGA TTGTCAATTT AAATATTGAT TCAATCGATA AAATCAATTA TTACAAATTT	500700
ATATTAAATA TGGGGATTGA TAATTTAAAT AATGAGGAAA AGGGTAATTA TTTTATAAT	500760
CTTGCGCTAA GTTTGGAAGA TGTTCAAGAT TACGATGAAT CTTATTTTAA TTATAAAAAA	500820
TTTCTTTCAA TTCCAAGGGC ACATTTAAAA ATAGATTCTA GAGACTATTT TAATGTTGTT	500880
ACAAAAATTA ATTACTTTAA TAATCCAGAG TTTGTTGTTT ATAGAAATTT AGGAGATTTA	500940
ATCCAGGATG TTAAAAATTT TGTTCTTTCT GGTAATACTT CTAAATTGCT TAATATAAGA	501000
GATAAGAATA ATTTTTTTAT TCAAAGCTGG GATCAAAAGG GTGGAAAGAG TAATTCCATT	501060
AATACTAATA GCTTTTTAAC CACTATGATT AGGCTTGGGG GGAGAAGAAA AAACGGAATA	501120
CAATTTGCAA AGCATCTTGA GGCAGATTCT AGTGACGATA TATCTTATCT TGAGTCAAGG	501180
GGCTGGGACC ATATTCATGA ATGGTATTTT GTTTTTAAAA GAATTGTTTA TCCTAAAGAT	501240
CCAGAAATTA ATAATGGCTG GACTTGGATA GCGTGTATT TAGGTAAAAA ATAATAGGAA	501300
GGAGATAATG CATTTTCTTA AGTTTCTTTT TAGTTATTTA TTTCTACTTT ATTCTAATGT	501360
TTCCATAATA AAGGATGAAG CTGCTGAGAC AAGTGTGCAC AGAATAATCG ATTGGGATAG	501420
GAAGGTTATT TGTTTTGACA TTGTAAAGGA AATTAATGAA AATGAATTTA GACCAGTGGG	501480
TTTAAATACA GCGTCTAAAT TAATAGCAAC CATTAATGAT TTTAAAGACA CGTTAATAAG	501540
AGAATCTCTT TTTAAGATAA TTATGGATTG TGAAAATACT TTTAAGAATT ATTTTGACCT	501600
GAATCCCAGC TTGATACTTA ATTTTTCAGG TCCTAATAGT ATTTTGAAAA GGTCTTATAT	501660
AAAATATTCA GAAGATTTAA GAAGTCTTAC TGTTAGGTAT GAGCTTAGTC TTTTCCCCGA	501720
TTTTATAAAT TTATTTTTTT CACATGAAAC TCCTTATAAA GCTTTTTATC CATTAGTAAA	501780
TTCTGATGTT GATAAAACCG ATTATACAGG AATTGTGATT TATGTAGGCG AAGTCTACAA	501840

TAATACTTCT	GGTTCATAAA	AATTAGAAGA	CTCTTTTTTT	ATCAAAATTT	ATGATGAAAA	501900
CATTAGGCCA	TATTTTGATA	AGAGAATGGT	TTCTTCAGAG	GCTTTGAAAA	AATGGGGAAT	501960
GCTTGAGTAT	AGCAACGATG	TTCTTTTATA	TAATAAAAAT	AGGGTTGGAC	ATCGTCCTTT	502020
AAAAATTGGT	GCCAAAAGTA	TTTATGGTAA	AAATAATACA	GATATTATAC	TTGATGAGTA	502080
TTCTATTAAT	AAGTTGTTTT	CAAATAGTAA	CAACATTAAA	CTTCTGCAAG	ATGGAAAACT	502140
TGTTGTAATA	AAGTAAGAAA	ATTAAATTTA	GTACTTGTTT	TTTTCTAAAC	AATCAACTAA	502200
GATAATAAAG	AGTTTTATAG	GGAATTAGTG	CCCTTATAGC	TCAGTTGGTA	GAGCACCACC	502260
ATGGTAAGGT	GGGGGTCGTC	GGTCAAGTC	CGATTGAGGG	CTTTTATTGG	TAGTTAGGAG	502320
TTTTGTTATA	TGGGTAAAAA	GAAGGGCAAA	GGAGCTGTTG	AGCTTATATC	TTTGATTTGT	502380
GAAGAAACAG	GAATTAGAAA	TTATACCACT	ACTAAGAATA	GACGCAATAA	GCAAGAAAAG	502440
TTAGAATTGA	TGAAATATTG	TCCAAAATTA	CGAAAAACACA	CTCTTCATAA	AGAAGGAAAA	502500
ATAAAATAAT	AAATAATAGG	TCAGTAGTTC	CAACGGTAGA	ACGACAGTCT	CCAAAACGTG	502560
ATGCTGGGGG	TTCAATCCC	TCCTGACCTG	TTGTTAGAAT	TAAAGTGAGG	CTTTAAAGTG	502620
TTTAGGTTTA	TCAAAGATAG	TATCTTAGAG	CTTAAGAAGG	TAACGTGGCC	TAAGTATAAT	502680
GAAGTTGTTG	GAAATGGAAA	GCAAGTTTTT	TGGCTGGTAT	TATTTGTTTC	AATTTTCTTG	502740
GGTATAGTCG	ATTATCTTAT	GTTTCTTGTT	GTAACCTATG	TATTTTAGTT	TTATTATAAG	502800
AAGGGTAAAT	TATGTCTAGA	GCTTGGTATG	TAGTTCAAAC	TTATTCTCAA	TATGAGAAAA	502860
AGATAGAGCA	GGACATAAGG	CTTTTAATAA	ATGAAGGTGT	TTTTGGCGGT	GTGGTATTAG	502920
ATGTTAAGGC	TCCTATTGAA	AAAGTAGAAG	AGATAAGAAA	TGGCAAGAAA	AGAATAAGGG	502980
AGAGAAAAAT	TTGGCCAGGC	TATATTCTTA	TTGAGCTAGA	TCTTCCAGAA	GTAGGCTGGA	503040
AAGATATTAT	TGCTAATATT	ATCAAAGTTC	AAGGCGTTAT	TAATTTTGTT	GGTGTTAGTA	503100
AGGGGCAAAG	GCCTATTCCCT	ATTAATGATG	AAGAAGTAAA	AAGTGTTTTT	ATGCTTACTG	503160
GTGAGATTAA	AGCAAATAAA	TCTATTTTTA	TGCTTTATGA	CTTTGAAGAA	GGAGAAAGAG	503220
TTAGAATTAA	AGGCGGACCT	TTGACTCCT	TTGAAGGACT	TATTAGTTCT	ATTGATTATG	503280
AAAGAAAGAA	ATTAAAAGTT	GCAGTTCAAA	TTTTTGGAAG	ATCAACGCCT	GTTGAAGTTG	503340
ATTTCCAACA	TATAGAAAAG	ATTTAAAATT	TAATACTAAT	GGGAGCTTTG	AAGGCGTTAC	503400
TACCATAAGG	AGATTATATG	GCAAAAAAAA	AAGCAATTTT	TTGGATTAAA	TTGCAGGTTC	503460
CAGCTGCTCA	AGCGGCTCCA	GGAGCTAAAA	TAGGGCAAGC	GCTTGGACCT	CATGGAGTTA	503520
GTGGTCCTCA	GTTTGTAAG	GAATTTAATG	AGAGAACCGC	AAAGATGGAT	CCCGGCATTG	503580
TGGTTCCTGT	TATTATTACT	GTTTATAGTG	ATAAAAGTTT	TTCTTTTATT	GTAAAGACTC	503640

CCCCAGCTTC	GATTTTAATT	AAAAAAGCTA	TTGGGATAGA	ATCAGGATCT	AAGAAATCTA	503700
ATACAGATAA	AGTTGGAACC	ATATCAAAAG	AAAAGTTGAT	GGAGATAGCA	AGAATTAAAA	503760
TGTCTGATTT	AAATGCAAAG	TCAGAATCAG	CAGCGTTTAA	AATTATTGCA	GGAAGTGCAC	503820
GTTCAATGGG	TGTTGAGGTG	GAGAAATAAT	GTCAAAAAAG	GGTAAAAAAT	ATATTGAAGC	503880
TTTTTCTAAA	GTGGATAAGA	ATAAATTTTA	TAACATTGAA	GATGCAATTT	TGCTGTTGAA	503940
AGAAATTAAA	TTTGCCAAAT	TTGATGAAAC	TATAGATATA	TCTATTAACC	TTAATTTAAA	504000
AAAAAATCAT	ACTGTTAGAG	ACACTATAGT	TTTGCCAAAT	CAGTTTATGA	AGCCAAAAAG	504060
AATACTTGTT	TTTGCAAAAG	GTGATCGAGC	AGATGAAGCT	AGAGCTTTTG	GTGCAACTTA	504120
TGTTGGCGAT	GATGATCTTA	TAAATAAGAT	TAAAAGCGGT	TGGGATGAAT	TTGATGTTGT	504180
TGTTGCAACT	CCTGATATGA	TGAAAGATGT	TGGAAGACTT	GGTCCTATTT	TAGGGAAAAG	504240
GGGTTTAATG	CCCAATCCAA	AGACTCAAAC	AGTCACAAAT	AATCTTAAAG	ATGCAATCAA	504300
CAGTCTTAAA	AAGGGTCGAA	CAGAATTTAG	GGCAAATAAA	AATGGTGTA	TAAGCTTTTC	504360
TTTTGGTAAA	TCTTCTATGG	ACAATGAAAA	GATAAAAGAA	AATTATGAGG	AATTTGTCAA	504420
GGAAGTTGTT	AAAAAAGAC	CGAGTGACTT	AAAGGGAGCT	TTTATAGATA	GTATTTATAT	504480
TTCATCTACT	ATGGGGCCTT	CTATAAAAGT	TAATTTTGTT	TGGAGGTAAC	ATTATGAGCG	504540
CAAAGATAAA	TGCTAAAAAG	TTGGAAATGT	TTGATTTATT	AAAACAGTTT	ATAGATAGCA	504600
AACAAAATCT	TTTTTTCTTA	GATTATAGAG	GTTTAAATGT	AGCTCAGTTA	ACAGAACTTC	504660
GCAATAAAAT	AGAAGGCGAA	CATGGATCAT	TAAAAGTTGT	TAAAAACAAT	ATAATGAAGA	504720
TGGTTTTTAAA	AGAAAAGAAT	ATTAATGTTG	TTGATTCTTG	TTTGGTTGGC	CCTACAGTTG	504780
TTGTTACTGC	ATTAGAAGAA	GCTAATGTAA	TAGCAAAAAT	TTTTTATGAT	TTTGTAAAAA	504840
GTAGTACTTT	AAAAGTAAAG	GGCGGTTTTG	TATTAGGAGA	GTTTTATGAT	GAGGC'TAAGG	504900
TTCAAGCTTA	CAGCAAGCTT	CCTACCAAAA	AAGAGTCTAT	TTCTTTATTT	GCTAGCGTGT	504960
TAAAAGCGCC	AGTTTCTAAG	CTTGCAAGAA	CATTGAAAGC	TTTGGCTGAT	GTTAAAAATT	505020
AACATGACAG	TGTTAGTCTT	AATTTTTGAG	TGCATGCTAT	CACTGTGAAA	TGAAAATATA	505080
TAAGGAGTTA	ATATGGCACT	AAATAAAGAA	GATATTTTAA	CCTGGCTTGA	AGGTGCAAAA	505140
ACTATGGAAG	TTGTTGACCT	TGTAACAGCT	ATTGAGGAAA	AGTTTGAGT	AACTGCCGCT	505200
GTTGCTGCTG	GTGTAGGGGG	AGCTGTTTCA	GTAGGTTTCGG	CTGATTCTGA	AGAACAAACC	505260
GAATTTGATG	TAATTCCTAT	GTCTTTTGGT	GATAGCAAGA	TAAATGTTAT	AAAAGAAGTT	505320
AGAGCTATTA	CAGGACTTGG	TCTTGGAGAA	GCTAAGGCGT	TAGTTGAAGC	CGCTCCTAAA	505380

GCTATTAAAG AAGGTCTTTC TAAGTCAGAT GCTGAAGAAT TAAAAAAGAA ACTTGAGGCA	505440
GTTGGCGCAA AAGTTGAAGT TAAATAAAAA ATTAAAAATA TATCAAAGTT GTTATTCCGC	505500
ATGTCGTTAT GATGTGCGGC TTGTTATGTC TTAAAAAAGG AGTCTTTTAA TGATAAAAAG	505560
AGTTCATCTG GGACAAGGAA GAGCTGATGA GATTTTAGAC CTACCTAACC TGATAGAAAT	505620
ACAATTAAAT TCTTATGAAA AATTTTTTACA ACTTGATAAA TTAAAAAGTA AAAAACCTTT	505680
ACTTAATGAG GGCCTTGAGT CTGTTTTTAG AAATATATTT CCCATTAAAA GTGGAAATGG	505740
TGATGTTGCT CTTGAGTATG AAAGATACTA TATAGAAAAC GATGCCCTTA ATTTTACAGA	505800
AAAAGAATGT AAAAGAAAGG GTCAAAGTTA TGAGGCTGTT TTAAAAGTAA GATTGAATTT	505860
GCAATTTTTG ACTACTGGGG AAATAAGGCA AAAAGACGTA TACATGGGAA CTATTCCTTT	505920
AATGACAGAA AGAGGCACTT TTATTATTAA TGGGGCTGAG AGGGTTGTTG TTTCTCAGAT	505980
TCACAGATCC CCAGGAGTTG TTTTTTATAA AGAAAAAGAT TTGTATTCTG CTAGAATAAT	506040
TCCTTATCGT GGTCTTGGT TAGAATTTGA GATTGATTCA AAAAAAGATT ATCTTTATGT	506100
AAAAATAGAT AGAAAAAAA GAATACTTAT AACTCTTTTT TTAAGAGCTT TAGGGTTTGA	506160
TACGAGAGAA AAAATAATAG AAACTTTTTA CAATATTAAA AAAATTAAAG TTGAAGACGG	506220
TACAAAAAGA GATCTTCCAG GGCAATATTT AGCTAAGAGT ATTAACATAA GAGAGAATAT	506280
GTATTATCGT GCAGGAGATA AAATTACTCT GCAAGATGTT GAAGATTTTT TACAAAATGG	506340
AGTAAATGAA ATAGAGCTTG TTGATTTTGA TGGTTATAAT GATATTTCTG GAAAGCGCTT	506400
TGTAAGTTCG AATGTTATTC TAAATTGTCT TGAAAAAGAG GATGCTTTCT TTGCTTTAAA	506460
GGATGGCTCT AAAGAGCTTC CAAAAGAATC AGTTATGCTA GCTGTTTATG GTTCTCTTTT	506520
TCCCGGTGAG CCAATATCAA TTGATAATGC TGAAAACGAT TTAAAAACCA TATTCTTTTC	506580
TGAAAGAAGA TATGATCTTG GACGTGTGGG GCGGTATAAA CTTTCTAAAA AATTGGAAT	506640
TGATGATTTA ACTACATCGG TTTTAACTAT GGATGATATT GTTAACACCA TATCTCATCT	506700
TTTAAGAATA TATGAAGGCC ATGATATTCT TGATGATATT GACCATTTAG GAAATAGAAG	506760
GGTTCGTTCT GTTGGTGAGC TTC'TTACTAA TATATATAAA GGCGCGATGT CAAGAGTTGA	506820
AAAAATTGCT AAAGATAGAA TGTCTAACAA GGAAGTTTTT AATCTAAAGC CTCAAGAATT	506880
AATAAGCGTT AAGCCTATTG TATCTGCTGT TAAAGAATTT TTTGCAACCA GTCAGCTTTC	506940
ACAGTTTATG GATCAGGTCA ATCCTTTGGC TGAGCTTACT CACAAAAGGC GTCTTAATGC	507000
TCTTGGACCA GGAGGACTTT CAAGAGATAG GGCAGGATTT GAAGTAAGAG ATGTGCATTA	507060
TACTCATTAT GGTAGAATGT GTCCTATTGA AACCCCTGAA GGGCCAAATA TTGGACTTAT	507120
TGTTTCTTTG GCTACTTATT CTAGAGTTAA TGATTATGGT TTTT TAGAAA CTCCTTATAG	507180

GAAAGTTGTT AATGGAGTGG TGACGGACCA ATTAGAATAT TTATCTGCTA TTGACGAAGA 507240
GAAAAAGTGT ATTGCTCAGG CTAATGCTGC TTTTAATTCT AATGGAAAGT ATCTTGAAGA 507300
TTTAGTTTCT GTTAGAATTT CTGGTGATTA TACTACAACA AGTCCCACAA ATATAGACTA 507360
TATGGACGTT TCTCCTAGGC AGCTAATTTT AGTATCTTCG GCGTTAATTC CTTTTCTTGA 507420
GCACAATGAT GCAAATCGAG CTCTTATGGG TTCTAATATG CAAAGACAAG CAGTACCTTT 507480
GCTTTTCCCT AAGCCTCCTA TTGTTGGTAC GGGTATGGAA AGCGTTGTTG CAAAGGATTC 507540
AGGAGTAGTT GTTAAGGCTA AAAGAAGTGG GGAAGTTATT CTTGCAACAA GTAGTAAGAT 507600
AGTTGTTAAA CCTTTTGAGG CAGAGAATGC TAAAGATTTA GATGAATATC ATATTGTTAA 507660
GTATGAAAGG ACAAATCAAG ACACTTGTTT TAATCAATCC GTTTTAGTTA AAGAGGGTCA 507720
AAAAGTTGAA AGGGGCGAGA TAATAGCTGA CGGTCCTGCT ACTAGATATG GAGAACTTGC 507780
TCTTGGAAT AATTTATTGC TAGGAGTTAT TCCTTGAAT GGATTTAATT ATGAGGATGC 507840
TATATTAATT TCTGATAGAA TTGTAAAGGA AGATCTTTAT ACATCTATTC ATATCAAAGA 507900
ATTTAGCATA GAGGTAAGAG AACTAAACT TGGTCCTGAG AAAGTTACAG GAGATATACC 507960
TAATGTTAGT GAAAAGATAT TAAATAAATT GGATGAAAAT GGGATTATAC GGATAGGAAC 508020
TTATGTAAAG CCCGGTGATA TTCTGGTTGG TAAAGTTACT CCAAAGTCAG AAGGAGACAT 508080
TACTCCTGAA TTTAGACTGT TAACTTCCAT TTTTGGAGAA AAAGCAAAAG ATGTTAAAAA 508140
TAATTCATTA AAAGTTCCTC ATGGTACTGA AGGTACAGTT ATTGATGTTT AAAGGATTAC 508200
CAAAGAGGAT GTTGGTAATC TTTCTCCTGG AGTTGAGGAG ATACTTAAAG TTTATGTTGC 508260
CAAAAAAAGG AAGCTTAAAG AGGGCGATAA AATGGCTGGA CGACATGGTA ATAAGGGTGT 508320
TGTTGCAAAG ATTCTTCCTG TTGAAGATAT GCCTTATCTT GCAGACGGAA CCCCTCTTGA 508380
TATATGCTTA AATCCTTTGG GAGTTCCATC TAGAATGAAT ATCGGACAGT TAATGGAATC 508440
TCAATTAGGC CTTGCTGGTA AATATCTTGG TGAATCTTAT AATGTTCTTG TTTTGAATC 508500
TGCTACAAAT GAACAAATTC AGGAAAAATT AAAAAGTCTT GGATTTAATC CAACTTCTAA 508560
AGAAATTTTA TATGATGGTT ATACAGGAGA GCCGTTTCGAA AATGAAGTAA TGGTTGGGGT 508620
GATTTACATG CTTAAACTAC ACCATCTTGT TGATGATAAA ATGCACGCAA GATCAACAGG 508680
CCCATATTCT CTTGTTTCTC AGCAACCTCT TGGAGGAAAG GCTCAATTTG GTGGGCAAAG 508740
ACTTGGAGAA ATGGAGGTTT GGGCTCTTGA AGCTTATGGT GCGGCGCACA CCCTTCAAGA 508800
ACTTTTAACA GTTAAATCTG ATGATATGTC AGGCAGAGTT AAAATATATG AAAATATAGT 508860
AAAAGGCGTT CCTACTAATG TATCAGGGAT TCCTGAGTCT TTTAATGTGC TAATGCAAGA 508920

GCTTAGAGGG	CTTGGA	CTTG	ATTTGTCAAT	TTATGATGAT	GCTGGGAATC	AGGTTCCCTTT	508980
GACAGAAAAA	GAAGAAGAAT	TGATTAATAA	AAGCTAGGTT	TTTGAGGTTT	TTATGAAAGA		509040
GATAAAAGAT	TTTGAAAGAA	TAAAAATTAA	AATAGCGTCT	CCCGATCAAA	TTAGAAATTG		509100
GTCTTATGGA	GAGGTTAAAA	AGTCCGAAAC	TATTAATTAT	AGAACTTTAA	GACCCGAAAA		509160
AGATGGGCTT	TTTTGTGAAA	GGATTTTTTG	TACTACAAAG	GAATGGGAAT	GTTATTGTGG		509220
TAAATTTAAA	TCGGTCAGAT	ATAAAGGTAT	TATTTGTGAT	CGTTGTAATG	TAGAGGTTAC		509280
CCATTTTAAG	GTTAGACGTG	AAAGAATGGG	GCATATTGAG	CTAGCAGCCC	CAGTTGCTCA		509340
TATTTGGTAT	TACAAATATA	TACCCTCTAG	GATTGGGCTT	TTGCTTGATA	TTACAGCATC		509400
TAGTTTGAAT	TCTATTCTTT	ATTATGAAAA	ATATGTAGTA	ATTGAACCGG	GCGATACTGA		509460
TCTTAAAAAA	ATGCAGCTTT	TAAATGAAGA	TGAGTACATA	GAAGCTAGAG	AGCGATATGG		509520
TATGTCTTTT	AATGCTTCAA	TGGGGGCTGA	GGCTATTAAA	ACTCTTCTTG	AAAATCTTGA		509580
TCTTGATGAG	CTTTCGTCTA	AGCTTAGAAT	TCAAATGATA	GATAAAGATG	ATAAACTGA		509640
TAAGAACTC	TTAAGACGTC	TTGAAATTAT	TGAGAATTTT	AAAATTTCTG	GCAATAAGCC		509700
AGAGTGGATG	ATTATGGAAG	TTCTTCCTGT	TATTCCTCCA	GAGATTAGGC	CAATGGTTCA		509760
GCTTGATGGG	GGGCGCTTTG	CAACATCTGA	TCTTAATGAT	CTTTATAGAA	GAGTCATAAA		509820
TAGAAATAAT	CGTTTAAGAA	AGTTGCTTCT	TCTTAATGCG	CCAGAGATTA	TTGTGAGAAA		509880
CGAAAAAAGA	ATGCTTCAAG	AATCAGTAGA	CTCTCTTTTT	GACAATTCTC	ATAAAAGAAA		509940
GGTTGTCAAA	GGTTCATCTA	GTAGGCCTCT	CAAGTCGCTT	TCCGATGCAT	TAAAAGGTAA		510000
GCAGGGAAGG	TTTAGGCAAA	ATCTTCTTGG	TAAAAGAGTA	GATTATTCTG	GTCGTTCTGT		510060
TATTGTTGTT	GGACCTGAGC	TTAAGCTACA	TCAATGTGGA	TTGCCTGCAA	AAATGGCCCT		510120
TGAGCTTTTT	AAGCCTTTTG	TGATAAGAAG	ACTGATTGAG	AGTGAAGCTG	TTTTTAATAT		510180
CAAAAGAGCA	AAGAATTTAA	TAGAGCAAGA	AGTAGATGAG	GTGTGGCAAA	TTTGTAGATCT		510240
TGTTATCAAA	GAGCATCCTA	TTCTTTTAAA	TAGGGCACCC	ACTCTTCATA	GACTTGGAAT		510300
TCAAGCTTTT	GAACCTGTGT	TAGTTGAGGG	TAAGGCAATA	AAATTACATC	CTCTTGTTTG		510360
TCATGCATAC	AATGCCGATT	TTGATGGTGA	TCAAATGGCG	GTACATGTGC	CTCTTACTCC		510420
GGCAGCACAA	GCTGAAAGTT	GGGCTTTAAT	GCTTTCAACA	AATAATCTTT	TAAATCCTGC		510480
CAATGGGCAT	CCTATTGTTT	TTCCATCCCA	AGATATTGTT	TTGGGCCTAT	ATTATTTAAC		510540
TATGGAAAAA	AAGAATGTTG	TTGGAGAAGG	TAAAAAGTTT	TTAAACTTTA	ACAATGTTAT		510600
TCTTGCCATA	AATAATAGGA	GTCTGGATTA	CAATGCTTCT	ATTTATGTAA	AAATTCATGG		510660
TGAGTACAAA	AAAACACGG	CCGGTAGGGT	TATATTTAAT	GAGGCTTTGC	CCAAGGGAAT		510720

TGAATTTGTA AATAAAACCC TTAGTGATTT GGAGCTACAA ATTTTAATAT CAAAAGTTTA	510780
TGTAGTTCAT GGTTCCTCTA TCGTAATTGA AATGCTTGAC ATCATCAAGG AACTTGGTTT	510840
TAGGTATGCC ACTAAGTTTG GATGCACAAT TAGTATGAGC GATATTATTG TTCCTGATGA	510900
AAAAAGAACT TATGTAGAAA GGGCCAATAA AGAGATTGCT AAGATTCAAA ATGATTATGC	510960
TAAAGGTGTT ATTACTGGCG AAGAGCGTTA TAACAATGTA GTTCTGTGTTT GGTAAAGAC	511020
CAATGAAGAA CTTACTAATA AGATGATGGA AATTTTAAAG AAAGATAGAG ATGGATTTAA	511080
TGTTATATAT ATGATGGCAG ATTCTGGTGC TAGGGGTAGT AGGAATCAAA TAAGACAGCT	511140
TGCTGGTATG AGAGGATTGA TGGCAAAAAC TTCTGGGGAT ATTATTGAGC TTCCAATTAT	511200
TTCTAACTTT AAAGAAGGTC TTTCTGTGAT AGAGTTTTTT ATATCTACAA ATGGAGCAAG	511260
AAAAGGTCTA GCAGATACTG CTCTTAAGAC CGCTGATGCT GGATATTTAA CTCGAAGATT	511320
AGTAGACATT GCTCAAGATG TTGTTGTTAG AATAGAGGAT TGTGGAAC TAATGGAAT	511380
AAAAGTTGAG ACTGTAAAAA ATGGTGAAGA AATATTAGAA TCTTTGAAAG AAAAAGCTGT	511440
TGGGAGTTAT TCTATTGAAA GAATAAAAAA TCCAATTACT GGCGAGATTG TTTTAGATGC	511500
AAATGAAGAA ATCTCAGAAG CTAAAATAGA ATTATTAGAG AAAATTGGTA TTGAAAAACT	511560
TGTTATTAGA TCTGTTTTAA CGTGTGAAGC TGAGCATGGC GTTTGTCAAA AATGTTATGG	511620
TAGAGACTTT TCTAAGAACA AACCTGTTAA TATTGGGGAG GCTGTGGGAA TAATTGCTGC	511680
TCAGTCCATA GGTCAACCGG GTACTCAATT AACCATGAGA ACTTTTCATA TTGGTGGAGT	511740
TGCTCAGGCT GGCAGTGAGG ATGATAAAAT ATCTTTAAAG AATGCCTTCA TACTTAATGG	511800
CATAGAAGGT TTTAATGTTA GAGTTGATAA TGGAATTCTT TTCACAAGAA AAGGAACTTT	511860
AAAAATAATC AATGTTTTTT ATGAGGAAAA AATTAAGAAC ATAAAAGAGA TTAAAGTTTT	511920
AGATTCTCAA AGAGTAATAA AAGGAATTCC TTTGTTTATT GATAAAAAGG GCTCAGAGAT	511980
TCTCTCTTCT TACATTGGTT ATGTTAAATT AAGAGACGAT AATTTTTTCA TAGTGTCAGA	512040
AGAGCAAGAA GTTTCCTTGA AAGCGGGTAC AAAGCTTGAA ATAGAGGTTG GTGATTATGT	512100
TGAATCAGGC AAAGTTATTG GTACATTTGA TCCATTTGCA GAGCCTATTA TTGCAGAGGT	512160
TAAGGGTAAA ATTAAATTTA AGGATATTAT TTTAGGAACT ACTCTTAAAG AGGAAATAAA	512220
TACTGAAACA GGCAATGTTG AAAAAAGAAT TACAGATAAT GTTTTGAAT CTCTTGATCC	512280
TAGAATTTTT ATTATTGATA GTAGTGGTAT GGAGGTTGCA TCTTATGTAT TACCAGGTGA	512340
TGCTTATCTT CAAGTTGAAG ATGGCCAGAG TATTAACATA GGAGATATTA TTGCGAAACT	512400
TTCTAAAGGT TCTGAAAAAA CTCAAGATAT TACAGGGGGA TTGCCTCGTG TTAATGATCT	512460

TTTTGAGACA AGAATTCCTA AGAATTTAAC TGAAATGGCT AAAGTAAGCG GAATTGTACA	512520
ATTTAAATCA ATTCAAAAAG GTAAAAGGCT TATTAATATT TTAGATGAGT ATGGGGTTGA	512580
ACATAAGCAT TATATTCCAG CTGGAAAACA TCTTTTGGTT AGAGATGGAG ATGTTGTAAA	512640
AGCAGGAGAT ATGCTTTGTG ATGGTAGAAT TAATCCTCAT GATGTGCTTG AAATTTTAGG	512700
TGGGATTAGT TTACAAGAAT TTCTGTTGGC AGAAATTCAG GATGTTTATC GAAAACAGGG	512760
TGTTAGCATT AATGACAAAC ATATTGGTGT GATAATCAAG CAAATGATGA AAAAAGTTAA	512820
GATTGTTGCA GTTGGTGATA CTAATTTTGT TTATGGGCAA AAGGTAGATA AGCACACTTT	512880
TTATGAGCAA AATAGAAAAG TAATCGAACA AGGTGGTGAG CCAGCAATAG CAAGTCCAAT	512940
TCTTATAGGA GTAACATAAA CGTCTCTTAA TATAGATTCT TTTATTTCCG CAGCTTCTTT	513000
CCAGGAAACA ACAAAGTAT TAACAGATGC TTCTATTGCT GGAAAAATAG ATGATCTTAG	513060
GGGATTAAAA GAAAATGTTG TAATTGGACA TTTAATTCCT ACTGGAAGTG GTATGGGTCT	513120
TTATAAAAAA ATTAAAGTTA GTGAAAATAT CGATTCTGAA GTTTAACTTG AAAATAAGTG	513180
ATATATTTGC TACCATTTTA TTAATAGTTT CAAGAAAAGG AGAGCGTTGA TAAATGCCTA	513240
CAATTAATCA GTTAATTAGA AAGCCTAGAA AAAGTCAAAC GGAGAAGACC GCATCTCCTG	513300
CGCTTCAAAA TTGTCCTCAA AGAAGAGGAA TTTGTACGCG TGTAATGACC GTAACCTCCA	513360
AAAAGCCTAA TTCAGCTTTA AGAAAAGTAG CGCGTGTTAG ACTTTCAAAT GGATTGGAAG	513420
TAACAGCATA TATTCCAGGA ATTGGACACA ATTTACAAGA AACTCTGTG GTTCTAATTA	513480
GAGGTGGTCG AGTTAAAGAT TTGCCTGGAG TAAGGTACCA TATTGTTAGA GGAGCTAAGG	513540
ATACCCCTGG CGTTAATAAT AGGAAAAAGG GTAGATCTAA GTATGGAACA AAAAAGCCTA	513600
AAGCTTAACT GAAAGGTGGG TTAATATTAA ATATGTCAAG AAAAAATAAA AAAATCAAAA	513660
AGAAAGTTTT TGTGATACC AGATATAATT CTAGAATTGT TGCAAAGTTT GCAAATAGAA	513720
TGATGTATGA TGGAAAAAAA TCAATAAGCG AGAGTATACT TTATAGTTCA ATTGATTTGC	513780
TTGCCGATAA GCTTGAAGAA AGCGACAAGA TGGCTGTTTT TTATAAAGCT TTAGATAATA	513840
TTAAGCCATT GGTAGAAGTA AGAAGTAGAC GAGTGGGTGG TGCTACATAT CAAGTTCCTG	513900
TTGAAGTTAG AGAAGAGAGA AGAGAAGCCT TGGCTATGAA GTGGATTATT TTTGCTGCTA	513960
GAAAGTCTAG CGGTAGGTCT ATGAAAGAAA AGTTGTCAAA CGAACTTTTA AATGCATATA	514020
ATTCTACTGG AGCTGCTTTC AAGAAGAAAG AAGATACTCA TAGAATGGCT GAAGCAAATA	514080
AAGCTTTTAC TCATTATAGA TGGTAAAAAG ACACCTTTTT AAGGTGTCTT TTTTGTTTA	514140
TATGCCGTGT ATTATGAGAT CTATTTTTTG TATTTTTTTA TTAAAAGCAA GGAGGATATT	514200
TTTATGTTAA AAAAAGTTTA TTATTTTTTA ATTTTTTTAT TTATTGTTGC TTGTTCTAGC	514260

TCTGATGATG GCAAGTCGGA GGCAAAAACA GTTTCGCTTA TAGTTGATGG TGCTTTTGAT 514320
GATAAAGGAT TTAATGAAAG TTCTTCTAAG GCGATAAGAA AATTAAAGGC AGATTTAAAT 514380
ATAAATATAA TTGAAAAAGC ATCTACAGGC AATTCTTATT TAGGAGATAT TGCAAACCTTA 514440
GAAGATGGTA ATTCAAATTT GATTTGGGGA ATTGGGTTTA GATTGTCAGA CATTCCTTTTT 514500
CAAAGAGCTA GCGAGAATGT TTCTGTTAAT TATGCAATCA TAGAAGGGGT TTATGATGAA 514560
ATTCAAATAC CCAAAAATCT TCTTAATATT AGTTTTAGAT CCGAAGAGGT GGCTTTTTTA 514620
GCAGGATACT TTGCGTCGAA GGCTTCTAAA ACGGGTAAGA TTGGATTTGT TGGAGGAGTG 514680
AGGGGAAAAG TTTTAGAATC TTTTATGTAT GGATATGAAG CTGGTGCTAA GTATGCAAAC 514740
TCTAATATTA AAGTGGTCTC TCAATACGTT GGTACATTTG GAGACTTTGG ACTTGGTCGT 514800
TCAACGGCAT CTAATATGTA TCGAGATGGG GTTGATATCA TATTTGCAGC TGCAGGGCTT 514860
TCTGGTATAG GGGTAATTGA GGCCGCAAAA GAGTTGGGGC CCGATCATT AATTATTGGA 514920
GTCGATCAGG ATCAATCATA TCTTGCTCCT AACAATGTTA TTGTTTCTGC TGTAAAAAA 514980
GTTGATTCAT TGATGTATAG TTTAACAAAA AAGTATTTAG AAAGTGGAGT TTTGGATGGT 515040
GGCAAGACCA TGTTTTTAGG GCTTAAAGAA GATGGTCTTG GTTTAGTTTT AAATGAAAAC 515100
TTAAATCAA ATTATTCTGA GATTTATAAC AAATCATTGA AAATTGGGCA AAGTATAATG 515160
AATGGTATAA TAAAAGTGCC TTATGACAAG GTATCTTATG ATAACCTTGT TTTGCAAATG 515220
GAAAATTAAT TTGATTTTTA TTGAGCTGAT TTGTGAAAAA TCTTTTTAAT TCTTTAAAGA 515280
TGTTTTAAAG GGTTTTTTAA TTGTTGTAAT TTGAATTTAA ATTAATCTTG CAAAAGGGTT 515340
TAAATTTGGA TATTATGGTG ATGTAGGAAA AATTATTTTT CCTACTACTG TGTTTTTATT 515400
AATGCTAGAA GTATTTTTTT AAAAGGGATT ATTAATTTT TATTTTATAA ATAAAGAATA 515460
CTACTTGTTA GTAAAATAAA GTTAATATTT TAATTTTTAA AAAATTTAGA ATTTTTAAAA 515520
AAAATATAAG GAGAGGATTA ATTTTGTTTA AAAGATTTAT TTTTATTACT TTATCTTTAT 515580
TAGTATTTGC TTGTTTTTAA TCTAATAAAA AGTCTATTAA ATCTGACAAA GTTGTTGTAG 515640
GTGTTTTGGC TCATGGTAGC TTTTATGATA AAGGCTATAA TCAAAGCGTT CATGATGGTG 515700
TTGTAAACT TAGGGATAAT TTTGGAATAA AGCTTATAAC TAAATCTTTA AGACCTTATC 515760
CTATTGAGGG TAAAAGACTT CTTACTGTTG ATGAGGCAAT GACTGAGGAT GCTTATGAGG 515820
TTCAAAAAA TCCTTTAAAT CTTTTTTGGT TGATTGGATA CCGATTTTCT GACTTGTCAG 515880
TTAAGCTTTC CTATGAACGT CCAGATATTT ATTATGGTAT TATAGATGCT TTTGATTATG 515940
GTGATATTCA AGTTCCTAAG AATTCCTTGG CTATTAAGTT TAGAAATGAA GAGGCTGCAT 516000

TTTTAGCTGG GTATATTGCT GCTAAGATGA GCAGAAAAGA AAAGATTGGA TTTTAAACAG	516060
GTCCTATGAG TGAGCATGTA AAAGATTTTA AGTTTGGTTT TAAGGCTGGA ATTTTTTATG	516120
CCAATCCTAA ATTAAGATTA GTTCAAAAA AAGCACCTTC TCTTTTGAT AAGGAGAAAG	516180
GCAAAGCAAT GGCTCTATTC ATGTATAAAG AAGATAAAGT AGGCGTTATT TTTCCAATAG	516240
CTGGTATAAC TGGTCTTGGA GTTTATGACG CTGCTAAGGA GCTTGGACCT AAATATTATG	516300
TTATTGGTTT AAATCAAGAT CAATCATATA TTGCGCCTCA AAATGTTATT ACTTCAATAA	516360
TTAAGGATAT TGGTAAGGTT ATTTATTCTA TTTCATCAGA GTATATTAAT AATAGAGTTT	516420
TTAAGGGTGG AATTATTATT GATCGGGGGT TAAAGGAAGG AGTAATAGAA ATTGTTAAGG	516480
ATCCCGATGT TTTAAACAAT AGGTGGTTG ATGAAGTTAT TGATCTAGAA AATAAAATAA	516540
TAAGTGAGGA AATTATTGTT CCTGATAGTG AATATGCATT TGATTTATTT AAATCAAAGT	516600
TATAAACTAC TTAAATATAG CTTTGTGTGT AAAGGGGAAA TAGTTTATGA ATAAATATT	516660
GTTGTTGATT TTGCTTGAGA GTATTGTTTT TTTATCTTGT AGTGGTAAAG GTAGTCTTGG	516720
GAGCGAAATT CCTAAGGTAT CTTTAATAAT TGATGGAAC TTTGATGATA AATCTTTTAA	516780
TGAGAGTGCT TTAAATGGCG TAAAAAAGT TAAAGAAGAA TTTAAATTG AGCTTGTTTT	516840
AAAAGAATCC TCATCAAATT CTTATTTATC TGATCTTGAA GGGCTTAAGG ATGCGGGCTC	516900
AGATTTAATT TGGCTTATTG GGTATAGATT TAGCGATGTG GCCAAGGTTG CGGCTCTTCA	516960
AAATCCCGAT ATGAAATATG CAATTATTGA TCCTATTTAT TCTAACGATC CTATTCCTGC	517020
AAATTTGGTG GGCATGACCT TTAGAGCTCA AGAGGGTGCA TTTTAAACGG GTTATATTGC	517080
TGCAAACTT TCTAAACAG GTAAATTGG ATTTTTAGGG GGAATAGAAG GCGAGATAGT	517140
AGATGCTTTT AGGTATGGGT ATGAAGCTGG TGCTAAGTAT GCTAATAAAG ATATAAAGAT	517200
ATCTACTCAG TATATTGGTA GTTTTGCTGA CCTGAAGCT GGTAGAAGCG TTGCAACTAG	517260
GATGTATTCT GATGAGATAG ACATTATTCA TCATGCTGCA GGCTTGAG GAATTGGGGC	517320
TATTGAGGTT GCAAAAGAAC TTGGTTCTGG GCATTACATT ATTGGAGTTG ATGAAGATCA	517380
AGCATATCTT GCTCCTGACA ATGTAATAAC ATCTACAAC AAAGATGTTG GTAGAGCTTT	517440
AAATATTTTT ACATCTAACC ATTTAAAAAC TAATACTTTC GAAGGTGGCA AATTAATAAA	517500
TTATGGCCTT AAAGAAGGAG TTGTGGGGTT TGTAAGAAAT CCTAAAATGA TTTCTTTGA	517560
ACTTGAAAAA GAAATTGACA ATCTTCTAG CAAAATAATC AACAAAGAAA TTATTGTTCC	517620
ATCTAATAAA GAAAGTTATG AGAAGTTTCT TAAAGAATTT ATTTAAATAA AGAATCAATT	517680
TATATATTTT ATTTTAAAGT ATAAAAACA CATTGTTTTT GTTTGAATAA TTGAAATGGA	517740
GAAGTGCTTT ATATGAGAAT TGTAATTTTT ATATTCGGTA TTTTGTGAC TTCTTGCTTT	517800

AGTAGAAATG GAATAGAATC TAGTTCAAAA AAAATTAAGA TATCCATGTT GGTAGATGGT 517860
GTTCTTGACG ACAAATCTTT TAATTCTAGT GCTAATGAGG CTTTATTACG CTTGAAAAAA 517920
GATTTTCCAG AAAATATTGA AGAAGTTTTT TCTTGTGCTA TTTCTGGAGT TTATTCTAGT 517980
TATGTTTCAG ATCTTGATAA TTTAAAAAGG AATGGCTCAG ACTTGATTTG GCTTGTAGGG 518040
TACATGCTTA CGGACGCATC TTTATTGGTT TCATCGGAGA ATCCAAAAAT TAGCTATGGA 518100
ATAATAGATC CCATTTATGG TGATGATGTT CAGATTCCTG AAAACTTGAT TGCTGTTGTT 518160
TTCAGAGTAG AGCCAAGGTG CTTTTTTGGC TGGCTATATT GCAGCCAAAA AAAGCTTTTC 518220
TGGCAAAATA GGTTTTATAG GGGGAATGAA GGGTAATATA GTAGATGCAT TTCGCTATGG 518280
TTATGAATCT GGAGCAAAGT ATGCTAATAA AGATATAGAG ATTATAAGTG AATATTCCAA 518340
TTCTTTTTCC GATGTTGATA TTGGTAGAAC CATAGCTAGT AAAATGTATT CTAAAGGGAT 518400
AGATGTAATT CATTTTGCAG CTGGTTTAGC AGGAATTGGT GTTATTGAGA CAGCAAAAAA 518460
CCTTGGCGAT GGTTACTATG TTATTGGAGC CGATCAGGAT CAGTCATATC TTGCTCCTAA 518520
AAATTTTATT ACTTCTGTTA TAAAAACAT TGGGGACGCA TTGTATTTGA TTAAGGCGA 518580
ATATATTAAA AATAATAATG TTTGGGAAGG TGGAAAAGTT GTTCAAATGG GATTAAGAGA 518640
TGGTGTTATT GGGCTGCCTA ATGCGAATGA ATTTGAATAC ATAAAAGTTC TTGAGAGAAA 518700
AATAATCAAT AAAGAGATCA TTGTTCCCTG CAATCAGGAG GAATATGAAA TTTTATATAA 518760
ACAAATATTA AAGTTATAAA CTTTTGAAAT AGAAAGATTT TAATTTTCCA GTTTTAAATT 518820
TTTTAATTAT GTTATATTTA TTGTGTTATA ATAAATAGAA GTACATTTCT GTTGTTTTAG 518880
AGGATTTAGC ATTGAATAAA AAAATGTTTC CCAAATTTA CTATTATGAT CAAGACTTTA 518940
TTGATATTTA TAATAAAAGT TTATCTTGGA TTCAAGATAA GGTGATTTTG CAAAAGTTG 519000
CTGATAGGGG CAAAAAGAT AAAAATTATT ATTCGGAAAA TTGTGATTAT ATAGATCAGA 519060
TGCAAGCTTG TATGTCAAGC TTTTTCTTG TCTATAGTAA TGGGGAATAT TCATCTACAT 519120
CTGCAATTGA TAAATTTTAT CAATTGCAGG AAGAATCTGG TGCAATCAGG GCTAGATATG 519180
ACAATAACAA TGCTATTATT GATCTTGATG AGAATGAAGA GAATATTGGA TTCCCTATTT 519240
TTGCATGGGC TGAATACAAC TTATATCATA AGACAGGAAA TAAAAAGAGA ATTTCTGAAG 519300
TTTTACCAAT TCTTGATAAG TATTATAAAT GGATAGAGAG CAAATTTTAA AAGGAAAATG 519360
GTCTTTATTC AATTGATGTA AATAAAATTT TTTATAAGAA CTCCCCAAGA GTAGATGCGT 519420
ACTATCCTAT AGATTTTAAT TCATTGCAAG TTCATAATGC ATATTGTATT TCTAAATTGG 519480
CAGACATTTT AAATGATAAA AATTTATCGC TTGAATACAA AAAACGATTT TTTCCCTTA 519540

AGGTCAAAAT	TAATTCTTTA	ATGTGGAGCG	AAAAAGATGG	ATTTTATTAT	GATCTTGATG	519600
TTAATGAAAA	TATTCTTGAA	ATCAAGACAA	TAGTAGGTTT	TTTCCCAATG	CTTTCTGAGA	519660
TTCCCAGTGA	GGACAGAATA	GAAAGAATGA	TTTTTTATTT	AAAAAGTACT	AATCATTTTG	519720
GGACTCCAAA	TCCTTTTCCA	ACACTTTCTG	TTAGTGAGCC	AGGTTTTAGT	GAGGATGGCA	519780
ATGGATATTA	TGGTTCAGTT	TATACTTATA	TGAATTTTTT	TGTAATCAAA	GGGCTTGAAT	519840
ATTGTGGTCG	TGCAAATATT	GCAAGAGAAT	TTACTATAAG	ACATTTGTAT	TATATATTAG	519900
ACACTTTAAT	GCCTTTTAAT	AAAATTAAGG	GGCACATTTG	GGAAGCTTAT	AGACCTATGC	519960
AAGAAGGACC	TGCATATTTT	GATTCTAATA	AAAAAECTTA	TACCGAGAAA	GGTCTTATTT	520020
GTTATCTTGC	ACTTTTTTAGT	ATTAGCTTAA	TGATAGAAAA	TATTATTGGG	CTTACAATTA	520080
GTTTGCCTGA	TAAAACTGTA	TATTGGAATA	TACCCACTCT	TGAGATTATG	GGGATAGAAA	520140
GCTTATCTCT	TAAAAAGAAT	CAAACTACAA	TAATTTGCAA	TAAGGGGAAA	AGAGGTGGG	520200
AAATAAAAAAT	GGAATCTGAA	AAACTTTATT	ATTTTACAAT	AAATATATTA	AATAAAAAAG	520260
AAAAAACCT	TCCTATTCCC	TCAGGAAGAT	GTTCTATGTT	ATTGGATAAG	CTTTGATGAA	520320
TTAGATTCAT	TAAATGTCTT	GTAAATTTA	AATTTTGGGA	GGCCTTTTAA	TGATAGATAT	520380
TGATGAGTTG	AGAATTTTTT	TTAAAGAGAA	GAGCTATTCT	AAAATTAAAG	AAAAATTTTT	520440
AAAGCATGAT	TCCTTTGATA	TTGCTGAGGC	TCTTAAAAGA	CTTAATGGAA	CTGAATTGAT	520500
TTTACTCTAC	AGATTTTTGC	CAAAAAAAT	AGCAGTTGAA	ACTTTTTCTA	ATTTTGACCA	520560
ATCTACAAAA	AATAAATTAG	CAAATTCCTT	TACCAATAAA	GAAATAAGTG	AAATGATTGA	520620
TGAGCTGAAT	CTTGATGATG	TTATTGACCT	TTTGGGAAGAG	GTTCCTGCAA	ATGTTGTTCA	520680
GAGATTTTTG	GCAAGTTCTA	CAGAAGAGAA	TAGAGAAATT	ATTAATAAAT	TTTTGTCTTA	520740
CAGTGATGAT	TCTGCAGGTT	CGATCGTAAC	AATTGAGTAT	GTTGAGCTTA	AAGAAGATTT	520800
CACAGTTGGC	AAAGCTCTTG	ATTATATTAG	AAGGGTAGCT	AAAACCAAAG	AAGATATTTA	520860
CACTTATTAT	ATTACAGATG	ATGAAAAGCA	TTTAAAAGGA	GTTATAAAAA	TTGAAGATTT	520920
AATATTGGCT	AAAGATGATG	TTATTCTCTC	GTCAATAATG	AGAAGTAGTG	GGTTTTATAT	520980
TGTGGGGGTT	AATGATGAGA	AAGAAGATGT	TGCACTTCTT	TTTCAAAAAC	ATGATATTAC	521040
CAGTGTTCCCT	GTTGTTGATA	ATGAGGGGAG	AATGATAGGG	GTTATTATTA	TTGATGACAT	521100
TTTAGAGGTT	ATTCAATCTG	TAAATACTGA	AGATTTTCAA	ATGATTGCAG	CTGTTAAGCC	521160
TTTAGATACA	TCTTATCTTG	ATACTTCTAT	TTTAGTTATG	ACAAAAAATA	GAATAATTTG	521220
GCTTTTAGTT	CTTATGGTGT	CTTCTACTTT	TACAGCTACA	ATTATTTCAA	ATTATCAAAA	521280
TTTAATGTTG	TCTTTAGTGG	TTTTAGCTAA	TTTTATTCCC	CTTTTAATGG	ATACTTCAGG	521340

CAATGCCGGC	TCTCAGGCAT	CTGCGCTAAT	AATTCGTGAG	CTTGCTCTTG	GTACTGTCAA	521400
GGTAAAAGAT	TTTTTTTAAAG	TGTTTTTTAAA	GGAAATATGT	GTTAGCATTC	TAGTGGGAGC	521460
AATTCCTTGCT	AGTGTTAATT	TTTTAAGAAT	TGTCTTTTTT	GTAGCTCCAC	ACCATTCTGA	521520
TAAGCTGAAA	ATAGCTTTTG	TAGTTTCATC	TTGCTTGATG	GTAAGTTTGA	CAGTAGCAAA	521580
GATATTGGGA	GGTCTTTTAC	CCATTGTTGC	TAAACTTTTA	AAGTTGGATC	CAGCACTTAT	521640
GGCAGGCCCT	TTAATCACTA	CAATTGCAGA	TGCTATTACT	TTAATAGCTT	ATTTTAATAT	521700
AGCAAAATGG	GTTTTAGTTA	GCTATGCTGT	TTAAATTTCA	TTTAAATATG	TTGATTGCTA	521760
TTTTTTTATA	ATAGGATATT	TTTAATGTAT	GATTGTATTT	TTTGTA AAAAT	AATAAACAAA	521820
GAGCTTCCTA	GTTATAAAGT	TTATGAGGAC	GATTTAGTTT	TAGCATTTTT	AGATATTAAT	521880
CCTTTAACTG	TTGGGCATAC	TCTTGTTATT	CCCAAAGAAC	ATAGTGAGAG	TTTATTAAAC	521940
ATGGATGATA	AATTTAACGA	GAGAGTTTTA	AAGGTATGTA	AAAAAATTTT	AAATGCTTTA	522000
AAAAGAATAA	ACTCAAGCAT	TTATGGTGGA	ATAAATATTT	ATTCTGCTTT	GGGGGCTGGC	522060
GCAGGGCAAG	AGGTTTTTCA	TACTCATTTT	CATGTAATTC	CAAGATTTAA	AAACGATGGT	522120
TTTGTTTTTA	AGAGAGGCAA	TAACTTAAT	CTTGAAGTTG	AAAAATTTAA	AGAGTTGTCT	522180
ATGCAAATAA	GTATGAATAT	TTAATTTTAT	TTTGCCCAAA	AGGATTCTTT	ATGAGAAGAA	522240
ACTTTTTTATT	CTTTTTTTGTT	TTTATGCTTA	ATGCATTTAG	AATTTATTCA	GGAATTCCTA	522300
GCTATCTTAA	TGTATACAGT	GGAGTTGGGC	TTGGTGTTGA	CAATTTTACT	CAAGATTTAT	522360
TCTTTTATGA	AAGACTTAAG	TATCAATTTT	TCAGTGGAGT	TGGTGTTAAT	GTTTCTCAAA	522420
ATTTAGCATT	TGGTGGAGAA	TTTAATTTAG	ATATTAAATT	TTACCAAGC	CATACTCCTT	522480
ATACCAATGA	GATTATATTT	ATGTTGGATG	ATCAAGCATA	TTTGAAGCAT	TCTCTAAATT	522540
ATTTCATAAT	AAAAGATGTT	TCATTTTCAC	TGAGAATGTA	TGGTAATTAT	TTCTTTTTAT	522600
CCTATACCCC	AATGTTTAGT	TTAATCTTTT	TTACAGGTTT	AAAATTTTCA	TACATTGGTG	522660
CAAAAATTTG	TTTTGTAGAT	TCGCGTGATT	GGGTATTATT	GGATAATTTT	GTTTTGGGAA	522720
TAGACATTGG	AGCTAGAATT	AATGTAGATT	TTATTTTTTT	GGAATATACA	ATCTCTCCAA	522780
TTTTTTTACAA	CAAACCTTTA	CTTTTAAATC	AAATGCATAA	AATAACATTA	GGATTTATTT	522840
TTCAGTTTGA	TGTAGCAACA	AAAAATGAAA	GCGAAATACT	TTCTATTTTG	TAAATTTTAT	522900
GAGCTAAGGA	TATTTTAAAT	TTTCTTCTTT	AATATTGTTT	AATATTTGTA	AGTATTTAGA	522960
AGATTCATAT	TTAGCCATAT	CAAGGTTATG	TTCTTTGTAA	TTCCGCATT	CCTTATCACT	523020
TGCGCCTGGG	ATAGGTTCTG	AAAAATTTAC	GATTTCGGAA	AAAAGCCATG	AGACTAAGTC	523080

AACAAGATCT TTACTTTCAT AGTCTCCAAA AATTATTAAG TAAAAACCAG TTCTGCATCC	523140
CATAGGGCCA AAATATACTA TTTTTCGGT CCAAACCTCA TTATTTCTAA GTAAAGTAGC	523200
TCCTATGTGC TCTATTGTAT GTATTGCTGC GTTTTCAATT ATTGGTTCGA TGTGCGGAGC	523260
TTTGATTCTA ATGTCTATTG TAGTAAATAT TACATTTTCA AAGGTATCTT TTCTTGAGAC	523320
ATATATGCCA GGGTTGAGTT TTGTATGATC TATTGTAAAG CTTGTTATTT TTTTCATTTT	523380
TTTAGCGCTG TTTGTATTTT TTTTACAAAA TCTAATTTT CCCATTCAAA TTCATTTT	523440
CCAAAATGAC CATAAGTGCA AGTTTAAAGA TATATGGGT GTTTTAGTTT TAATTTTTC	523500
ATTATACCGT TGGGAGTTAA ATCGAAGTTA TTAACAATAA AATTTAATAT TTTGTTTGCA	523560
TATTTAGGAT CATTTATTCC CCCAGTTATT TGAATAGATA TTGGGTTTTT AATTCCAATT	523620
GCATATGCGA GCTGTAGTTC AAATTCTTTA GAAATCCCG CTGCCACCAT ATTTTTTGCA	523680
ATATATCTTG CCATGTAGGC AGCTGATCTA TCTACTTTTG TGGCATCTTT TCCGCTGTAT	523740
GCTCCCCCTC CGTGTCTTGC AAATCCTCCA TAGCTATCTG CAATAATTTT TCTTCCTGTA	523800
AGCCCAGTGT CTCCGGTAGG GCCTCCAATT ACAAATTTT CAGAAGGATT AATGCAATAA	523860
GCAGTATTTT CATCAAGCAT TGAATTGTCT TGAACAGTGG GCTTGATGAT TTCTTCAATT	523920
ATTGTTTGTT GTATTAGTTT TTGGGAGATG TTTGGATGGT GTTGATGAGA GACTATAATA	523980
TTTTTTATTT TTACAGGGTT TCTGTTTTTA TCGTATTCTA TGGTAACTTG AGATTTTGAG	524040
TCAGGCCTTA ACCATTTTAT TGCTCCTGAT TTTCTAAGAT TGCTAGCTTT TTTTAGAATT	524100
GAATTGGCTA GTTCATAAGG AGCAGGTAAA AAATTTTTTG TTTTCATCGCA GGCATATCCA	524160
AATATTATTC CCTGATCCCC TGCTCCAAGG GCATTGGATC CCTTTTTTTC AATTGCGTTT	524220
ATAATGTCAC GTGATTGATT GCCAATAGCG TCTATTACCG TTATTGTTTT GTAATCAAGC	524280
CCATAATCAA TATTTGTATA GCCTATATCT TTGATGATAT TCTTAGCAAC CTCTTTTATA	524340
TCTATGTTTT TTTTACAGG ACTATTTATT TCTCCTGCTA TTACTACTAA ATTTTGTGCA	524400
ATTATGACCT CGCAAGCTAC TTTTGCAATT TTATCTTCTT TTAGTATTTT ATCAAGGATG	524460
GCATCAGAGA TTTGATCTGC AATTTTGTCT GGATGTCCTT CAGATACAGC CTCAGAAGTT	524520
AAAGTTTGGT TCGCTGCTAT TATTTTATTC ATATTAGCCT AATAAGTTCC TTTGTCATTT	524580
TGCTTGAATT TATTGATGAT GTTTTAAAA ATTTATTAAA GTCTATATGG TTGTCTTTAT	524640
TGTTTGGTAG ATCAGAAATT GAACGAATTA TTATGAATGG TATTTTAAAT ATGTGTGCTA	524700
CTTGAGCTAT TGCAGCTCCT TCCATATCTA CAGCTAAAGC ATCTTTGAAA TTTTTTTTAA	524760
TTGTTTCAAG ATTTTTTTTCA TTGTCAACAA ATTGATCTCC TGTTAGTATT AAGCCAATAT	524820
GGATATCAAT GTTTAAAAGC TTGTTGTCAA CAATATTGGC CACTTTTTTA AGTAGCTCTT	524880

CATCTGCTTT	AAACTTTTGT	GGCAAATTAG	GGACTTGTCC	TATTTTGTGT	CCAAACTTAG	524940
TTAAGTCAAA	GTCATAGTAT	GCTGTTTCTG	AGGATACTAT	AATGTCTAAT	ATTTTAAGGT	525000
TAGAGTTTTC	TTTTATCCCC	CCAGAACTTC	CAGAGTTTAT	TATGTGAGTG	ATTTTATACT	525060
TAGAGATAAT	TTGACTACTC	CAAGTTGCTG	CGTTAACTTT	TCCAATTCCT	GTAGTTAAAG	525120
ATATTACATC	TTTTCCTAGA	ATTTTTCCTT	TATAAATCTT	TTTATTTTCT	AAGTAGTCGT	525180
TTAATACAAT	TTCTTCTTTG	TTGTCAAGTA	TTTTATTTAT	TTCTTCTGAT	TCTTCTTGCA	525240
TAGCTGATAT	TATCAAAATC	ATATTTTTTC	TCCTTTTAAG	TGTCTTATAT	AATATCTATT	525300
AAAGAATATT	TATTTTTAAT	TAGCTCTATT	TCATTTTGAT	TGAGTATTTT	TTTTATTCCCT	525360
GTATTTGTAT	TTGGTATAGA	TTGAACACTA	GATTGTTTCAT	TTTTGTCTAT	AACTTTTCCA	525420
TTTTTTATTA	TGTAGTTGAT	GTATGGAAGA	TTTGGGTTAG	ACTCATCTAT	ATCTACTATT	525480
TTGGCTATAG	AATTGTCATT	AAGTTCTACA	ATAAAGTCTA	AGGGACAAGA	AGATATTGCA	525540
TTGATTATTA	GCTTCAAAAC	CCTTTTGTCA	AATTTTTTGT	CAGCATCTTT	GATTAATTCA	525600
ATAATAGATG	CTCCAGAATT	AAAAGATTTT	TTGTATGCCT	TATCTAAAAT	GATAGCAGAA	525660
TAGGCACTAG	CAGCGCCTAT	TATATTTGAT	TCTATGCTGA	TATTTTCACT	TGTTAATCCT	525720
TTAGGATAGC	CAGTTCCGTC	TAGATTTTCT	TTATGTGTTA	AAAGTGTCAA	ACATATTGAT	525780
CGTGATAAGT	TACTCGTTGA	AGCTATTTTG	TAGCTTATTA	TGGGATATTT	TTTTATTATT	525840
TCTAGTTCTT	CCTCAGTTAA	TGCTTCTTTT	TTTTCGCTGA	TTTTTGATGG	AATAAATAAA	525900
AATCCTATTT	TATGTAAAAG	AGCAATACTA	CAAAGCTCTA	CTGTTTTATA	GTTATTTAGT	525960
CCCATTTTCAT	TGCCAAGGGC	TACTGTTAGG	ATAGCTGTAT	TTACCGAATG	AATAATGTGA	526020
TAGTTTGCAG	AAAGCTTGGG	AATTCTAAAA	TATTTGATAA	AAATTTTCTT	CTGTTTCTTG	526080
TAAAATTCTA	TTACTTTTTT	TACAGTAGGC	ATAATATCTT	GGTAATATAT	TTTTTTATTT	526140
CTTTTGCAAT	TTTCATAAAT	TTCTTCTAAA	TTGCTTATTA	TTACATGATA	ACTGGAAATA	526200
GCCTCTTCGT	TGAATTTTTT	GTGTATTTCT	TCATATTCTT	TTTTAACAGA	ATCGTCACTG	526260
AAAAAATTTT	TTCTCTCTTT	AATGTATGAC	TTTAGATTCC	ATTTTTC AAT	AAGCTCAATG	526320
TTTTTGCTC	CAATAAATGC	ATTCTCAGGC	CAAATAAAA	ATTCCTTGTC	TATTAAATAT	526380
GATGAATTTT	TTATATTTTT	AATAATGCTT	TCAGAATTTT	GCATTTATTC	CCTTGAAATT	526440
AAGCTCTATT	AACCATGTAT	ATCATATTAT	TTATTAATTG	TCTATCTATT	AGTATAATGT	526500
ATTTATTATA	TCTCAATTTT	TGAATTAAGC	TTTTTTGAAG	AGATTTTTAT	GGTAGAAAAA	526560
ATACGCTTAG	GTTTTAATAT	TATTTTCTT	GGATTATTTA	TTTATTTTCT	GGCAATTTTA	526620

AGATTTCAAA TGAAATTAAG CTTCAATTTG TTAAATTACC AATTTATTGT AGTTTATTTT	526680
TTATTAGTGA TTGTTTTTAA TGTATTATTTAT TCCCAATATT TTTTCCAAG ATTGTATTTT	526740
ATTTTAAATG GGATGGAAGA TGCATTCCTT TTTTGAAGC TTAAAATGGT TCGCAAAAAG	526800
CTTAAAAGTG TTTTGAAT ATCTATTCTT CTTAGGTTTA TTTTAATAAA ACAAGATAAA	526860
AAAAGCCTTG ATGAGCTTTA TTTTATTTA AAAGACACTA GATTAAGACA TAAAACAATA	526920
ATAGAGCTTT ATTCTGTTCT TATTAGCTTT AGAGAAAAG AAAAGGCTTC TAGTTTAATT	526980
TTAAATTACA AGTACAGTAG AAATAAGTGG GTGAAATATT GTGAGGCTCT TAGTATGTTG	527040
TCATTTGAAG AGCACTCAAA GCTAAAAGAG TTGGTAAATT TTTTAGATAA GTTTTTTTTG	527100
AAAAATGATA TTTTACTAT TTATTTTTAT TATTTATTGC GAAAATCAAA AACATCTTTT	527160
GATTTGCTTG AAAGCAAGAA AATTGAGATT AGAAATCGAT ACTATAAATT TAAAAACAGG	527220
ATAGATTCTA AGCATACAAA GCTACTTGGT TCGAATTTAT TTTTGTGTGT TTTTATTAT	527280
ATTTATGATT TTTCTAAAAA AGATGTTTTT TATTAAAGGA GTTGTGTTTT GAGTACAAGA	527340
GTTGCTTATG CGCCTTCTCC AACGGGTTTA CAACATATTG GCGGGATTAG AACAGCTTTG	527400
TTTAATTATT TTTTGC AAA GTCTTGCGGA GTTAAATTTT TGCTTAGAAT TGAGGATACA	527460
GATCAGAGCA GGTATTCTCC AGAAGCTGAA AATGATCTTT ATTCAAGTCT TAAATGGCTT	527520
GGCATTCTT TTGATGAAGG CCCTGTTGTA GGGGGTGATT ATGCGCCTTA TGTTCACTCT	527580
CAAAGAAGTG CAATATATAA GCAATATGCT AAATATTTGA TTGAATCTGG GCATGCTTAT	527640
TATTGTTATT GCAGTCCCGA AAGGCTTGAA AGAATTAAGA AAATTCAAAA TATTAATAAG	527700
ATGCCACCTG GATATGATAG GCATTGCAGG AATTTAAGTA ATGAAGAGGT TGAGAATGCA	527760
CTAATTA AAAA AAATCAAGCC TGTTGTTAGA TTTAAAATTC CTTTAGAAGG AGATACCAGC	527820
TTTGATGATA TTTTACTTGG AAGGATTACA TGGGCGAATA AAGACATTAG TCCTGATCCT	527880
GTAATTCCTA AGTCAGATGG ATTGCCGACT TATCATCTTG CCAATGTTGT TGATGATTAT	527940
TTAATGAAAA TTACCCATGT ATTAAGGGCT CAAGAATGGG TTTCTTCAGG TCCATTGCAC	528000
GTACTTCTTT ATAAGGCTTT TAAATGGAAA CCCCTATTT ATTGTCACCT TCCAATGGTT	528060
ATGGGAAATG ATGGTCAAAA ATTAAGCAAA AGACATGGCT CAACAGCTTT AAGACAGTTT	528120
ATTGAAGATG GGTATCTTCC AGAGGCTATT ATTAATTATG TTACTTTGCT TGGCTGGTCT	528180
TACGACGATA AGAGAGAATT TTTTCAAAA AATGATCTTG AGCAATTTTT TTCAATTGAG	528240
AAGATCAATA AATCTCCTGC TATTTTTGAT TATCATAAAT TGGATTTTTT CAATAGCTAC	528300
TATATTAGAG AAAAAAAGA TGAAGATTTA TTTAATCTTT TACTCCCTTT TTTCCAAAAA	528360
AAAGGGTATG TTTCTAAGCC TAGTACTTTG GAAGAAAATC AAAAATTAAT GTTATTAATT	528420

CCTCTTATAA	AGAGTAGAAT	TAAAAAATTA	AGTGATGCTT	tAAATATGAC	TAAATTTTTT	528480
TATGAGGACA	TTAAATCTTG	GAATTTAGAT	GAGTTTTTAA	GTAGAAAAAA	AACAGCTAAA	528540
GAAGTTTGTT	CTATTTTAGA	ATTAATAAAG	CCTATTTTAG	AAGGGTTTGA	AAAAAGATCA	528600
TCAGAAGAAA	ATGATAAAAT	TTTTTATGAT	TTTGCTGAGA	GTAATGGTTT	TAAATTGGGA	528660
GAAATTCTTC	TTCTATTAG	AATTGCAGCG	CTTGGTAGCA	AAGTCTCTCC	GCCGCTTTTT	528720
GATTCTTTAA	AATTGATAGG	CAAGCTCTAA	GTTTTTGAAA	GAATAAAATT	AGCACAGGAA	528780
TTTTTAAGAA	TAAATGAATA	GCTATTAAGG	ATATTTTTAT	GGTTAGAATG	GAAGATATTA	528840
TTTCTCTTGC	AAAAAGAAAA	GGATTTGTAT	TTCACTCTTC	AGAGGTTTAC	GGGGGCCTTT	528900
CAGGAGCTTG	GGATTATGGT	CCTTTGGGGG	TTGAGCTTAA	AAAGAATATA	AAGAAAGAGT	528960
GGTGGAAGAG	CATGGTGTAC	TTGCATGAAA	ATATTGTAGG	TTTAGATAGT	GCTATTTTTA	529020
TGCGCCCTGA	AATTTGGAGA	GCATCTGGTC	ATGTTGATGG	TTTTTCGGAT	TCTATGGTTG	529080
ATTGCAAAGA	TTGTAAAAGT	AGATTTAGAG	CTGATTTTAT	TGATTTGTCA	AAAAATTGTC	529140
CGAATTGCAA	AGTTGGAAAT	AATTTTACCT	CCCCAAGAAG	TTTTAATTTA	ATGTTTAAGA	529200
CCCACATTGG	AGTAGTGGAG	GATAGTTCTA	GTGAAGTTTA	TTTAAGGCCT	GAGACAGCAC	529260
AAGGAATTTT	TGTTAATTTT	AGAAATGTTT	TGATTCTTTC	AAGGCTTAAG	ATTCCTTTTG	529320
GGATTGCTCA	GGTAGGTAAA	GCGTTTAGAA	ATGAGATAGT	TACTAAAAAT	TTTATATTTA	529380
GAAC TTGTGA	GTTTGAGCAA	ATGGAAATGC	AGTTTTTTGT	TCATCCCAAG	CAAATAGACG	529440
AGTGTTTTTG	TTATTGGCAG	CAAAATAGAA	TGAATTTTTT	TATAGAAACT	CTTAAAATTA	529500
GTCCCGATAG	ATTAAGATTT	AAGGCGCATG	ATTCAACGCA	GCTTGCTCAT	TATGCAAAAG	529560
CTGCATTTGA	TATTGAGTAT	GAATTTCCGT	TTGGATTTC	GGAAGTAGAA	GGAATTCACA	529620
ATAGAGGTAA	TTATGATTTA	ACTCAGCACG	CTAAATTTTC	TAATAAGCCC	AAAGTATTTG	529680
AGTATCATGA	TTTGTTGACA	AAAGAGAAAT	ATGTGCCTTA	TGTTATTGAG	ACTTCTGCTG	529740
GTCTTACAAG	GTCTGTTTTA	ATGACTCTTT	GTGATGCTTA	TTCTGAGGAA	GAGCTCTCAG	529800
ATGGAGACAA	GCGTATTGTT	TTACGCTTAC	ATCCCAAGTT	GGCTCCTTAC	AAGATTGCTA	529860
TATTTCCCTCT	TGTTAAAAAA	GTtGAGCTtA	CTGAGATTGC	TAGAAGGATT	TATATGGAGC	529920
TTTGCGATGA	TTTTCATATA	TTTTACGATG	ATAGTGGAAC	AATAGGTAAA	AGGTATAGAC	529980
GTCAAGACGA	AATAGGAACT	CCTTATTGCG	TAACAATAGA	TTACAATACG	ATTGAGGATG	530040
AGACAGTTAC	TGTTAGAGAA	AGAAATAGCA	TGACTCAGAA	GAGAATTTTT	ATTAATGATT	530100
TATATTCATA	CATTAAAACA	GAGATTTTAA	ATTACAAAGA	GGATTTTAAT	AAATGAATCT	530160

TGCTTTAAGT	CTTTTACATA	AACGCGGATT	TTTAAAGCAA	TGTACATCTT	TAAAAGTTTT	530220
AAGTGATTTA	ATGGATAGGG	AAAAAATAGT	TTTTTATGCA	GGAGTTGATG	CAACATCTAG	530280
TTCTCTTCAT	ATTGGCCATT	TGATTCCCTT	TTTAGCAATG	ATGCATCTTA	GGCAACACGG	530340
GCACATGCCA	ATTGTTTTGA	TTGGAGATTC	TACAGCAAAA	ATAGGCGATC	CTTCTGGAAA	530400
AAGTGAGATG	AGAAAGATTT	TATCTTCAGA	AGAGATTGGC	AATAATGCTT	TGTTGATAAA	530460
AAATCAACTT	CAAAGAATAA	CTAAGTTTAC	TTCAGAATGT	TTTATTCATA	ATTCAAATTG	530520
GTTAGATAAT	CTCAATTATA	TTGAATTTTT	AAGAGATGTT	GGCATGCATT	TTTCTGTAA	530580
TCGTATGTTA	AGCTTTGAAA	CTTATAAAAG	AAGGATGGAT	TTCGGACTTT	CATTTATTGA	530640
GTTTAATTAT	CAACTTTTGC	AGTCTTATGA	TTATTATATG	CTTAATAAAA	TTAAAAATTG	530700
CCGACTTCAA	ATTGGTGGTG	ATGATCAATG	GGGGAATATT	ATTTCAGGGG	TTGACCTAAT	530760
TAGAAAAAAA	AATGGATCAG	AAACTTTTGG	GCTTACTTTT	CCATTAATTA	CAAGAAGTGA	530820
TGGAAAAAAG	ATGGGTAAAT	CAGAAAAAGG	CGCTGTTTAT	CTTGATTCTA	ATCTTTTTAG	530880
TATTTATGAT	TTTTATCAGT	ATTTTAGAAA	TACTTCAGAT	TCTGATGTGA	AACTTTTTTT	530940
ATATCTTTTT	ACTTTTTTTAG	AAGAAGATGA	GATTGAATTA	ATTTCAAATT	TTAAGGGGAA	531000
TTCTTTAAAT	AAGGCCAAAG	AGATTTTGGC	TTTTGAGATA	ACTAAAATTG	TTACCGGAGA	531060
GGCAGAAGCC	TTGAAAGTTC	AAGAGGCATC	TTTTGCCGCA	TTAGGGGAA	GTGGAGATAG	531120
GAGCAATATT	CCATTTTTTA	AATTTAGCTT	TTCTAGCCTA	AAAGAAGAGA	TATTATTGGT	531180
TGATTTAATG	TTAGATTCAA	AAATTGTGCC	CAGCAAATCA	GAAGGCAGAA	GATTGATTGA	531240
TTCTGGAGGT	GTTTATATTA	ATGGTAAAAG	GGTAGAAAGT	CAGAGTCACC	TTCTTACCAA	531300
AAAGGATTTT	AATAACAATG	AAGTTGAATT	AAGAGTAGGT	AAAAAAAAT	TTTTACGAAT	531360
TGTTATATAG	TTGATTTTGG	ATGTATGATA	GAAGAGCTTT	AAATTGTTTA	TTTTTTAACA	531420
CCTTTTTGTT	TTTCATGGAA	TCTAGGCACC	TTGTGTTTAC	AGAAGAGCAC	ATTTTTTATG	531480
GGCTTATTAA	AAGTGATAAA	GTAAAGAAC	TACTTAATTT	GTGTGCAATT	GATTTTTATA	531540
AACTTAATAA	ACAAC TAGAA	GAATTTTTTA	GTAAACTTCC	CTTAAGAGGC	AATTATATCC	531600
CAGACTATGT	TTCTAGTATG	GATTATTTGT	ATGACGATAT	AATTAGTGTT	CTTTTTTTTT	531660
ATAAAAAACC	TTATAAAATA	CAAGAAAAAG	ATCTATTGTG	GGTGCTTGTC	AAAAAAGAA	531720
AAAATAGTAT	TTTAGATGCG	CTGCTTAGCT	CGGGTTTTAA	TTTGACTATT	TTTGATAAAC	531780
TTATTGAAGC	TCATGATTAT	TTAGCTGTAA	ATACTAAATC	TGCCTCAGGC	GACAGTGAAT	531840
TAATTGCAGA	ATATATTCAT	AATAATGCGC	CAAAAAGGAA	AGGAGGCTTT	CATATTTTTG	531900
ATGATAAGCG	TGATGAATTG	GATCAAAATA	ATATTTTCTT	AGAAAGTAAA	GACTCTATTG	531960

GTAATTTTTT	AACAAACGTT	ATTGATACTT	TGGATTTAAA	ATACAATCCT	TTAATTGGTA	532020
GAAGTCAAGA	ATTATCTCGG	TTAATCCAGG	TGATACTTAG	GAAGCATAAA	AGTAATCCTA	532080
TTTTGTTTGG	AGAGCCTGGT	GTTGGAAAAA	CAGTATTAAT	CCAAGGTCTT	GCATATAAAA	532140
TAAAAATAGA	GAATGTTCCA	AAGGATTTAA	TAGGGTATGA	AATCTATTCT	CTTGATATTG	532200
GTAGGCTTGT	TTCGGGTACT	AAATATAGGG	GAGATCTTGA	GAGTAGGGTG	AATAGGGTTT	532260
TAGATTTTTT	AAGCTCAAGA	AAAAAAGTTA	TGCTTTTTAT	TGATGAAATC	CATATGATAG	532320
TAGGGGCAGG	GGCTACTTCA	TTTGGCAGTA	TGGATATTTT	CAATTTGTTA	AAACCCATTC	532380
TCACTTTAGG	AAAAATTAAA	TTTATTGGAG	CTACTACAGA	ATATGAATAT	AGAAAATTTT	532440
TTTTTAAAAGA	TAAGGCCTTA	ATGAGAAGGT	TTTCAAGTAT	AGAGCTCAAA	GAGCCTAATT	532500
TTGAAGACGC	TTATAATATT	TTGCAGGAGA	TTAAAAAAGA	TTACGAGAGG	TATCATAATG	532560
TGGAATATAC	AGACGAGGCA	ATACAAGCTT	GCATTCTCAT	GTCTCAAAAA	TATATTAAAG	532620
ATAGATTTCT	TCCAGACAAA	GCTTTTGATA	TTTTAGATGA	ATTAGGCTCT	AAGTTTAAGC	532680
TTGAAAATAT	AAAAAGGATT	ATAACAAAAG	ATGATGTTTG	CGATCTGATT	AAATCTATTG	532740
TTGGTTCTAA	TATTTTTTAAT	TTTGAAGAGT	ATGATGGTGA	ATTGCTAATT	AATTTAGAAA	532800
ATAGAATAAA	AAAAGAACTT	ATTATACATG	ATAACTTGGT	ACTTGATTTG	ATATTAAATA	532860
TTAAATTATT	AAAATTCAAT	TTGCTTGCCA	ATAGAAGTAC	TATTGGAATA	TTTGCCTTTA	532920
TTGGTGCTTC	TGGGTCAGGA	AAATGCAAAT	TGATGGATAT	TTTATCAGAA	GAGTTTAAAA	532980
TTCTTAAATT	TAGTCTTAAC	ATGGGTGAGT	ATAATGATTT	TAATTCTCTT	GATAGATTGA	533040
TTGGGCCTGT	TTTAAGTAAT	GAAGGATATT	ATGAATCTAC	CAGATTTTTT	AAATTTTTGA	533100
ACAAATCTTC	TAATTCTATT	ATTTTCCTAT	CAGATTTTGA	TAAATGTAAT	AAAAGGGTTT	533160
TAGATTTTTT	TTTAGAGGGG	TTTAAAACAG	GTAAACTTTT	TGATGGTCTT	GGAAAAAAGG	533220
TAAGCTTATC	AGAAAGTTTA	ATAGTAATAA	GTATCAATGC	TGAGAGCAAA	GAGCTTAATA	533280
GCATTGGTTT	TAGAAATAAA	ATGGCGGGGG	AAAATGATTT	TAACTTTATA	TTAAAGAAGA	533340
GATTGCCCAA	TGAGTTTTTA	GAATTAATAG	ATCATGTGTT	TGTATTTAAA	TCTATTGATG	533400
AGTTAGATTT	TGAAAAAATC	ATTTTAAATG	AACTTAATTA	TTTTGCAAGG	ATATTAAGAG	533460
ATAGAAAATT	TGATGTTTTT	TTTGAAAAAA	GTGTTGTTGA	TTATATTCTG	GAAAAGATTT	533520
ATGGAAAGGG	GTACAGCTTA	AAAAGTGTTA	GAAAATTTAT	ATTCAAAGAA	TTGGGAAAGC	533580
TTTTAATAGA	TGAAATTCTT	TTTAAGAAAA	TTGAAAATTC	TGGTAAAAATA	AAAATCTATT	533640
TAGATGAAAC	AATAAAATAT	GAGTTTTTTT	AAGGTTATAG	GGGGAGTATT	TATGAAAATA	533700

TCAGTAATAG	GGGCAGGTGC	TTGGGGAACA	GCTATTTCAA	AGTCTTTGGC	AGATAAATTT	533760
GATTTTAATA	TTTTTTTATG	GGTCTTTGAA	GAAGATGTTA	AGAATGATAT	TAATAATGAT	533820
AATGTTAATA	CTAAATATTT	AAAGGGAATT	AAATTGCCAA	AAAATTTAGT	TGCAAGTTCA	533880
GATTTATTTG	AAGTTGTAAC	AATGTCTGAT	TATATTTTCA	TTGCAACACC	TTCTCTTTTT	533940
ACCGTTGATA	TTTTAAAAAA	ATTGGATCAA	TTTTTACATT	TTCTGGAGAT	AAAACCAAAG	534000
CTAGCAATAC	TTACAAAAGG	GTTTATTACT	TTTGATGGTA	AAACTCAGAC	AGTTATTGAA	534060
GCTGCTGAGA	GAATTATGAA	AGGATATAAA	GACGAAATTA	CTTATATTGT	TGGTCCAAGT	534120
CATGCTGAGG	AAGTTGGGCT	TGGTGTGATA	ACAGGGCTTG	TTGCGGCTAG	TAATAACAGA	534180
GAAAATGCAT	ATTGTTTAT	TAATTTATTT	AGTAAAACCC	CAATTTCTTT	ATTTTATAGC	534240
AACGATGTTT	TTGGGGTGCA	AATAGCAGCA	GCTTTAAAAA	ATGTGTTTGC	TATTGCATTT	534300
GGAATTTTGG	ATGCCTATAA	ATTGAATTAT	CCTAATTTAA	TAGGTAATAA	TACAGAATCA	534360
TTTTTATTTT	CAATATCCTT	AAATAATATA	AAAGATATTG	CAATGGAGCT	TGGGGGAAGA	534420
AATATTGAAA	CGTTTTTATT	TTTGTCTGGT	TCTGGCGATT	TAGATGTTAC	TTGTAGAAGC	534480
ATGTTTGGAA	GAAATAGACG	ATTTGGCAAT	GAAATTGTTA	GCAAAAACAT	TTTAGAAAGC	534540
TTTTTAAGTA	TAGATGACTT	GATAAGTAAT	ATTGAAAAAA	TTGGATATTT	ACCAGAGGGA	534600
GTTTTGGCTG	CTAAATCAAT	TTTTTTCTTT	TTTAAACAAT	TAAATCGTGA	TCTCAATCCT	534660
AATAGTTTGT	TAAGCGTTAT	ATATAAAATT	TTGAATAAAG	AGTTGGAGCC	CAAATCTGTT	534720
ATTGAGTATA	TGAGAGATGT	TAGACAATAA	AATAAAGCCT	CTGCAGAGGC	TTTATTGTTT	534780
TTGCTCATTC	ATCATATATA	AAATTTTATT	ATAAACATCC	TCGATTATTT	CAAAATTTAT	534840
TACAACCTCT	GTAAGTTCAT	TAGATTTAAT	AGTTCCTATT	ATGTTGTCAT	TTTTTGTTAA	534900
ATCGTCTCTT	TTGACTAAAG	AATTGCTGTC	TACTAAAATT	TTTATTCTTG	TTAGGTCTTT	534960
GTCTATGTTT	TTAATATTTT	TAATTCCCCC	GAAGCATTC	ACAATATGCT	CTGCTACTTT	535020
AATTTTATTT	ATTTTTTCTA	AATCTGCCAT	AGTAATTTTA	TTCTCTGTAG	AAAGCTTTAT	535080
ATGCTAAGTA	AGCATTGTAT	AAATCAAATT	TAGAAGTTAT	TTCCATTGGA	GAATGCATAC	535140
TTATAACAGC	AGGCCCATG	TCTATTGTTC	TTATTCCATA	GCCAGCTAAG	AATTTAGCAA	535200
CAGTTCCTCC	TCCTCCTTCT	TCTACTTTTC	CGAGTGTGTC	TACTTGCCAG	GCTATATTGT	535260
TTTTATTTAA	TAATTGTCTA	ATATAAGAAA	CAAGCTCAGC	ATCAGCATCG	CTTGCCATAC	535320
TTTTTCCACC	ATGTCCTGTG	TATTTCATTA	TAGGTATTCC	ATAGCCAAGT	TGGGGAGCGT	535380
TTTGTTCGTC	ATGAACTGAA	CTAAATAGTG	GGTTTATTGC	TGCACAAACA	TCAGCAGAAA	535440
TGCTTTTTGA	ATTCCACAAA	GCTTTTTTGA	CGTGAAGATT	GTTGTATTCT	GATTTTTTTAA	535500

TTTTGAAGAT CATGTCAGAA ACAAATATT CAAGATATCT TGAGTCTAGT CCGGTTGAAC 535560
CTGTTGAACC AATTTCTTCT TTATCTACAA GAAAGCAAAT GGCTGTTTTA TTTGGAGTCT 535620
CTTCAAGATC AAATATGGAT TCTAGTGAAG TGAAGACGCA TATTTTGTCA TCTTGTCCGT 535680
AAGCCCCAAT TAACGCTTTG TCAAATCCAA CGTCTTTTGC TGTTCTTGCA GGCATATTT 535740
CAATTTCTGA TGATACAAAG TCCTCTTCTT CTATTTTGTA TTTTCTTTT ATTAGTTGCA 535800
AAGTTGCCAG TTAACTTTA TTTTTTCTT TTGTTTCGAT TGGCAGGCTT CCAATTAAAA 535860
TTTTTAGATT TTCCCCTTCA ACAATTTCAT CTGATTTTTT ATTTCTTTGT ATTTTCTAT 535920
CAAGATGAGG CAAGATGTCG GGAATTACAA ATACAGGATC GTTTCATTG TCTCCAATAT 535980
TGATTTCAAC CTTTTCTCCA TTTTTTAAAA ATACCACCCC TCTTATTGAA AGGGGTGTAG 536040
ATAACCACTG ATACTTTTTT ATTCCCCCAT AATAGTTGGT TTAAATAAAT GTAAGTTCAT 536100
TTTCTTCAGA GATTGGTGAG GGTTTTCAT CAAGTCTTGG TGAATCTGTG TGAGAAACAA 536160
TAAAATTCAT TCCATCTTCA ATGGGATTTT TGCCAATAAT AGCAAAGCA ACAGATTTTT 536220
CTCTACAGGT ATAAAAAATT TTATCACCTG GCATTAAATT TTTTTTCTCT TCAGCGTTAA 536280
TAAACCCCAA TTTTTTTGCT TTATCTAGGG CATAGGCTGT AACTTCTCTT TCTGTTTTGA 536340
ATTTGCTTAT AAATTTTTTG TAACTTTCAG AAAAATTAA AATTTGATTT TTTTCTTCTT 536400
CATTTAAATA TATCCATGGA TTTTGTTTTT TCATATTAAT AAGACCTCCT GTTTCATTTT 536460
AACATTTTAA TTGTTTTTAA AGTGTGTACA AAATAAATTA TTTATTGTAA ACTTACTTTT 536520
AATTTTAATA TGATTAATAA ATTATAAGGG AGAATTTTTA TGTATAAAAA TGGTTTTTTT 536580
AAAACTATT TGTCATTGTT TTTAATTTTT TTAGTAATTG CTTGTACTTC AAAAGATAGC 536640
TCAAATGAAT ATGTTGAGGA GCAAGAAGCG GAGAACTCTT CTAAGCCTGA TGATTCATAA 536700
ATAGATGAAC ATACTATTGG GCACGTTTTT CACGCTATGG GAGTAGTTCA TTCAAAAAG 536760
GATCGAAAAA GTTTGGGGAA AAATATAAAG GTTTTTTATT TTTCTGAAGA AGATGGACAT 536820
TTTCAAACAA TACCCTCAA AGAGAATGCA AAGTTAATAG TTTATTTTTA TGACAATGTT 536880
TATGCAGGAG AGGCTCCAAT TAGTATCTCT GGAAAGAAG CCTTTATTTT TGTGGGATT 536940
ACCCCTGACT TTAAAAAGAT TATAAATAGC AATTTACATG GCGCTAAAAG TGATCTTATT 537000
GGTACTTTTA AAGATCTTAA TATTAAAAAT TCAAATTGG AAATTACAGT TGATGAGAAT 537060
AATTCAGATG CCAAGACCTT CCTTGAATCT GTTAATTACA TTATCGACGG CGTTGAAAAA 537120
ATTTACCTA TGTTAACGAA TTAATTTATA TTTTGTATTT TATAGGCTTT AATCTAAATT 537180
AAAGCCTATT TTAAAAATC AAGCTCTCAA GTCCTTTTAT TAAAATTTCT GCTGTTTTTA 537240

CGTTGGTTGC	AAGCGGTATT	TTATGTACAT	CGCAAAGCCT	AATAAGAGCT	GACACATCTG	537300
GTTCGTGAGG	CTGGCTTGTT	AGGGGATCCC	TAAAGAAAAA	TATAGCTAAG	ATATTTCCCTT	537360
CAGCTACTTC	AGCTCCAATT	TGTTGATCTC	CTCCCATAGG	GCCTGATTTA	TATTTAAAAA	537420
TCGTAAGATC	GGTAGCTTGT	TGGATTTTAG	ACCCCGTTGT	TCCTGTTGCA	ATAAGCTTGA	537480
ATTTAGATAA	GAAGAGATAG	TTTTGTTTGA	CAAATTTTAC	CAAATCTTCC	TTTTTTTTTAT	537540
CGTGTGCAAT	TAATGCTATT	TTTTTTTCCA	TTAATTTTAT	TCCTTTTTTCA	ATGTAAAATA	537600
ATTTTTGTG	AAATTTAATA	AAATTTAGGC	ATAAGTATAT	TTTTAGATTT	CACTTTTTTTA	537660
GAATTTATAT	TGGTCTGGT	TTGTGCCATA	AAAATCCTTG	CCCATAGTCT	ATTTCTAGTT	537720
CAATTATTTT	TTTTAATATT	TCCTCATTAT	ACACAAATTC	GGCAATAATT	TTTATATTTT	537780
TTGTATCTGC	TATTTTTTTA	ATAGATTTTA	TTATTACAAA	ATCTATTTCA	CTAGAGTTTA	537840
TTGCTTTTAT	GAAAGATCCG	TCTATTTTAA	GTAAGTCTAT	TGGTAGTGTT	TTAATATATG	537900
AGAGTGATGT	ATGTCCGCTT	CCAAAGTCAT	CAAGTGCTAG	CTTGATTCCA	AAACTTTTTTA	537960
ATTCTTGAAA	ATATTTGTTT	ATTATCTCAA	AGTTTTCAAG	AATTCAGTT	TCTGTTATTT	538020
CCAAGCATAT	ATTTTGAAGT	GGGATTTGGC	TTTTCAATAA	AGTATCTCTT	AAAAAGATTC	538080
GAAAGTTTTG	GGATTTTAGT	GAATAAGGAG	ATATGTTAAT	TGAGAAAATG	TGAATTCCAT	538140
TTTTTGATAC	AAAGCTTTTG	TATTCTCTTA	AAGCCTTTTT	AACCACCAAT	GTATCAACCT	538200
CAACAGTTAA	ATTATATTTG	TCTATTAAGT	TAAAAATTTG	ATTGTTTGGA	ATTGGTTTGC	538260
CCATGTGGTC	AAAAAGTCTT	GTCAAGATTT	CTATTTTGGG	CTTTAAGTTC	TTTTTAAGAG	538320
GATTTATTTT	TTGATAATAA	AGAGTAAAAA	AATCATTTTT	TATTGCTTTG	AGTATATATT	538380
GAAAAATTTT	GTTTTGATTT	TTTAAAATCA	CCGCTTCTGG	TAGTTCCTCT	TTGTATATAG	538440
TGGGATTAGA	TTCTTTGTAT	TCCGATGATA	TTTTTGTAGC	CATCATTAAT	TTGGGGATTT	538500
TGAATCTTAA	GTTTTCTTTT	AAATTTACCT	CTATTATTCC	AATGTTGAAC	TTGAATATAA	538560
TAATATCTTC	TTTTTTTAAAT	GCCAGAGCAA	TTGTTTTTTT	GATTTTTTTG	GCAATTGAGA	538620
TTATTCGCTT	TTCTCCGCCA	CTGTGCTTA	TGATTACTAT	TAAATTGTTG	TGTTTTAACT	538680
TAAAAATATA	TTCAGAGTAT	AATGACATTA	TTTTTGAATA	CATTATTTTA	AGTATTTTTG	538740
CATTAAGTTT	TTCTTGATCT	TCTTTGTATT	CATATTCTGC	TGTTAGGGAT	ACGTCTAAAT	538800
TAAGTAAATA	TATGCTTTTT	TTTTTGTAAG	TATCCATATG	GTTTACTAGT	AATTTTTCAA	538860
TTTCTTTGGC	ATTTTGAATC	TCGTCTTGCG	AATCAATAAT	TTCTAGATAT	TTATAGTTTT	538920
CTATTTTATT	AGAGTTTGAT	ATTTCTTTAA	TTGTTATTAA	TTTATCGATA	TTGTTTTGAG	538980
CAATTGTGCT	AATAAATATA	TCCACATGTA	GTTTTTTATT	ATTTTTTAAA	GTAAAAAGAC	539040

AATCAGTTAT	TAATATATTT	TTAAATTCAG	GAATAGAATT	TGTGTGATAA	CTTAAATTTA	539100
TTTTTCTAG	CTTTTCCCA	TCTCTGATAT	CTATGTCGGT	TACTTTGATT	ATATTTCCAG	539160
AGGTTTTCAT	TGGAAGATTA	AGATTTTTAC	TACCTTTTTT	ATTGATATAA	ATAATTTTAT	539220
TTTtagtGTT	TGTGATGATT	ACTATTTCTT	TTATGAGTTC	TGATAAATTT	AAAAAGAAAT	539280
CCAGAGTTGT	GTTTTTATTG	TCGCAAAATA	ATTTTTTTTT	ATGTATTAAG	CTTTGCTTAT	539340
ATTCTAATTC	GCTTATATCT	TTTATTATTT	CTATGTGATC	AAGTTTTTAA	TATTCCTCAT	539400
CAAATTTTTT	TTTGCTAATT	ATGATAGAAT	GGATTTTGTT	TGCATTTTTT	AATTCGTTTG	539460
CAATGTTTAT	TGAAAAATCT	ATTGGTTTTT	CATAATTATA	AATAATAGCG	AATTTAATAT	539520
TATTTTGTTT	TACATATTCG	CTGTATAAAG	CTTTTTCAGA	TTTTACGATT	TGAATTAAGT	539580
TAAAAATAGA	TTTAAGCTTT	ATGAGATCTC	TAAGTCCAAC	TTCTTTTTTA	GAGATTATAA	539640
CTGAATTTAT	ATTTTGATAA	TTATTGACTT	TGTTTATTTT	ATTGGCTTGC	TCTTATTTTA	539700
ATTTTGTAT	GCCAAGTTGG	TGTTATTTTT	TATTTTTTTA	TCTGCAATTT	TTTTAGTGAC	539760
TATTATCCAG	ATTAATCCTG	AGAGCATCAG	CGTTAGCGAG	AGAATTTGTC	CCATTGATAT	539820
GTTTAAAAAA	GAAAATTCGG	ACAGGCTTGT	AATTGGCTTG	TAGGTTATTA	TAAATCCAAG	539880
TTCTTTGTCC	GGTCTCTTA	AATATTCAAT	AAAGAATCTG	AAAAAGCGT	AAAGCATTAC	539940
ATATACACCA	AAAATAAATC	CATCATATTT	TTTGATTTTT	TTAAATAAAA	ACCATAGTAA	540000
CAGAAAAGTT	ACAGGTCCTT	CGAAAAATCC	TTCAATAAGT	TGAGAAGGTA	TTCTTGGAAG	540060
GTTGATTAGC	AGGTCATGAG	GCGAAATTTT	AAGCCCTACT	GATGATGCAA	ATTCTTTTAC	540120
ACCCGGTATA	TTTGTGTCAA	ATGGTTCTGC	ATTAGGGAAT	ATTATTCCCC	CTTTCATTAC	540180
TCTTCCATAA	AGTTCTGCAT	TTGCGAAATT	AGCAAGTCTT	CCAAGTATGT	AGCCAGAAGA	540240
AAAAGCTATT	GATCCATAGT	CTGTTAGTTT	TAGAAAATAT	TTTGAACAT	TTGTATTTTT	540300
GAGATTTGTA	TTTATTGTTA	TTAAAGGAGC	AATTATTGCC	CCCCAAAAAC	CACCATGGAT	540360
GGCCATACCT	CTAAAGCCTG	TAAAATTCCA	ATGCTGGTCG	AATGGCAAAA	GGATTAGCCA	540420
GGGATTAGAA	TAATAAATTC	CCGATTTGTC	GTAAACTAAG	GATGATGCTA	GTCTGCCTCC	540480
TAAAATTGCT	CCAAGTACAA	GTGAGAACAT	GAATATTTCA	TAATCTTCTT	TTTTAATATC	540540
AACGTTGTCT	GATTGTATTT	GATACCAAAT	AACTTATAA	GAGATTAGTA	TGATTAAAAT	540600
ATAAGATAGG	CTATACCATG	TAATTGGTAT	ACCTTGAATT	ACTTCAGGAT	GTAACCAACT	540660
TGGGTAATTT	ATGTAATTTG	GCATTAGACC	TCCTTAGCCT	TTTCAAGCTT	TTCAACAAGC	540720
TTTTTTTTTA	ATAACATATT	TTGCTTTCTT	AAGGTTTCGA	TTTCTCTTTT	CTGAGATTTT	540780

ATTATATCAA	TAATTTCACT	ACTTTCTATT	GTTTTGTGTTT	TTATCAATGA	TTCAAGGTAT	540840
TCAATTTTTT	CAATATATTC	TTCTTGAGCC	TCTCTTAGTA	CAAAATCATA	ACTTTCATTT	540900
AAATCTTCTT	CGTTTAAAAG	CTCGGCATCA	TTTGTTAAAT	CTTCAATTC	GATTAATTTT	540960
TTTGCAATTT	TTTTTATACT	TTTAGAAGTT	GAGCTTGTAG	GTTTGTATAT	AGTGATGGGT	541020
ATTTTGCTGT	TTAAAGCCTG	ATCAACTATT	TCATCTTTAT	AGATTGCTCC	AATACTTTGT	541080
AAATTTATGC	TTAAATAGTT	TTTTGCTGAT	TTTATTATTT	TTTCGGTTTT	TTCAATGTCT	541140
TTGGGAGCTT	TGAGCATATT	AAATATCATG	AAAGGGCTAA	TTGTCCTAAA	CAATTTGTTA	541200
AATTTAGAAT	AATTTTCAGG	ATCTTCGCTT	TCAAGTTTTA	ACAACAAATT	AGGTATATAA	541260
ACCCTTTGAA	GATCGATTGA	ATTTTGTTTT	ATTGTTCTGA	GAATTTTCATT	TCCTTTTGTT	541320
CCTCTTTTAA	ACACACTTGA	TAACAATCTA	AATATTATAT	TTTTAAGAAA	TAAATATGCA	541380
TTCATTGTAG	CTGTTACTGT	TGGTGTTGTT	ACTATTACTC	CTCTTTTTGA	CATTAAAAAA	541440
AAGTCTATAA	TATTAAAAGC	TGTTCCCTGCT	CCAAGATCAA	TCACTAAGTA	ATCATATTTT	541500
AAAGATTTTA	AATTTTTTAT	TATGATTTTT	TTTTGGGAAG	CAGCTATATT	AGCAAGTTCT	541560
GGAATGTCAG	AATCTCCTGC	AATGAAGTTT	AGATTTTTTAA	TTCCAGATTG	AATAATGATG	541620
TCTGAGAAAT	TAATCCTTGT	TTTTAAAAAT	GTTCCCTATAC	TTTTTTTAGG	TATAATGTTT	541680
AACATTGAGT	GCAAATTAGA	TGCTCCGAGG	TCAAGATCAA	CAAGCAATAC	GCTTTTTTCCT	541740
TCGTTTGCCA	GGCAAATTGC	TATGTTTGTT	GAAAAAAGAG	ATTTGCCAAC	TCCCCCCTTA	541800
CCACTGGCTA	CAGGAATAAT	AATCAAGCTT	TACTCCAGGT	TTTTTATTTT	TGCTTTAATT	541860
AGCACTAATA	TTGTTACATT	AAATACTAGG	TAAACTACTG	TAATTCCTAA	AATTATGGCT	541920
AGAGAGGTTT	GATAGACGTA	TATTTTAAAA	ATAAATCCCA	AGATGAATAA	TAATAATGTT	541980
AATATTATTT	GGAATAATTT	AGTTATTACT	ATAATGCTGT	GAAGAATTTT	AAATTTTTTCG	542040
TAGATAAAGT	AATAGGTTGT	TAAATTGGCC	ATGAAAAATT	CAGGTGAGTA	TAAGATAAAT	542100
GTTAACATAA	ACTTTATGGA	GTAATTATTA	ATGAAAATTA	ATTTATTAAT	GGCTTGATAT	542160
AATAAGGCTA	AGATTAAAAG	GCTTTCAGTA	ATTTGTAAAA	CAACAAGTCC	TGCTCTGTAA	542220
AGGCTTTGTG	TTTTTTTAGG	ATGTGAGTTT	AACATAGTTT	TAAAATATTA	TATTATGGAA	542280
ATAAAATCAA	GTTTTAATTT	TTGCATTAGG	AATGAATAAA	TGAAAAATAA	ATTTTTAATA	542340
TGTGTATATT	TTTTATTGAC	TCTGGGTATA	AGCTCTTTAG	TAATTGTTGA	ATCTATTTTT	542400
GCTTTTGATG	AATCTAATAA	TAAAGTTATCA	AGATCAAATT	ATGAGCAGAT	GATGATTCAA	542460
GCTTTTGAAT	TTGTAAAAGA	AAATTATGTT	GATCCTGTAA	GTGATGAAGT	AATTTTTGAA	542520
GGTGCTTTAA	AAGGAATATT	TCAATCCCTA	GGCGATCCTT	ATTCTCAATA	TTTGACAAAA	542580

AAAGATTTAG AAGAAATTTT AAAACAACA GTAGGAGATT ATGTTGGCAT TGGAATTTCT	542640
ATAATAAAAA AAATGCATTC CCAAGATAAG CAAGACAAGG CAAAAGATTT TGATCCTAAT	542700
AGTGCTTGTG TTTCTATTGT TACGCCTTTT GAAGGAGGTC CGGCTTATAA GGCTGGAATT	542760
AAATCTGGAG ATTGTATTAC CGCTGTTGAT GGCAAGAGTG TTTATTCTAT GGAAGTAGAT	542820
CAAGTTGTTG ATCTTTTAAA AGGTAAAGAA GGCACAAAAG TTAAAGTATC TATTCTTAGG	542880
GGAAAAAATT TAACATTGGA TTTTGAACCT ACAAGAGAGA AGATAGAAAT ACAAACAATC	542940
AAGTATGACG TTATTAATTC AGATATTGGC TATATAAGAA TAGTAAGCTT TAATCCACAC	543000
ACCTCTGTAG ATTTTAGAAA AGCTTTAGAT AATCTTAAGA ATAAAAATAT TAAATCTTTA	543060
ATTTTAGATT TAAGGCTTAA TACCGGAGGA TATTTTCAGG CAGCTATAAA AATGGCGGAT	543120
GATATTTTAT CTAAAGGAAT TATTGTTTCC ACAAATCAA GAAATCTAG CAAGCCTATT	543180
GATTATAAGG CAAGCTCAA ACAAGTTTTG CCTTCAAATA TAAAAATTGT TGCTTTAATA	543240
GACAGATCAT CAGCCTCAGC ATCAGAGGTT TTTGTAGGAG CCTTAAAAGA CAATAAGAGA	543300
GCATACATTA TAGGGGAAAA GTCTTATGGC AAGGGGCTTA TTCAGCATGT AGTTCCTTTT	543360
TATACTGGTG GATTTAAAAAT TACAAGCTCA AAGTATTATA CTCCATCTGG AAAGAGTATT	543420
CATAAGGTTG GAATTGAGCC TGATTTGGAA ATAAATCTC CAGATTTTTC TGAGGAGGAG	543480
GCATTAATAT ATAAAGAAAT TTTTGATAAA AAGCTGATAG AAGGTTTTTT GAAGGGTAAA	543540
AAATTCATTA CCGAACAAGA GATTGATTTT TTTGTTGAGA ATCTTGTAAG AGAAAATCCA	543600
AAATATAAAA TTGATAAAGA ATTTTTAGGC AAGTATGTGT TTTTAAATTA CTATCAGGAC	543660
AATAATAAAG AATTGCCAAT TTATAATCTA CATTATGACA AAGTTTTAAA AACAGCTTGT	543720
GAGTATTTGT CTAAATTAGG TAATTAAATT GTGAAGCAAA TTGTTTTGGA TGAGAATTGT	543780
TTAGCAGGTA ATTTTATTAT TGTTAAAGAT GCAAAAATAT ATCACCATCT TGTTAATGTA	543840
AGACGACTTA AAAAGGGTGA TAAGCTGAAC ATTCTTTTAA AAGATAAAGA ATTAAGGGCC	543900
TCAGAAATAG TAAAGATTGG TAGTAATTTT ATTAAGTTTA CTACCAATAA AATAGATAAA	543960
ATTGAAAAAA ATAATTTTGA GATAAGTATT TTTATTTCTA GTTTAAAGGG CAGAAAAATA	544020
GATTTGGTGT TAAGACAGGT TGTGAGATT GGAGTTTCAG AAATCAATAT TATTAATGCG	544080
GATCGTTCTG TGTCGAAAAT AGATATAAAC AATGCATCTG CAAAATTTT AAGATTTTCA	544140
AAAATAATAG ATGAGGCCTT AAAGCAAAGT GGTAATAAAA TTGTTCTAA AATTAATTTT	544200
TATAATAATT TTTTTTATTT ACCTTATTCT TTTTGTACTA CCAGATATTA TGTTGCTCAT	544260
CCAAGTGGA TGATTTTAAG CAAGAATGAA AGTTTGTACA ATTTTGCAA AATTGGAATT	544320

ATAATAGGTC CTGAAGGATG CTTTTCGGAG TCCGAAATTG TCTTTTTC	GGAGAAAGGC	544380
TTTAATTTTG TAAGGTTTAA CACTCCAATT TTACGAGCAG ATACGGCTAT	TATTTATTCG	544440
CTTGCTTATT TTAAGGCATT GTTAGAGGAT TATAATGGCT AATTTAAAAG	ACATATATTC	544500
AAAACCAGAC AGATTTTATT TTTTAGGTGT GCCTATAGAT GTTTTGTATA	GTCCGAGCAG	544560
CTTATAAGCA GATTTGTCTA TCTTTCAGGG CATCCTTATC ATTCCAATAG	TAATTTTAT	544620
CGGGCTTAAA GCTTTTCTAA AGGCTTTGAT TTTTAAAAG TTTAGAAATC	ACATTAAAAA	544680
TTCTTCTCTT GTTTTTTTAA ATCTAAAAT TGTAAGATTT TTTTATAGGA	TTTTTAAAAG	544740
AGTTAATATT GATTGTTATG ATTCAAATAC AGTTCTTCTC ATTTTAATGG	AAATACTAGA	544800
AAATGCCCAT AAAACATGTT ATATTATTGA CAAGGATAAA GTGATTTCAA	AGAAAAAATT	544860
TTTAAGATTG AAAGAATCTC ATAAAGAAAT TAGTTTTATT GGGTATTATG	ATTTAAAAGC	544920
TGTAAAGAGA AATAAAGAAA TGTTTTTTGC AAATATTAAT AACTTACTC	CTAGTGTAAT	544980
AATAAGCTTT TGTAATGATA GATATCTTGA AAATTTATTT TATGAAAATA	AATTTAATAT	545040
TAGAACCAAT TTAAGTGTTT TTTTATGAAC TTTTAAATTT TAACATCTA	TATTTTATGA	545100
GGTAAGTATG GCATTTTTGC TAAATCAATC AGTAGTTTAT CCAATGCATG	GAGTAGGTAC	545160
GATTAAGGAT ATTAGGACTA AAGAGTTTAA TGGTGAGATT ATTGATTATT	ATGAAATACA	545220
TTTTCCATTT AATGATATGA TTTTATGGT TCCTGTTGCT AAAGTTGATG	ATTTTGAAT	545280
TAGAGCTTTG GTTAGCAGGG AAAAGGTAGA AGAAGTTTTT GATGTTATTA	AAGAGTTTGA	545340
AGGGCAAATA GATTCAAAAA AAATAAAAGA TGGTGGTCAT GAATTTTATA	AAAAAAGCGA	545400
TATTTTAGAT ACAGCAAAGT TATATAAGTT TTTATATAAA AAATCTACTC	AAAAAGAACT	545460
TCCTTTTTTAC GAAAAAAGGA TTTTGAATGA TTTTGAGTTA ATATTGGAGC	ACGAGATTAG	545520
CTTAGCTTTG CAAATTAGCT TTGAAGAGGC TAAAAAGAAG ATTAAAAATA	TTTTGGTCTGA	545580
TAACAAAAAG GCTTAAAGTT TTTTCAATTT TCGAGGGGGG AGGATTTGCT	GTGTTTGATT	545640
CTTTAAGATT GATCTTTTTA ATAATTTGTA GGTTTATCTT AATATTTTGC	CTTTTTTCTT	545700
TAATGTTTAT ATGTACATTT TATTTGAAAT ATAAGTTTTT GTATTTTAAT	TTTTCTATTT	545760
TTAGCTATAG TCTTTATTAC AATGCTTATA TTTATCTTT TCCTTTGTCC	CTTGTTGTTA	545820
CTTTTATGAG AATATCTTGT CCCTTTTATG GAATAGTTTT AAATTCATCT	AGAGAGTCTT	545880
TCTATTTTTA TTGTATTATC TTTGTTCTTA TTTTATTGTT TTCTTATTTA	GGATTTTATG	545940
TTAGTCATAG TTTTCATTCT TACTATATTA ATAGCAATAG AAATGATAAT	TTTATCCTTA	546000
AAGATGAGAT TGTGCATTTT TTAAATGATA AGATAATATT TTCTAGTAAT	AGGCCTAGAA	546060
TTTATGGTTT TAATGGAGTT TTAATCGTTT CGGAGAATGA CAAAGGGGAT	AAAGGTTTTT	546120

CTTACCAATC	AAATATTTCC	AATTCTAGTA	AGATTGATTT	TGTTGAGAAT	AATTTTTTAG	546180
AGCAAAAGAT	TTATAATAAT	TTTGTTGATT	TTCTTTTCAG	AGATTTAAAA	ATTTTGAATA	546240
ATTTTCTACT	CTCGCTAAAT	TATTTAAATT	TAATTTTTTA	TATATTGGGA	ATTTCTTTAT	546300
TGTTATTTGC	TTTTTCTTAT	GTTTTTAATC	TTATTTTTTC	AAATAGTTTT	GCAATATTTT	546360
TTTATCCTAT	TTTTATTATA	CTTTTTTTAA	AAATTTATAA	TGTTTATTCA	ATTGAGTTTC	546420
CCAAGATTTA	CAATGTAAAT	ATAGGAAAGA	GCATGATCTC	TGATTTTATT	CCTTTTATTT	546480
TTTGTGTTTT	AACTTTTTTT	TCTACCTATT	TATTTGGTTT	TGTTTCAGAA	TATATTAAAA	546540
TCAGCAAAGA	TTTGGATAAT	AATTTATATA	AGGGTAGTTA	ATTCTTAAAG	CTTATGAAAA	546600
GAGAAATATA	TGCATTTTTG	AGCAATTTTA	TTATTTTTAT	GTGTTTTTTT	CTAGGTTTGC	546660
TCTTTAGTTA	TTCATATTTT	TTTGGAGAAA	ATTTTTTAGA	AAAGCATAAA	TTAATAGCAA	546720
CTTTTTTTGA	TTCTATTTTG	CTTTTTTATA	AGTATTTTTT	TGGGTTTTTT	ATTTTTATTG	546780
TTTGTATTTA	CTTTGCTTTT	TTTGTTTCAGC	AAGAAATAAA	GATTCATTTA	AAATCGCATA	546840
ATGGATATTT	ATTTTCCAGG	CTTTATGCAT	TTTTACTATT	ATTTTTTATT	ATAGGACTCT	546900
TTTTTACTTT	TATATTTAAT	TTAATTTTGC	CTTATATAAT	TGCTCAGAGA	AATGAGTATA	546960
AGTTTAGTTA	TGATAGATAT	AATCTTCTTG	AAAGTGAAGC	AAATGAAATA	TCTCTTAAAA	547020
TTAAACATAT	AGATATAAGT	TTGGCTGCAA	ATAGATTTTT	TTTATCTTCT	GATTTGACAG	547080
ATTCAATGAA	GCAAAAGAGA	AAGCATCTTG	AAAATTTGAT	TAGAATATAT	GATAAAATGC	547140
GAATTATTTA	TGTAAATAAT	GAAGAGCTTT	TAACAAATTA	TTATTTAGTG	AAATCTGAAT	547200
ATAGTAAAAT	TCCAAGTTAT	GACGTTGATT	TAGAAAAAGT	TAAAAAACT	TTTTCAAAAT	547260
ATCCTTTGCA	AAGTCTTAAA	AAGCAAGATT	TTTTTAATAT	TGTCAATGAA	TTTATTTCTA	547320
AAAATGATTA	TTATACAGCC	AATTATTTTG	CTTATATTGC	TTATGTTGCA	ACAAAAGACG	547380
ATAATTTTGT	TGTGCTTTTA	AATTTGACTT	TAAAGTTTAT	TAATGAAAAC	AGGAATTTTG	547440
AAAAAGAAAA	AATGCAGTTG	ATTTCCGAAG	AAAAGCAAAA	AAATTTTTTG	TTTCTTAATA	547500
CTGAAAAATT	TAAATTAGCT	TATTACGGGT	TTTCGAATCT	TTATAAGTTA	TTGCCCAGCG	547560
ATAATGAAAT	TTTGAATTAT	AAAAATAAAT	CTCTTGAAAA	GCTTAGGAAA	AGATATCTTT	547620
TTTTTTGATGA	GATTGAAAAA	TATTTTGAAT	ATTACGGAAT	AAACGATGTA	TTTTTATTGC	547680
AACCAGATTC	TAAGAGAGGT	TTTTATGATT	ATATTTATAT	GCAAAAAGTT	GTGGCCTTTA	547740
ACAATCATTC	TAAAATAATA	AAAAATTTTG	AAC TTATTAG	ATTTAATAAT	ACAGGGAATG	547800
TTATATTACA	TATTAAAATT	CCATTTGCTA	CTTTGAAGGG	TAATTCTGTG	TATCAAAAATA	547860

TTTGTAGATAA	AGACAATGAG	CAGAGCGAAA	TTACTCTTAC	CAAGGTCTTT	GTGTCTACGG	547920
ATAGCTTTGA	TACAAATGTT	TTAGAGGTTG	TCAAAATTAA	TGAGAATGTA	GAAAATTTAG	547980
CTTTATTTTC	AAATTTTACT	GAGTTTGGAT	TTTTTTTAAA	AATTCAAAAT	TTGCCAAGCG	548040
CTTTTCATAG	GGTTGCTATA	TTAAATTTGA	AATTAATTAA	TACTTTTCC	TTAAGTTTGG	548100
TTTTGCTGAT	TTCTCCTATT	TCGCTAGTTT	TAATAGGGGC	ATTTTTTATC	TCTTTGTTTT	548160
CTAAATAGA	ATTTAATTTT	AATCCAAGG	CTATGATTTT	TCTAGTTTCA	TTAATGATAG	548220
CTATTTTCTC	AGGGATTACT	TGTCTTTTTG	TAAATTATTT	TCTAATTGTT	TTTACCTCTC	548280
TTCTTATATA	TGTTTTTAAT	AGCGTTTACG	TATCTTTAGC	TATTCFTTCT	GCATTATTGT	548340
TTTTTCTTAT	TTTTAAAATA	ATTACTTTGA	ATTACAAGGA	AAGACTTATT	TAATTTTTTAT	548400
TTTTTTTTTAG	ATTATTAGCT	TTAGAGAAAA	ACCATTCATT	TATTAGTAAG	TTTTCTTTTT	548460
CAATTGTTTT	TTTGCTTAAT	ACATAGGAAT	GGCTATTGAT	TTGAGTTTCG	TCAATAATAA	548520
AAGGAGATAT	TCCATCAATT	GAATGTTTTA	TTTTTAAATT	TAATTCCTTG	TAAGGGGTAA	548580
AACCATTGGC	AAATCCAAAA	CATATATTTG	ATTGGGATTG	ATTGTTAAAT	CCAATTAGGG	548640
TTTTTTGAGT	TTTTTTATAC	AATATCCAGT	TGATAAATTT	TTTAGTTAAA	ACAGATGTTT	548700
CTAAATGCC	AATAAAATTT	GGGTTTGAGA	TAACAATTTT	ATTGTTATCG	TTTATTAAAT	548760
AGGAAAATTT	TATTTGTGAC	TTCTCTTGTT	CGCTTAAGCT	ATTGTAGAAG	GTTATATCGC	548820
TCAATCCTGC	TATTAAAAGA	GATTTTTTAT	TAAGCAATAT	TTTATTTAAC	TTTAGGTAGC	548880
CGTATTTATT	AAAGAAATCT	TTTGTGCAAGT	CCATTTGTTT	TGTATTTAAA	AATGATGAGA	548940
AATATTCTAG	CATTTTTTAA	ATTTGATTCT	CATTATAATT	TAATTTATTT	TTTTCAAAAG	549000
AAAATCTCAC	ATTATTTATT	TGAGAAATCA	CATAAAATAA	ATTTTCAGAA	ACATAAGGCG	549060
ATATAAAAAA	TTTTCCATCT	TTAATGAAAT	TTTCGTATTC	TTCTTTTAGA	TATTTAGTGT	549120
TTATGTATTT	TTTAATATGA	TGTGTATTTT	TATAGATTAA	AATAGGAATG	TCAAAGCCCA	549180
ATGGAATAAT	TTTGTAGTTA	AATTGCTTGA	AAATATGCTT	TAAGATAGGA	TAATCTGGAT	549240
TATAATTGAT	TTTTACAGAT	TTAAAATGGT	TAGCAATATT	TGTGTTACCA	ATGTTTTTAG	549300
AAATAATTAT	TTGTGCATTT	TCTTTTTCTA	TTGTTTGCAG	ATCAATATTA	TTTCTAAACT	549360
TAATTATAAA	ATTTGCTTTA	TTTTCTATAT	TAAATTGATT	TATATAAAAT	GGTATTGTTT	549420
TATTGTCAGT	TAGTACAACG	ATGTTCTTAT	TTGTTGAACA	GCTAGGGCTA	ATTAATAAAA	549480
TTGCTATTAG	TATTAAATTT	TTTATTCTCA	TAAAATTATT	CAAGTTTTTT	CTTTTATTTT	549540
ACAATAAATT	ATGTATAATT	TTTATAGTTA	TATTAATTTT	CATGCTTAAT	TGGAAATTAG	549600
AGTAAGGTGG	CTTAAGAGCT	TTTAGGGGGA	TGATGAATTT	GGGTTTATTT	GATTTTATAC	549660

TTTCTATGTT	TAGTATTAAT	AAAGAACTTA	CTTCTGAGCA	AATAAAGCAA	AAAAGGTTAA	549720
AAGAAGTTAA	AGTTAGTTTA	GGCAGAGTAA	GTAATTTTTT	TAATGCTTCA	AAAATTCAGG	549780
CTTTACCTCA	ATTTTCTAGA	TTTCTTTATA	ATTTTATAAA	AATTTTTTCT	CCCTTAAGGC	549840
CATTTGCACA	AAGATATAAA	AATTCTAATA	AAATTGTTCA	TTTTGTTGTT	GAAAAATACT	549900
TAAATGAAAA	CCAAAAGAAG	TCTTTAGATT	ATATTTATTC	TTTTTCTGCA	AGCGATAACA	549960
TAAATTTTGC	CTCAGATCTT	CCTAAAAACT	TACATAATAA	TTTATCTTAT	TTGTTTAAAA	550020
ACATAACTCA	AGAACAAATT	AAATTGATAG	ATGAAACTTA	TGAAGCTTTG	CATAATTTTT	550080
TTGATTTAGT	CTTATATCAA	TATCATTTGG	TTCTTAAAAA	TTTTGACAAC	TTGCTTCCAG	550140
AAGATGATTT	TGTGTATAGG	CCTAGATTCA	GCTCTATAGG	TTGTGGAGTT	ATTATAGATG	550200
ATCTTAAAGA	TTTGTTAGAA	TGTATTTCTT	GCATTAAGAA	TATTTCTATT	TGGAAAAACC	550260
TTTATGACAT	TATTTTAGAA	ATTTATGGGA	ATAAAGAAGA	TTTTCCTATT	AAGTCTAATG	550320
TATGGATTAA	GGTTATTTCT	TCTATTTTGG	ATATAAATAA	GAGTAAAGAA	ATTTTATATC	550380
TAATAAGATA	TGTTAGTGGG	GATCCAGATT	ATTTCCCTAT	TTCTGTTGGG	CAAAAACCCA	550440
ATCCAATAGC	AAGAATGTTT	TTTAATGATC	TTACTAAGCA	TGTTGCCACT	GAAATTGAAA	550500
AGATTAAAGT	TTTGCAAAAA	AATAATAAAT	CTAAAAATAT	AGCCGAGCAG	CTTTTCCCAG	550560
GAATATCTTT	TTTAAATTTG	GATAATTATA	ATGAAAAAAT	GAATGAAAAG	ATTGTATCTA	550620
AAATTATGAG	CACTACGGGG	TATATTTATT	GCGAACTTTT	AGTTTATTTG	AGAACATATA	550680
CTATTTATTT	TGTTAAAAAA	GATCTTAATG	ATATTATTAA	TTTACTTATT	ATTAAAGGAC	550740
AATGGAAGCT	TATAGAGCTT	TCAAGAGAAA	TGTCTAACGA	CATGCATGCT	TTGATTAATA	550800
TTTATGCAAG	TCTTATTGAT	TTTGATTCTA	ATTTGGGGGA	ACAAGGCGGT	TATGGCAATA	550860
GAATAAATGC	ATTATTGCAC	AGAGCTTCTT	TGGGGGATAA	ATCTTCGGAG	AAATTGTTGT	550920
TAAATATAAT	AGCAGATGTT	AATAAAAAGG	CGTTTGCTAT	ATCAAGCGAA	TATTATTCCA	550980
AAATATATTC	TATTGAGCAG	CGTTTGCAAG	ATTGTCTTTC	AGACTATTCA	AAAGTCTCTT	551040
TGGAAAGAGA	GCTGATTTAT	AATTGGAAAG	AGCTTGATAT	GGATCTTGCT	AAAAGCTATG	551100
GAAACAATTT	AAACTTTGGA	GGTATGATGA	AAAATATTTT	GGGTAGTTTA	GCTTTATTTT	551160
TAAAGTTAAT	GGATTTATAT	TTGGAGAAAA	AATCTTAATT	TGAAGGAGTG	TTAAATGGC	551220
TAGGAAGTGT	GAGATAACAG	GAAAAAAAAC	TATGTTTGGA	AACAATGTTC	CAAGGAAAGG	551280
GCTTGCCAAG	AAAAAAGGTG	GAGCTGGACA	ACATATTGGA	GTAAAAACCA	AAAGAACCTT	551340
TAAGGTTAAT	TTAATAAATA	AAAAATTTTT	TATTCCAAAT	CTTGAAGAA	GTGTTAGTAT	551400

TAAGGTTTCT	GCTAATGCGC	TAAGAAAGTAT	TTCAAAGATA	GGGCTTGATG	CTTTTTTAA	551460
GAAAACTGC	AAAAAATAG	AAAACCTTTT	ATAAATTTTA	GTTTTGATAA	TTTTATCTTA	551520
TTAGAATACT	GTTTGATATC	AAGTATTCTG	GGGAGTTAAA	TGTTATTTTT	GAGTCTGTAA	551580
ATTCGAAATG	TTTAAAAAGG	CTTGAAATGG	TCATGATTGC	ATTTATATTT	TCCGGAAATA	551640
TTTTTTTTGA	TTTATAGTTT	TCTAGTATTA	GGTTAAGATT	AGGCAATTTT	TTTTCAAGAA	551700
GGATATGCTT	TAAATTTTCT	TCAAACCTTA	AGGCTTTTTT	TATATTTGTA	GATTTTGAAA	551760
TAAAGCAAGA	TAGAAAAATA	AATGAATTTT	CTTCTCTGTT	TATAAAAGGT	TTTAAAAACT	551820
CGCAAAATTT	TAGTAAATGT	TTATTGCAAG	TTTTTCCAAA	AATTATTGGA	ATTATTTTTA	551880
TGTTTTCCCTT	TATGTTGCTA	ATAAAATTCA	ATGTAATTTT	AATTTTATGA	TCATTTTCGA	551940
TTAATTTATC	GTCTATATTA	ATAAAATTTA	AGGTTTTTAA	TAATTTTAAT	ATCTTTAGGT	552000
TTACTTTAAT	ATTTTTATTA	AAAATTTTCC	ACACATTGTG	ATTGGATATA	TTAATTAAAA	552060
AATTGCTTTT	GGCCTCAGAG	ATTATAAATA	CATTATTAGT	TTGATTTGAT	ATTATTTTTT	552120
TAAACAAGCA	TTCATTTTTT	AAAAAAAAC	CATAGCTCCC	ATAACTTGTT	AGGAGGGCTT	552180
TGTGAGTTTT	TTTTTCTTCC	AACTTAAATG	ACAAGTCGTT	TGTATTATCT	GAATAAAATA	552240
TGTTTTCAAC	CAAGGAGTTT	CTAGCTTGCT	TTATATATTT	CGTCCTTTGA	TTGCATCTTC	552300
TACTGTGTTT	ATTTCCATAA	ATTCTGTTCC	TTTTTCAATA	TTTCTATTTG	GATTTCCAGA	552360
AATAATTATT	ACAGTATCTT	TGTCATTAAC	AACACCTTGT	TCTTTTAACA	TTTTAAGAGA	552420
AGTTACTACA	AATTCGGTAG	TTCTTTTGAA	ATTATTGTCT	ACAAGATTAG	AATAAACCCC	552480
GTAAGATAAT	GCTAATTCTC	TTGCTAGTCT	TTGCTATTTT	GTTGTAATGA	ATAATGGAAC	552540
ACTTGCTCTG	TAGGTTGCCA	TTATTCTTGC	GGTTTTGCCT	TTTAGAGAAT	CTACAATAAT	552600
TGCTTTTATG	TCCATAAGTT	TTGTGGCATC	AATTGCACAT	TTGATAATAT	AGTTTCTTGT	552660
GATACTTTTA	TCGTAAAAAA	GTTTCATCCTT	ATATAAGGTC	ATTTTTCTGT	GTTTTTCAAC	552720
TTTTTTAGCA	ATGCTTGTC	TCATTTTTAC	AGCTTCAATT	GGATATTTCC	CGTAGGCGGT	552780
TTCTCCGGAT	AACATAATTG	CGTCTGTGCC	GTTTAAAATA	GCGTTAGCGA	TGTCAGACAC	552840
TTCTGCTCTA	GTAGGTCTTG	GATTTTCAAT	CATTGTATGA	AGCATTTGAG	TTGCTGTAAT	552900
CACGGGTATT	CCATACCTTA	TACAGGTTTG	TGTTATTTTA	AGTTGAGCAA	TGGGTACATC	552960
TTCTGCAGGA	ATTTCAACTC	CCATGTCTCC	CCTTGCAACC	ATTATTCCGT	AAGAAGCTTT	553020
TGCAATTTCT	TCAATGTTGT	CAATTCCCTC	TTGATTTTCG	ATTTTGATA	TAATTTTTAC	553080
ATCAGGATTT	CCAGAGGCAG	TTAAAATTTT	TTGAACATCT	TGAACGTCTT	TGGAATGTCT	553140
TACAAACGAA	TGGGCAATAA	AATCAACATT	ATATTTTGCT	GCAAGCTCAA	TAAATCCTTT	553200

GTCTTTTTTCG	GTTACTGATT	GTAGCTTAAG	AGAAATTCCG	GGGGTATTGA	TTGATTTTTT	553260
ATTTTAAATT	TGGCCGTCAT	TTTAAATTC	ACAAATTAAT	CTGTCAGGCA	ATTTGGCAAC	553320
AACAGTCATT	TCAAGTTCAC	CGTCATCAAT	TAGCACTTTA	GATCCTTGGG	GTACTTCTTT	553380
AACAAATCCA	TCATAATTGG	TTTGAAAGTT	ATTAGGCTCA	TTAATAGGCG	AGGTTGAAAT	553440
GATTACCTTG	TCTCCAGTTT	TTACAATAAT	AGGATTTTCA	ATATTTGCTG	TTCTAACTTC	553500
TGGTCCTTTT	GTATCAATCA	TTAAAGCTAT	TTTATTTGAA	ATTTTCTAA	CATTGTCTAT	553560
TACTTTTATT	GTATCTTCGT	GTGATTGATG	AGCAGTATTT	AGTCTTATAA	CATTTACCCC	553620
TGCATCGTGT	AAATCTTTTA	TATGTTCTGG	TTCGCATCTA	AGATCAGATA	TTGTTGCTAC	553680
AATTTTTGTT	AACTTTGAAA	TCATAAAGTT	CTTCCTCCAC	TTTTATAAAT	TTTATGCTTT	553740
TTGTCATTGA	ATAACAATAT	TTTGTAAGAA	ATTCAAAACT	TTACTTTGCT	ATAAGCAGTG	553800
TTTAGGTTTG	ATTTTTTATT	TTTTTTATTA	GATTTTCATC	TAGCTTAATA	TGTAAATTTT	553860
TTTCTGCTTT	TGGAATTACA	AGGCCCAGCT	TTTTATTTTT	AACTCTTCTT	AAATTTTTTAA	553920
CTTGAGTGTA	GTAAAGATCG	GCTTTTCCCG	ATTTTTTTGC	TAATTTTGTG	TAAAATACGC	553980
ATAAATTACC	AGCACCTAAA	AGGACATCAA	GGCTAGGAGT	TTATTTTTTT	TGATTTTTTAA	554040
TAAAAACATA	AGCTCCAGGA	TAATCTCTTG	TATGAAGCCA	ATAGTCATTT	CCTTTAACGC	554100
AATGTCTTAA	AAGTTTATCG	TTTTCTTTTG	CGTTTCTTCC	AATAAGAATT	TCAAATCCAC	554160
AATAGGTAAA	ATGCAAGCCT	ATTTTTGGCG	TTTTTTCTTT	TTCTTTAATA	GCAGTTTTTT	554220
CTTGATTATA	TTCTTCTTCC	GGAATTAAAT	TTTCGACTTT	TAACATTGTT	ATTTTTGATT	554280
GAATTAAATT	AAATTTATCT	AGATTATCTT	TTAATTGATT	TTGTATGGTT	TTGAAAGAAT	554340
TTTTGCCCTT	TTTATATGCT	TTAAAATATT	GCAAGGCATT	TTCTTTTGGT	GATAATGATT	554400
GGTTTAAGGA	TATTTTAATT	TTTTCTTCTT	TATAATTTAA	GAGGTTTATT	TCTTTAATCC	554460
CTTTTTGTAT	TTTGTTAATA	TTTAATAAAA	TCAATTCGCC	TTTTTCCTTT	TCGTTTTCAA	554520
TGTTTTCAAG	CAGTTTAATT	TGTTGTTTTA	AAGAGTCTAT	TCTTTTTTCT	AAAACAATTA	554580
ACTCTTTTTT	ATATTTTTCA	ATAAGCAATT	CTTTTATATT	GGTTTTTTTA	ATTTGATCAT	554640
TAAGCGATTC	GTAGTAATTT	TCAAGAAATT	CAGAATAAGA	TGTATAGCTG	GTATTATTAT	554700
ATTCTTCCTT	TAGTTCCATA	ATTTTTTTAT	CAGACATTTT	ATTGCTTTCA	TGTATTTCTT	554760
TAGCTTTTAA	AAAGATTTCA	CCTGTTGTTT	CTTTTATTTT	TGGCCTTCTG	TAATATGCAT	554820
CTAGTATTTT	AAAGTTTGAA	TTTGTAGCTA	TTATATTGGG	CGAGGATGGC	CACAATTTAA	554880
TAAATAAGAT	AATCATATCT	TTTTTGCAAAA	TCTCAAGAGA	AATGATTCTT	TCATTTTTCA	554940

TTTGGAAGC	TTTTATAATT	TTTCCATTTT	GAATTTTGA	TTTTAAGAAG	TCAGAAAATC	555000
TTAATTTTAA	AGCATTCTTT	TTGAAATTTT	TTTTTGTTAT	ATGGAATCTT	GTAAGTGTG	555060
GATTTAAGCA	GATTAGTATT	TTAAATTTTT	TATTGTCAAT	TTTATTGTAA	ATCTCTAAAA	555120
CCAAACTTTT	GTAATCCGGT	TGTATTATTT	TTGTTATTAA	AGAGTTTGTG	AAAGGAATTT	555180
CTTTAATCAA	AGTATTTATT	TCAGTGTAAT	TCAAAGACAT	TTTTATCAAA	TCCTAATTCT	555240
TTCAAGGTGT	TTATATCTAA	GCTTTAAATT	TTTATTTTAT	GTATTAAACT	AGTACTATTA	555300
ATAATAGTTT	ATTTCCATGA	TATGTAGTAT	TATGGAAATA	AAGTTTATTG	ACAATAAATA	555360
GTTTAAATGT	AGTTTTTGTTA	ATAGCTTAAG	CTTAATAATA	AGAGTTCATA	GAATGATAAA	555420
AACAATACTT	TTATTAGTTT	TGTATCCTGT	TGTTGTGTTT	TCTCAAATAT	CTGCAAATCA	555480
ATATTTTGAA	GGAATTTATG	CTAAATATCA	AAATATAGAG	GACATGCAAG	CAACAATTAA	555540
TTTTACTTTA	AAGGGGTAA	AGCAAACAGG	TGTTTTGCTT	TATAAGTTTC	CAGACAAGTT	555600
TATTATCAAT	TTAGATTCAA	ATAATCAAGT	TTTTGTAAGT	GATGGTGAAT	TTTTGACAGT	555660
TTATGTTCCA	TCTCTTGGGA	CTTCTTTTAA	TCAGCAATTA	TTAAAGGGTA	GTAAGTGGGG	555720
AGGTCTTATG	AAAGTTTTTAA	ATAGTGAGTA	TAGCGTATCT	TATACCAATT	CTCCAAATTT	555780
AGAAGATCTC	GATTCATCTG	AGCCTGGAAA	ATATATTAAA	TTAACCTTTT	CTAGAAAGCT	555840
TTACAAGGGG	GCTGCTACTA	TTAATTCTTT	TATTATTGCT	TTTGCTCCGG	ATGGAATAAT	555900
TAGAAGAATT	ACTGCTTTTC	CTACTAGTGG	TGGGCGCGAA	ATAGTTATTG	ATTTGACTGC	555960
TGTGAAGTTT	AATGTTGGAA	TTCTTGATAG	CAAATTTAAA	TATGATCCTC	CAAAATCTTC	556020
AAATAAGGTA	GATAATTTTT	TATATGATAT	TAAAAAAAT	TAAGGTTTAA	ATCTATGAAA	556080
GAAAATGATT	TTATTAAATT	TGGGAGTTAT	TTGAGAAAAG	TTAGAGATAG	TAAAAATTTG	556140
ACTCTTGAAA	TGGTAGCTGA	GGATATTAAA	ATTTCTATTA	AGTATCTTAA	GGCTCTTGAA	556200
GAATCTAATA	TTGAAATTTT	CCCAAACGAA	GTTTTGGCTG	TTGGATTTTT	AAGAACTTAT	556260
AGCGAATATT	TAGACATTGA	TTCTAGATTG	ATATCAACAC	TTTTTAAGGA	TTATAAAAGT	556320
AGACTTAATA	ATAGTTATAT	TGGGATTAAA	TCTGAAGATA	AAATTTCAAA	TTTAGGATTT	556380
TTAAGCGACA	ATAAAGTTTC	AGAAAAAAA	ATATTTTTTT	TTAGTTTAGA	ATCTTTAAGT	556440
ATTTTTTAAAG	TCTTTTTTAGG	CATTGTTGGT	GTTCTTTTAT	TATTTGTGTT	TCTCTATTTT	556500
AGAGAAGTGG	AAGGCTATTT	TAAAAAATTT	TTCAATCTTA	GTCAGGATGA	AAAGATAATT	556560
TCAAATATTC	ATGAAGTGTC	TTTTGATAAA	AAGAATTTTT	GGAACGTTTC	TCTTAAAGAG	556620
GGAGATTTTT	TATCTTTAAC	GTATAGTGAT	GATATTGCAA	AATATAGAGC	ATCGTTTATT	556680
GGCGATGATT	TAGTTATTGT	TGATGAGTCT	AAAAAAAGTA	AGAATATTTT	AAATTTAGGA	556740

GAGTTTAAAG	AGATAAATCT	TGATGATAAT	ATTAGAGTCA	AAATTATTTA	TGAGAATTAT	556800
TATTATGATA	AGTTGAAAAT	AGCTCATGTA	AGTTTAGAGT	CTTTTGCTTT	AAATGTTAAA	556860
TATGTATCTG	AAACTAATAT	TGACAATAGA	TTTAATATTT	TAAATTGGCA	GTTTGATGTT	556920
AAGGGAAGT	AAAAATTGCC	GAGCAGCAAT	TATCTTACCC	TATATTCTTC	TCAAAAACCT	556980
TCAAATGTTG	ATTTGAAAAT	CGATTTTTTA	AATGATACAT	TTTTTAGATA	TGCCGATGAA	557040
AACAATCTTT	ATGGGAAGTC	TCTTTTTGCA	TCCAAAGGTA	TTCTATTAA	TTTAGCTTTT	557100
GAAAAATCTT	TGATACTATT	TTTTTCAAGA	CTTCTGATG	TTAATATCAT	TCTTAATGAC	557160
AGAGACATTA	CTCCTTTTTT	AAAAGAGCAG	GGAAAAGAAA	TTTTTGCTGT	TCAATTTTTT	557220
TGGGTAAAGA	CCCCCTCAGG	GTTTGATCTT	AAGGTTTCTG	AAGTTTATTA	GTGATGGATA	557280
AAATAAAAAA	ATTTTTTTCT	AGCTTAAATA	CTTCTCAAGA	AAAAATTGTT	TTTAGTAAAA	557340
GTAAAAATCC	AATGCTTGTT	TTAGCAGGGC	CTGGAAGTGG	TAAAACAAGA	GTTATAATTG	557400
CAAAAATTGT	TTATTTAATC	AAATATATGA	ATATAGATCC	CAATGAAATT	TTAGCTTTAA	557460
CTTTTACCAA	TAAAGCTGCA	AATGAAATGA	ATGATAGGAT	AAATGATCTT	TTAAAATTTG	557520
ACAAAAAACT	TCATATTCAA	ACTTTTCATT	CTTTTGGGTC	TTGGCTTTTG	AGAGTTTACT	557580
ATAAGGATTT	TAACGAAAAT	TACGATTCAA	ATTTTACAAT	TTGGGATACT	AATGATGTTG	557640
TTAAATTTGT	TAAACAAATT	GATCTTGCTC	CAAATCTTGA	AATGGCAAAA	CATATTGCAG	557700
CTTTGATTTT	AAAAGACAAA	GAAAATTTTT	TCTTAGAAAA	ATTTATTCAA	TTTACAGAAA	557760
AGGAATATGA	GTATATTAAA	ATTTATGAGG	AAGAGAAAGC	TAAAAATAAT	GCTTTTGATT	557820
TCTCAGATCT	TATTATTAAG	CCTATTTTAA	TGCTGAGGCA	ATCTAAATCT	TTAAAAGAGT	557880
CTATTCAATC	TAGATTTAAA	GTTATTTTTG	TAGATGAATA	TCAAGATACA	AATTATTCAC	557940
AATTTTTATT	TTTAAAAGAA	CTTTATTTAG	ATGGTATGTA	TTTTATGGTC	GTAGGAGATG	558000
AAGATCAGTC	AATATATTCT	TTTAGGGGAG	CTAGAATTGA	AAATATTCTT	GAATTTGAAA	558060
AAACTTTTGA	CAATGTTATT	AAATTTTATT	TAGTGCAAAA	TTATCGTTCA	AATTCAAATA	558120
TAGTGGGCAT	TGCAAATGAG	GTTATTTCAA	AAAATAAAAA	TAGATATGAA	AAGCAAATAA	558180
CAACTCAAAA	TAGTTCTAAT	AAAAGGATGA	AATTTTTAGT	TTTCAAAGC	ACTTCAGATG	558240
AAGCTGAATA	TTTTTCTAAT	TTGCTTATTT	CCAATGATAT	TAAGACAGCA	ATACTTTATA	558300
GATTTAATTC	TCAATCTTTT	CATTTTGAAA	CATCTTTTTT	AAAGAAGAAT	ATCCCATACA	558360
AGGTTTTAGG	ATCAATTAAA	TTTTATGATA	GAGAGGAAAT	AAAAGATATT	ATTTGTTTGC	558420
TTAGGCTTTT	TATAACAAG	AAAGATAAAA	TATCTTTCTT	GAGAATGATA	AACAAGCCTT	558480

CTAGAGGAAT	TGGAAAACT	ACTCTAGACA	AAATAATTAG	TTCTTTAAAC	GATAAAGATG	558540
TTAATTTCAA	TTTGTTTTGT	GCAAGTAAAA	AGACTTTAGG	TTTGCTTAAA	AATAGAGCCA	558600
AAGAGTCTCT	TTTATTATTT	TTAAATGTTT	ATGAGGAGCT	GGGTAAAAAA	CTTTTGAAG	558660
ATAATTATAT	TAATTTATCT	GCTTTTATTG	AGGATGTAGT	AATTAGGTTT	GGTCTTTTAG	558720
ATTATTATAG	AAAATTTGAT	AAGGACGAAA	AATTAAGAAA	TATTGATGAA	CTTATTAATA	558780
GTGGAATTGA	ATATTCAGGC	ACGTTTGAAG	GTCTTGCTAT	ATTTT TAGAA	AATTCTTCAC	558840
TTTCTCCTTT	AATTTCTGGA	GATTTTAAAGT	CCAATATACT	TTTGTCTTCA	ATTCACGGTG	558900
TTAAGGGGCT	TGAATTTGAT	AGAGTTGTGA	TTTCTGGGCT	TGAGAAAGGT	CTTTTACCTG	558960
CTGAAATTGA	AGAATTAACA	GAAGATAGAC	TTGAAGAGGA	GAGAAGGCTT	TTTTATGTkG	559020
CGATCACAAG	AGCTAAATCA	GAGCTTATTG	TTACCTTAAA	CTTAAGGCGA	GCTTTTAGAG	559080
GTTCTTATAA	GGGCACTTTG	CCTTCTGTTT	TTTTCCAAGA	TATTGACAAA	AACTCTTATG	559140
ACATTATCTT	TATCCCTGAG	TATTTAAAAG	AGAATTTTAA	TAATTTTTTTT	ATTAATAACA	559200
AAAGGGATAT	TGGATTTAAT	ATTGGAGATT	ATATAATTTA	TAATGGAGAA	AAGGGAATAG	559260
TTGTTGATAG	CTGGTACCAA	AGCAACTTGC	AGTTTGTTAA	AATTAGTTTG	AGAAATGGTA	559320
AGAAAGCTAT	TTTGAGTCCT	GAGTATATTA	AAAAAATTGT	CAAAGTTTAG	AGGTTTATTT	559380
TGAAAGATAT	ACATTTAAAA	AATAGCTTAA	AATTAAGCTT	AGTGACACTT	AGTAGAGAGA	559440
GTGAAGATAA	ATTTATTTCA	AAATTTGAGA	AAGTTATTAA	ATTGGTTAAT	AAAATTTCAA	559500
ATTTTGAGGT	TCAAATTAAT	TTTAATGCTA	ATAAGAAAAA	GATTTCTACG	TTGCGCGAGG	559560
ATAAAGTAGA	ATTTTCTCTT	TCTATTGAAG	CAATTAAAAA	ACTTAGTAAT	TCGTTTTTAG	559620
ATGGATATTT	TTCATCTCCT	AAAATATTGG	AGTAAGGATA	AGGTGTTGGA	CTTAAGTAAT	559680
TTAACTTTAA	CCAAAATTCA	AGAATTAGTT	TTAACTAGAA	AATGTAAAAT	TTATGATATT	559740
TTGCTTGCTT	ATAAAAATAA	TTATGAGCTA	AATAAGATA	TCAATGGATA	TATTGAATTT	559800
TTTGATGATT	CTTTAGAGAT	TGCAAAAAGG	TATGACGATT	GTTTAAAAAA	TTGTGAATTA	559860
GAAGATTTGC	CTTTAATTGG	TATGCTTATT	GCAGTCAAAG	ATAATATTTT	AATTCAAGAT	559920
AAATCTTTAA	CTTGTGCTTC	TGAGATTTTA	AAAGGTTATA	TTTCTCCTTA	TGATGCGACT	559980
GTTATTAAAA	GGCTTAAGAA	TAAAGGAGCA	ATTTTAATTG	GTAGAACCAA	TATGGATGAA	560040
TTTGCCATGG	GTTCTACTTG	TGAATTTTCT	TATTACGGTG	CAACTTTAAA	TCCTTTAAAT	560100
AGAGAATATG	TTATAGGTGG	TAGTTCTGGA	GGCTCTGCAG	CTGTAGTTGC	AGCTTTTCAA	560160
GCACCTTTTT	CGCTTGGTAG	TGATACTGGA	GGTCTGTGTA	GGCTGCCCCG	ATCTTTTTC	560220
GGAATTTTGG	GTTTTAAACC	TTCTTATGGA	GGTCTTTCTC	GCTATGGGCT	TGCATCTTAT	560280

GCTTCGTCTT	TTGATCAAAT	AGGATTTTTT	TCTCATTCTA	TTGAAGATAT	TGCTTTAATT	560340
TTAAAGCATA	CTTGTGGATC	TGATAAAATG	GATTCTACTA	GTGTAGACAT	TTTTGATGAT	560400
TTTTATCCTT	TAAAAAATGA	GTCGTTGCAA	GGTAAAAATT	TAGCTGTAAT	CAAAGAGCTT	560460
AGCGAAGATC	TAATGGACAA	AAATGTTGCA	AATAGTTTTG	CAAAGTTTAA	ATTAGACCTT	560520
TTGTCAAAGG	GTATTAATAT	AAAAGAAGTT	TCAATAGAAG	AGATTAATTT	TATTTTATCA	560580
ATTTATTATA	TAATTTCTCC	TGTTGAAGCA	TCCTCCAATC	TTGCTCGTTA	TACTGGACTT	560640
TGTTACGGCA	AGAGAATCTC	TGAAGGTTTG	AGTCTTAATG	ATTTTATTTT	TAAACATAGG	560700
AGCAATTTCT	TGTCAGAAGA	AGTTAAAAGG	CGTATTGTTT	TTGGAAATTA	TTTGTTATCA	560760
GAAAGGTATG	ATTCTAAATA	TTATGCAAAA	GCTTGTGAAA	TTCTTCAAAA	TTTGATTATT	560820
CCTAAATTTA	ACAAGCTTTT	TGAAAGCTGT	GATTTTATTA	TTACCCCAAC	AAGCTTTGTT	560880
AAACCTTTTA	GACTTGGTTT	GGATTTTGAT	GATCCTGTTA	AAATGTATTA	TTCAGATATT	560940
TGTACTGTTA	TTGCAAATCT	TATTGGAGCC	CCTGCTATTT	CGCTTCCATA	TTCTAAGGAT	561000
GAGGAAGGAT	TGTCAATTGG	GATGCAAATT	ATTGGGCGTA	GCAAAAAGGA	TTTTGAACTT	561060
TTAAGTTTTT	CAAAAAATGT	GATTAGGGAA	TTAGGATTGA	ATGGAATATA	AATTAGTTAT	561120
TGGATTAGAA	ATTCATGTTC	AAC TGGGTTT	AAAAACAAAG	GCTTTTGTG	GATGTAAAAA	561180
TGAGTTTGGA	GGAGTTCCCA	ACTCTCGTGT	TTGTCCAATT	TGTCTTGGAT	TGCCAGGTTC	561240
ATTACCAAGT	GTGAATGTAG	AGCTTATTAA	TAGTGCAATT	TTAGCGGGGC	ATGCCACAAA	561300
TTCAAAGATT	AGAAATGTTG	TTAAATTTGA	TAGAAAGCAT	TATTATTATC	CAGATTTGCC	561360
AAAAGGATAT	CAAATCTCGC	AAAATGATAA	GCCAATTTGT	GAGGGGGGAA	GCTTATTGAT	561420
TGAAACCCCT	TCTGGACCCA	AAAAGATTAA	CATTATTAGA	ATTCATATGG	AAGAAGATTC	561480
TGGCAAGAGT	CTACATTTAC	TGGACAGTGA	AAATCAAAGT	TATGTTGATT	TTAATCGCTC	561540
GGGTGCTCCT	TTGCTTGAGA	TTGTTTCTGC	TCCAGATATT	AACAGTGGAG	ATGAAGCAGT	561600
TGCTTTCCTA	AGCTCTTTAA	GAGAAATTTT	TAGGTATCTT	GATTTGTCCG	AATGTAATAT	561660
GGAGAATGGT	TCTTTTAGAT	GCGATGTAAA	TGTTAATTTA	ATTGTTAAAG	AGAATGGTGT	561720
TGAACATAAA	ACTCCTATAG	CTGAAATAAA	GAATTTAAAT	TCTTTTAAAT	CTATTAAAGC	561780
GGCCATTGAA	TATGAAGAAT	TAAGGCAGCA	ACAGGAGTGG	ATTCAATTTA	AGAAAACCTC	561840
TAATAGTTGT	GGTAAGCACA	CTAGAGGATT	TGATGATAGG	AGCGGAGTAA	CGTTTATTCA	561900
AAGAAATAAA	GAGACAGTAT	CTGATTATCG	CTATTTTCAA	GAACCCGACC	TGCCTTTAAT	561960
AGAGATTGAT	GATTCTTATA	TTGATAATAT	TAAAAATTTA	AAGTTGATTG	AACTTCCATT	562020

TCATGCAAGA	ATTAGGCTTA	AGGGCCAATA	TGGGCTAAGT	GATTTTGATG	TTATTACTTT	562080
AACAGCAGAT	AAGCATCTGC	TTAAATATTT	TGAAGAGGCT	GTTATTAATT	CAAGCGATCC	562140
CAAAAAAGTA	GCCAATTGGA	TATTGTCTGA	AGTTTAAAGC	GTTCTTAATG	ATAAAGGAAT	562200
TAGTGTTCTT	GAATTTAATT	TGCTTCCAAG	CTATATTACA	GAGCTTGTTG	AATTTATGT	562260
TGCTGGCAAA	ATAAGTGGCA	AAATGGCAAA	AAGGGTATTT	TCAGAGATGA	TGACTAGAGG	562320
AGTTTCTGCC	TCTGTTGTTA	TAAGTGAAAA	TCAATTAGAG	CAAGTAAGTG	ATAAGTTTGT	562380
TATTAAGCAG	ATTGTGCTTG	AAGTTTTAGA	TGAAAATCCT	AAATCAATTG	AACTTTACAA	562440
AAAGGGCAAA	GACCATGCTA	TCAAATTTAT	GATGGGGCAA	ATAATGAAAA	AATCTTCAGG	562500
AAAGATTAAT	CCTATACTTG	CAAATGAAAT	TCTTTTAGAA	AGTTTATCAA	ATGTATGATT	562560
TGCCTTTAAT	AGATAATTTA	CCAGTGATTA	AAAGGGCAAG	ATTTTTTTAT	CTTTACGATA	562620
TTCATGGTAA	GAGGTATTTG	GATTTATATT	TAAATGGTGG	AAGAAATTTT	TTAGGTTATA	562680
GGGTTC AAG	TTTAAATCGC	CTTTTTAAAC	AACTATGTC	AAGGGGTTTG	ATATCCCCTT	562740
ATCCTTCTGT	TTTTAAAAAT	CAGTTTATCA	ATTTGGTATT	TACTTTTTTT	AAAGAGGCTG	562800
GGTCTGTTTA	TATTTTTAAG	CTAGAAAAAG	ATGCAAAAGA	ATTTTTATTA	TCTTTAACTG	562860
GTAAAAATAA	ATTTTTTATG	CCCTGGGAAA	AAGAAGAAGG	AATATATGAG	TTTAGAGTAG	562920
GATTTAGTAA	TATTAAATAT	CCTATGATTT	TTAATATTCC	TTGCCTGAT	TTTATGTCTG	562980
TTAGCATTGT	TGTTATGGAT	AATCTTTCTA	GAAAAATAGA	ATTTAAAGAT	AATTTTGATG	563040
CTGTAAC TTT	ATCTTTAGCT	AGACATACAT	TAAGCAAGCT	TTTATTTTAT	AAGAAAAATA	563100
TCGATATTGA	TTTTAATTCT	TTTGCCACAC	CTTTATTTAG	AATAGCTGAT	AGGTATATGC	563160
TTCTCTTTTA	TGATGCTTGT	TATCATGCTG	AAATTTTTAA	TGAATTTCTC	AAATTTGGGT	563220
ATTTAATTAG	TCCAAATTTT	AGTATTCCAT	CTATTGTTCC	CCTGAAGTTC	TCTAAAGGAG	563280
ATCTAGATAA	TTTTAAAAAA	CTTTGTTTTG	CTCTTAAAAA	TAAGTTTATT	GATGGGCTTG	563340
ACAGTGATCC	TTACAAATAA	TACAATGAAT	GAGATTTATG	CATAAAATTA	TAAAGGGTAT	563400
AGCGCTATTA	TGAATAAAAT	AACCAATAAT	GATACGATTT	GGATCAAGCC	AAAGACTGTT	563460
GAGAAAAAAT	GGTATGTAAT	TGATGCAGCA	GATAGAATTT	TAGGTAAAGT	TGCTGTGGAT	563520
GTTGT TAAAA	TTTTAAGAGG	CAACATAAA	GCTTATTATA	CTCCCCATCA	AGATTTAGGT	563580
GACAAATGTTA	TCATTATTAA	TGCTTCTAAA	GTTAAGCTGA	CGGGGAAAAA	ATATCAACAA	563640
AAACTTTATT	ATAGGCATTC	AAGATATCCT	GGAGGTCTTT	ATTC TGACAC	TTTTAGAACA	563700
TTGTCAGAGA	GAAAGCCTTG	TGCTCCTCTT	GAAATTGCTA	TTAAGGGTAT	GTTGCCAAAA	563760
GGCCCTTTGG	GGCGTAATCT	TTTTAGAAAT	TTAAAAGTCT	TTTCTGGTTC	AGAGCATACT	563820

CTTAAAGCTC	AAAATCCTAT	AAAGCTGTAA	gCTAATTTAG	AGAGGTAAAA	TGAAAAAATC	563880
AAATTTTAGC	AATGTTAATT	TATCAATGGG	AACTGGTAGG	AGGAAATCTT	CTGTTGCTAG	563940
AGTTTACATT	AGAGAGGGTA	GTGGCAATAT	CAAAGTAAAT	AATAGAGACT	TTGACTCTTA	564000
CATACAACTT	GAAAATTTAA	GAACAATGGC	TTTATCGCCT	TTGGTTTTGA	CAAATACACT	564060
TGGGAAATAT	GATCTTTATA	TTAATGTTTA	TGGGGGAGGG	ATTTTCAGGTC	AATCAGGGGC	564120
AATAAGGCAC	GGCATTTCOA	GAGCTCTTTT	TAAACTTGAT	GAATCTAATA	AGATGATTTT	564180
GAGATCTAAT	GGGTTTTTAA	CAAGAGATTC	AAGGAAGGTT	GAACGTAAAA	AATTTGGGCA	564240
GAAAAAAGCA	CGAAAAAGTT	TTCAATTTTC	CAAAAGATAA	TTTTATTTTT	TTATACATTT	564300
TACATTTTTTA	TTTAATTAAA	AAAAATCCCT	TTTACAGGGA	TTTGATTTAT	TTTTGTTTAA	564360
TAGAATAAAA	GACGCTCTTA	CCGTGGTATT	CAGCAGTTGT	TTCCAATTCT	TCCTCTATTC	564420
TTATGAGTTG	ATTGTATTTT	GCTATTCTAT	CTGTTCTTGA	GAGTGAACCA	GTTTTGATTT	564480
GTCCTGTTCC	AAGAGCTACT	ACAAGATCAG	CTATTGTTGT	ATCTTCTGTT	TCTCCCGATC	564540
TGTGAGAGAC	TATTGCTGTG	TAACCCGCTT	TTTtagccat	TTCTACAGCC	TCAAATGTTT	564600
CTGTTAGTGT	TCCAATTTGA	TTGACCTTAA	TAAGGATTGA	ATTGGCAACT	CCCATTTCAA	564660
TTCCTTTTTTT	AAGAAACGAG	GTATTTGTGA	CAAATAAATC	ATCTCCAACA	AGTTGTATTT	564720
TGTTTCCAAT	TTTGTCTGTA	AGTTTTTTCC	ATCCATCCCA	ATCTTCTTCA	GCCATTCCAT	564780
CTTCAATTGA	AATGATTGGA	TATTTTTTCTA	CCCACTTTGC	CCAATATTCA	ACCATTTGTT	564840
CGGAAGTAAG	TTTTTCTTTT	GTTGACCATT	TAAGTACGTA	TTTTTTTGTT	TTTGGATCAT	564900
AAAGCTCAGA	TGTTGCGGGA	TCAAGAGCTA	TTGCAATGTC	TTTCCAGGT	TCATATCCTG	564960
CCTTCTTTAT	TGCCTCTATA	ATCACTTCAC	AAGCTTCTTC	ATTTGATTTC	AAATTTGGAG	565020
CAAATCCCCC	TTCATCTCCA	ACAGAAGTTG	CATACCCTTT	GCCACTTAGA	ATGCCCTTTA	565080
GCGTATGAAA	AACCTCTGCT	GCCATTCTTA	TTGCTTCACT	GAATGTTTTT	GCTCCTATTG	565140
GCATTATCAT	GAACCTCTGA	AAGTCAACAG	AGTTGTCAGA	GTGTGCACCG	CCATTAATAA	565200
TATTACACAT	AGGTGTAGGC	AAAATGTTGG	CTTTGTACGC	TCCAAGATAT	TGATAAGGCC	565260
TAAGTCCAAG	GTACTTTGCA	GCAGCTTTAG	CTGTAGCCAT	TGAAACTGCT	AAAATTGCAT	565320
TAGCACCAG	CTTTTCTTTT	GTAGGGGTGC	CATCAAGTTC	AAGCATTTTT	CTGTCGATTG	565380
CAACCTGATT	TAAGGCACCT	ATACCTTCAA	GTTCTGGGGC	AATTATGTTT	TTTATATTTT	565440
CAATTGCCTT	TAAAACCCCT	TTTCCCATAT	ATACAGACTT	ATCACCATCT	CTAAGCTCAA	565500
CAGCCTCGTT	AATTCCTGTT	GATGCACCTG	ATGGTACGGC	AGCTCTTCCG	TAAGTTCCAT	565560

CTTCTAAAAT	GACATCAGCT	TCAACTGTTG	GATTCCCTCT	AGAATCAATG	ATTTGTCTGG	565620
CTTTGATTTT	ATAAATGTGA	AAACCCATTT	TTTGTACTCC	TCGTATTATT	TACTTTAATG	565680
TATATTTTTA	GTATAATGTT	AAAAAGTTTA	AATGTGTAGT	ATTTTCCAA	AAGAATTATT	565740
ATTGTGAGCT	TTGTGTATAA	TCTATGAAAG	AAAGGTGTTT	GTATTTATTG	GTTTTTGTAG	565800
CTTTATGTGT	TAACAATCTT	TTTTCAGATG	ATTATTTAAT	TTATGACTTT	GATTTAAGTT	565860
TAAATGAATT	TCTAGAAAGT	TCAACAAGAA	AAGACAATCT	TGAGCCTATG	GTTGATTCCA	565920
ATCGTATATT	ATTGTTTTAT	CCTCCTAAAA	AAGAAATTAG	AAAAATTTTT	GCTGCCTTTG	565980
ACTTTGATCA	GSTATCTAAG	AAATATTTAT	TCAAAAAAAA	TGAGCATGGA	GTTTTTTTTG	566040
TTAAAGTTAA	TATTCCTCAT	GGCACAAGCA	GTATAAAATA	TAGGCTTATT	GTAGACGGTG	566100
TTTGGAATA	TGACGAGTAT	AATAAAAATG	TAGTTTATAA	TGAGGATTTA	ATCCCATTTT	566160
CTAAAATTGA	GATCGCTAAA	GAGAAGTCCA	GCTATATTTT	TTTGAGAAAT	CCAATACAAT	566220
CATATGATAA	CAATGAAATT	GAAATTTTTT	ACATAGGTCG	TCCTGGACAA	ATAGTTACAA	566280
TAGCTGGTAG	TTTTAACAAT	TTAATCCTT	TTTTAAATAG	GCTTATTGAG	AAAGAGGACA	566340
ATAAGGGAAT	TTATACTATT	AAGCTTAAAA	ATTTACCCAA	GGATAGAATT	TATTATTATT	566400
TTATTGATTC	TGGTAACAAA	GTAATAGATA	AAAATAATGT	TAATAGAATT	AATTTATATT	566460
TTGTTGAGGG	AATTGATAAT	AAAATAGATT	TCGAAGTTTC	CTATTTTGAT	CATAAGTAAG	566520
CTTTTAATTA	TTTATCTGTT	CATCTCATCA	AAAAGGTATT	TAGATACAAA	GTGATCTTTT	566580
TCTACTTCTT	CGAGCTTTGG	ATGTACTTGG	GTTGATAAAT	GAATTTTCT	AATGTTTGCT	566640
AGAGTTTGCT	CGTCTAGTTT	TATATTTTTA	TTTTTCTTTT	TTTCAGGGTT	GATTTTCAGGA	566700
ATTGATGCTA	TTAGCATTTT	AGTATATGGA	TGAATTGGAT	TTGAAAATAG	CGTTTCTCTA	566760
GGTGCAAGTT	CCAGGATAAC	TCCAAGGTAC	ATTACAGCAA	TTTTATCACT	CATATATTTT	566820
ACTACGGCAA	GATCGTGAGA	AATAAATAAA	TAAGACAAAT	TGAATTCCTT	TTGCAGAGCT	566880
TTTAGAAGAT	TTAAAATTTG	AGCTCTGATT	GATACATCAA	GTGCAGAAAC	GGCTTCGTCT	566940
AAAAGCAAAA	GCTTAGGATT	TAAAGCTAGT	GCTCTAGCAA	TTCCTATTCT	TTGTCTTTGT	567000
CCTCCTGAAA	ATTCATGAGG	ATATCTGGTT	AACATACTTT	TATGTAGTCC	GACAATATCT	567060
GTTAGTTCGT	TTACCCTTTG	TTCTATTTCT	TGTTTTGTTT	TTGGAAGAAT	TTTGTTTTCA	567120
TTGTATATTT	CTAGTGGTTC	TGCTATTATT	TCTTTTATTG	TCATTCTTGG	GTCAAGCGAA	567180
GTATGGGGAT	CTTGGAATAC	CATTTGCATA	TCTTTTTTTG	TTTTTAAGAG	CTCTTTTTTTT	567240
GAAAGTTTAG	TTATGTTTTT	TCCGTAAAG	TAAATATTTT	CAGAAGTTGG	CGTGAAAAGT	567300
TGCATTATTG	AGCGAAGAGT	AGTAGATTTG	CCGCAACCAG	ATTCTCCTAC	GAGTCCTAAA	567360

GT'TTTATTTT	TTTCAACTTC	AAAGCTAACA	TTGTTTACCG	CATTTACTTT	TTGTTTGTTT	567420
TTCCAAAATA	AAAAATCTTC	TCCTGTTGTG	AATGTTTGCA	TTAAGTTTTC	TACTTTAAGA	567480
ATTATTTCTT	TTTTACTACT	CATTTAAAAC	TCCTCGGTGC	TGGTTTTTGT	GATCTTCATA	567540
GGGTTTTCTT	TTGTTGAATA	AAGCTTTTTA	TTTGATCGT	GTTCTAGCGT	AAGAATTGAT	567600
TTTAAAAGCC	CAATGGTGTA	AGGATGCTTA	GGATTGTTAA	ATATTTCCCTC	TACTGTTCCCT	567660
TCTTCTACAA	TTTTTCCTTG	ATACATTACA	GATACTGTAT	CACAAATTTT	AGCAACAACC	567720
GCAAGATCAT	GAGTTATAAA	TATGGTAGAA	GTATTGAATT	TTTTAGATAG	GTTTTTGATT	567780
AATAATAATA	TTTGCTCTTG	GATTGTAACA	TCAAGGGCTG	TTGTTGGTTC	ATCTGCTATT	567840
AATAAGGATG	GATGACAGCT	AAGAGCCATG	GCAATCATAA	CTCTTTGTCT	CATTCCTCCT	567900
GAAAATTGAT	GTGGGAAATG	TTTTATTCTT	TCTTCTGCGT	TTACAACACC	AACAGTTTTT	567960
AACATTTCTA	TTGCTTTTTT	TTTGGCTTCT	TTTTTCCCTA	ATCCTTGGTG	TAAGATTATT	568020
GTTTCTTCAA	GTTGAGTTGA	TATTCTTAAA	AATGGGTTTA	ATGAAGTCAT	TGGGTCTTGA	568080
AATATCATTG	ATATTTTATT	CCCTCTGATT	TTTAAAAGTT	CTTTTTCGCT	AAGTTTTAGC	568140
AGATCTTGAT	TTTCAAATAG	TATTTCTCCA	CTTTTATATA	CTGTTGTAAG	TTCTGGTAAT	568200
AATTTTAAAA	TAGCCATACT	TGTTACGGAT	TTTCCGCTTC	CAGATTCTCC	AACAATAGCT	568260
CTAATTTCTC	CTCTTTTTTAC	AGATAGGTTA	ACATTGCTTA	CGGGATGAAT	TGTTGTATGT	568320
TTTAATCTAA	ATTCAATTGT	TAAATTTTTT	ATTTCCAATA	TATTTTCTTT	TTCCATTCAA	568380
TTTCTCCTTA	GATGCTATCT	TTTGATCAA	AAGCATCCCT	TAGCCCATCA	CCTAAAAAGT	568440
TCATAAATAA	TAGAAATATT	GTCATAACTA	TAGCTGGAAT	AAAAACTTTC	CATGGATATT	568500
CAACAAATGT	AGCAATTCCA	TTTTGCACTA	ATTCTCCCCA	GCTTGTCATT	GGAGCTGAAA	568560
TTCCAAGTCC	TAAAAAGGAT	AAAAATGCTT	CAGCCATAAT	AAAGCTTGGA	ACCCTTATTG	568620
TTGTGAATAT	AACTATCATT	CCAATGCTAT	TAGGGATCAA	GTGTTTAAAG	ATTATTCTTT	568680
GATTTGTTGC	ACCAAGGGTT	TTGGCTGCTT	GTATAAATTC	CGAACTTGAT	AGTGATTGTA	568740
CTTGGCCTCG	TACAACTCGA	GCTACTGTTA	ACCATGATAC	AAATGCAAGT	GCTATGAATA	568800
AGCCGATTAT	ACTTCTTTCC	ATTATTGCCA	TTAATATTAT	TACAATAAGT	AAATAGGGCA	568860
ATGCATAAAG	AATTTCTATT	GGTTTTAGTT	ATTATTTTGT	CGGGCAATCC	CCCAAAAAAT	568920
CCTGCTATGG	ATCCCAGGAT	AGTTCCTATT	ATCATAGACA	AAAAAGCTCC	AATAAATCCT	568980
ACAGAAAGAG	AAATTTGACT	ACCTTGATT	AATCTTGCAA	GCAGATCTCT	TCCAAGATTG	569040
TCTGTGCCAA	GCAAATATAC	TCTTTTATGT	ATTTTACTT	CCTTTTATC	TATTATTGTA	569100

ACTTCATTTT	CTATTTTCT	TTTTATGTCT	TCGAGTTTTT	TTAGTTCTTC	TTCATTTATT	569160
TCTCTTTTTT	CTTTTTTGC	TAATTTTTCA	ATAAATTTTT	TTTCTTTATT	ATACCAGAGT	569220
TCTCCAGCAG	CCTGGAAAGA	TGGTGGCAAA	TCAGAATGCT	CTACTATTTG	AGTATGGTAT	569280
TTATATATTG	GCAATATTGG	TTGCAAAATG	GCAATTGAGA	TATAAAATCC	AATTACAAAA	569340
AGACTGCCAA	ATGCGAGTTT	ATTTTCTTTA	AATCTTGACC	AAGCTCTTCT	TTCTAGTTTA	569400
GAATTGTTTT	CTTCATTTTG	TTTTTCAAGG	CTATTCATTT	TGATTTCCCC	TTATACTCTT	569460
GGATCTAATA	TTTTATATAT	AATATCTGAT	ATTAATATAG	AAATAAGCAG	TATTATTGAA	569520
TATACTAACA	ATCCGCCCAT	TAATACTGGG	TAATCTCTGT	TTAGTGCGGA	TTCTGTTATA	569580
AACATTCCCA	TTCCAGCAAT	TCTAAATATT	TTTTCAATAA	CCACGCTTCC	AGATATTATA	569640
GCAGCAAATG	CTGGACCTAT	ATAGCTTACT	ACAGGCAACA	TTGCTCCTCT	TAACATATGC	569700
TTTATAACTA	TCTTTTTGAA	GCTTAGCCCT	TTTGCACGCG	CAGTTCTTAT	AAAGTCGCTT	569760
TGTATTATTT	CTAGCATTGA	TCCTCTGATT	ATTCTTGCGA	AAATAGCTAC	GTTGGGCATG	569820
CTAAGAGTTA	TTATGGGTAG	AATTAAATTT	GAAAATCCTC	CTCTTTCTGT	AATCCATCCA	569880
GAGGTATAAA	GCAAACCCCA	TTAATTGCA	AAAAAATATT	GTAAAATTGG	CCCTATTACG	569940
AATAATGGTA	TTGAAATCCC	CAATATTGCT	ATTGATGTTA	TTATATAATC	CACATAAGTA	570000
TTTTTATAAA	TGGCAGCTAA	TATACCTATT	GGTATTCCCTA	TTGATAGTGA	TATAATAAGG	570060
GATATTACTC	CTAGTGTAAG	TGATTTTGGA	AATCCTAATT	TTATGTATTG	ACTAACTGTA	570120
AGGTCTTTCT	TTTTCAAAGA	AGGTCCCAGA	TCTCCCCTGA	GAGCGTTTGT	AATGTAATAA	570180
AAAGCTTGAA	TATAAAAAGG	CTTGTCGAAGG	TGATATTTTT	CCATCAATCT	TGCTTTTACT	570240
TGAGGATCAA	TAGGTTTTTC	AGAATCAAAT	GGACTTCCAG	GAGCCATTCT	CATTACAAAA	570300
AAGCATAAAA	AAATTATTAC	CAGTAAAGTT	GGTATTATTC	CTAATATTTT	CTTTAAAGTA	570360
AACTTTAACA	TTTTTGCTCC	TTTGTAATA	GATATTGATA	ACTTACGTAT	TAGTCAATTA	570420
TATCATATAG	TCTTTATTGT	TTTTCAAGCT	ATAGTTGATA	ATTTTTGATA	GAATAGGAGG	570480
TTTTTTGTAT	TATAATGAGT	AATTTAATTT	TCAATAAAAT	GTATTTTTTG	TTTTTAATTT	570540
TTTATTTAAA	ATTTTATTCT	CTTGATTTGA	GAAGAATTTT	TTTGTGTAAG	ATTCTAAGTA	570600
AAATTATCAT	AGAATCTTAC	ACATTATTTA	TGTATTTTTG	TTTTAAATAA	AGCTACTGTC	570660
TTAAGCTTAG	TCAGCTTTGC	TTTTAGACTT	AAATATTGTT	TTTAATTTAT	ATTAAAATCC	570720
TTTTTAAATT	AATTATGTTT	TGCATTTTTA	ATTGGTTTTA	ATTCAGAAAG	ATAATAAACC	570780
TCTGATACAT	TAGGATTCCA	TCCAGTCCAT	TTATCGTTTC	TAAAAAGATA	ATGCCCAGAA	570840
TATATGTATA	TTGGTGCAGC	AGGAAAATCT	TTTTCAATTA	TTATTGATTC	TGCTTTTCTG	570900

AGTAATTGTT TTCTTTTTAT AGGATCTTTT TCAAGATCTG ATTCTCTGAT GAGTTTGTCA 570960
AATTCTAGGT TTGAATATCC GTATGATGCA AGTTGTGAAT TTTCTCTTGT GAATATAGTA 571020
AAGTATGTGT GTGGATCTAA ATATTCCCCA ATGCGTCCAA CTCTTATTAT TTCAAAATTG 571080
CCAGTATTTT TGCTGTTGGT AAGAACAGGC CAATTTTCGT TGGTAAGCAT AAGATTGATA 571140
TTTAGAATTT TTTTCCATTG GTTTTGAATA AATGCAGCAA TTTTTTTATG AGTTTCGTTT 571200
GTATTATATT TTAGTGTTAG CATTGGGAAT CCTTTCCCAT TAGGATACCC TGCATCTGCC 571260
AAAAGCTTTT TAGATTTTTC AGGATCAAAAT AAAGCCAATT TTTTACCGTA ATTGTAATTT 571320
TTAAGATCAG GAGTTATTTT TCTTGTAAGG ACTGTGCCAT CATTTAGCAC TTTGTAAGTT 571380
AAAGTTTCTC TGTC AATAGC TAAGGTAAA GCTTCTCTAA CTCTAGCATC ATCAAGGGGT 571440
TTTATTTTTG TATTAAATGA ATATAAATAA ATTGCATTAC TTTTGTGTTG GTAATAGTCT 571500
TTTTGTAGTT TTATTTCAAT TACAATGTCC GGC GGGATGC TGTAAAAAAT AGCATCAATT 571560
TCGTTGTTTT TGTACATATT GTACACAGTA AGATCATTGT CAGACGTAAT GTAGACAAGC 571620
TCATCAAGTT CTACTTCTTT TGCATTATAA TAACGTTTCGT TTTTTTCAAA GATAATTTTT 571680
TCATTAGGTA ATCTTTTTTT TAATTTAAAA GGACCGCTAG TAACCATGTT TTCAGGGCTT 571740
GTCCAATTTT CCTTATATTT TTCAATCACA TGAATAGGTA CTGGCATGAA TGCGTAATGT 571800
AGAAGCAGTT CAAGAAAATA TGGCTTTGGG GCCGTAAGTG TTATTTCCAG CGTTTTACTA 571860
TCAATTGCCT TGATTCCAAG TTCAGAATCG GATACTTTCC CGTCAAAATA CTCTGTCCA 571920
TTTTTTATTA TTGATTTGAG CATGTCAACA TTTGTAGATC CTGTTTCTTT ATTTAAAAAT 571980
CTTAAAAAAG ATTTTCTTAT CCCTTCAGCG GTAATTTCAA CTCCATCGCT CCAAAAAAGG 572040
TTGTCCCTTA GATAAAATTG ATATGTTTTT TTATCTTTTG AGGCTTCCCA ATTTT TAGCA 572100
AGTCCGGGCT TTAGCTTTCC TGTTTTGGTA TTTAATGTCA AAAGCCCTGA GAATATTTGT 572160
TCTAAAATTC TTGCTCCTAT TGTCTCATCT ACCAAATGAG GGTCAAGCGA TGAGGGCGCT 572220
CCCCCTATGT AACTTTTAAA TGCTAATTTT TCTTTTTCTG AATTATTATT GCATGCAATT 572280
AAAGACACAG CAAGCATAAG TAGTGTTACT ATTTTAATTT TTTTACCGAT TTTTTTAGTT 572340
TTATTAAAGC TCATATTAAC CTTTCCCCCA AATTAAATTT ATTTATAAGT TTAAACTAT 572400
CTTTTTTTTA TAATAAAGTC TATAAAAACC GTCCATAAGG AATAAATAAT AGACGATTTT 572460
TATTTAATTA AATTTAATAT TATAAAGTTT ATTATATTAT TTATTTTTTA ATTTTAGCTG 572520
AGATAAATCA AATCTTTCTA AAATATTGGT GTCCACCCT GTCCATTTGT CATTTCTGAA 572580
AAGGTAAGT TTCCCATATA TGTATATTGG TGCTATTGGA AAATCTTTTT CAATAATTAT 572640

CTCTTCTGCT	TGTCTTAAAA	TGTCTTGTCT	TTTTATTGGA	TCAAGCTCAA	GGTCGGATTT	572700
CTTTATAAGT	TCGTTGTATT	CTGGGTTTGA	GTAATTATGA	GATGAGAATT	GTGTGTATCC	572760
TTGTGTGAAT	ATGCTTAAAA	ATGTCAAAGG	ATCAGCATAA	TCGCCTATCC	ATCCTGCTCT	572820
TGCTATTTCA	TAATTTCCAT	TTGCCTTAGT	GTTTAAGTAT	GTTGTCCATT	CTTCGTTTTTC	572880
AAGTTCCACA	TCAATATTTA	AATTTTTTTT	CCATTGGTTT	TGAATAAATT	CACAAATTTT	572940
TTTATTTGCT	TCGTTTGTAT	TGTATTTTAA	TTTTAAAATT	GGAAATCCAT	TGCCATTAGG	573000
ATATCCAGCT	TCAGCTAGAA	GGGTTTTTGC	AATTTTCAGGA	TTAAATAATT	CTAAACTTTT	573060
TGCATAAGAA	TATGAACATA	AGTTGGGAGT	TGCTCTTCTT	GTAGGGGTAG	TCCCCTTGTC	573120
AAGAACTTTA	TATGTAAGCG	TTTCTCTGTC	AATAGCAAGA	GTAAAGGCTT	TTCTAATTTT	573180
AACGTTGTCA	AGTGGTTTGA	TGTGTGTATT	GAACGCGTAA	AAGTATATGG	CATTAACAGC	573240
TGATGAGTAA	TAGTCGCTTC	TTAATTTTAG	ATTTTTGATT	AGATCTGGGG	GTATGGAACC	573300
AAAAATTGCA	TCTAGCTCTT	CATTTTCATA	CATTTTATAC	GCTGTTGAGC	TGTCATTTGT	573360
TGTGTAAAAT	GTAATCTCTT	CTAATTCTAC	TTCATTTGAG	TCGTAGTATT	TGTTATTTTT	573420
TTCAAAGACA	TATTTTTTCGT	TAGGAATTCT	TTCTTTTAAT	TTAAAAGGAC	CACTTGTCAC	573480
CATGTTTTTCG	GGGCTTGTCC	AGTTTTGTCC	ATACTTTTCG	GTAACATGAA	CTGGTACTGG	573540
AATAAATGAT	TGGTGTACTA	ACATATCAAT	AAAATAAGGT	TTTGGTGATT	CCAGTGTTAT	573600
TTCTAATGTT	TTTTTCATCAA	TCGCTCTAAT	TCCAAGTTCA	GAGTCAGTCA	CTTGTCCATC	573660
AAAATATTTT	TGACCATTTT	TAATTACCGA	TTTAACCAT	TCAACGTACT	TTGAGCCAGT	573720
TTCTTTATTT	AAAATTCTAA	GATAAGATTT	TCTAATTCCT	TCTGCAGTGA	TTGCAACTCC	573780
GTCACTCCAA	GTGATTTTTT	CTCTTAGGTT	AAATGTGTAA	ACTGTTCCAT	CAGAAGAAAT	573840
ATCCCACCCT	TTTGCAAGTC	CCGGTTTATT	TCCCCCTGTA	TTAGGATCTC	CTGTAACAAT	573900
CCCTCTAAAC	ATTGTGTCAA	TCATTTTTGA	TGCGACATTA	TCCTCTGCTA	ATTGAGGGTC	573960
AAGACTGCTT	GGCTCTGCTC	CCAAGCTTAT	TTTAAATGAT	ACTCCTTCTT	TTCTTTCCCT	574020
GTTATTACAA	CAAAGAAAAG	TTAGAAAAAA	TATTATTAAA	AATAATGACC	TTTGTAATTT	574080
CATAATTTTT	TATACCTCCA	TTTCAAAGTT	TGTTTTAAAA	TTTAACTTTA	ATTTCATAAT	574140
TTTCTTTCCG	TAGATATTAA	TTTTAAATCT	TAATTTTAAA	ATTACTTATT	TTACTTAATT	574200
TTATTATTTT	TTAGTTTTTA	TATCTTCATA	TAAATAGCTT	TCTGCGATAT	TTGGTACCCA	574260
CCCTGTCCAT	TTATCATTTT	TGAAAAGATA	ATGAGATTTG	GGTATATATA	AAGGTGCCAT	574320
AGGAAAGTCT	TTTTCTGCTA	TTATCTCTTC	AGCTTGCTCT	AAAATGTCTT	GTCTTTTTAT	574380
TGGATCAAGT	TCAAAATTAG	ATTTTTTTAT	TAAAGCATCA	TACTCTTTGT	TTGAATATTT	574440

GTACGCTCCT	AAAAAATGAT	TTTCTGTTGT	AAATAAGCTG	TCTAAGAATG	TTAAGGGATC	574500
AAAATAATCT	CCTATCCACC	CCACGCTTGA	CATTTGGTAA	TTTCCAGTTC	TTCTGCTTCC	574560
TAGGAATGTT	GTCCATTCTT	CATTCTCGAT	TTCTAAGTTA	ATGTTTAGTA	TTTTTTTAAA	574620
TTGTTCTTGC	AAAAATTCTG	CTGTTGTTGG	TCTTCCCTCC	GATATTTTAT	ATTTTAATGT	574680
GGGGAATCCT	TTCCCATCCG	GATATCCAGC	TTCAGCTAAA	AGTTTTTTTTG	CATTCTCAGG	574740
ATCAAATAGT	ATTAAATTTT	TTCCATAAGA	ATAATCATCA	AATTTTGGAG	TTAGATTTCT	574800
TGTTGGATCT	GAACTTCCCT	TTAAAACTAC	TTTAGTTAAA	GTTTCTCTGT	CAATGGCAAG	574860
GGAGATGGCT	TGTCTAACTT	TTAAATTGTC	TAGTGGTTTT	ATTGTTGTAT	TGAATGCTAT	574920
GTATGCCATT	CCGTTTTTTA	ACCCAGAATA	ATAATCATCT	CTTATTTTAA	TTTCTTCTAA	574980
ATTATTCCTT	TCTGCTCCTT	GTAGAAAATC	GAGTTCACCG	TTTATGTACA	TATTGTAAGC	575040
CACGCTACCT	TCTGTTGGGT	AAAATATTAC	TTCATCAATT	TCTACATTTT	TTGCATTATA	575100
GTATTTTTCA	TTTTTTTCTA	TTACGATTTT	ATCGTTAATT	GATCTTTCTT	TAAGTTTGTA	575160
TGCGCCACTA	ACAACTATAT	TTTCAGGATT	TGTCCAATTT	TCTCCATATT	TTTCAACAAT	575220
ATGCATTGGA	ACTGGTATGT	ATGCTGAGTG	TGTTAGCATA	TCAGGAAAAT	AAGGCTTTGG	575280
AGATGTTAAT	GTTATCTCTA	AGGTTTTGCT	GTCAATAGCC	TTTATGCCAA	GCTCAGATTC	575340
AGGCACTGTC	TCATCGAAAT	ATTCTTGTGC	ATTTTTTATT	GTAGATTTTA	TTAAATTAGC	575400
ATACATTGCA	GCTGTTTTTT	TATTTAAAAT	TCTTAGGTAT	GATTTTTTTA	TCTCCTCGGC	575460
AGTAATGGCA	ACTCCATCGC	TCCAACTAT	ATCTTCTCTT	AGGTAAAATG	TGTAAATAAT	575520
TCCATCTTCA	GAAATATTCC	AACTTTTTGC	AAGTCCTGGT	TTATATTTTC	CAGTTTGAGA	575580
ATCTTTTACC	GCTAGGCCTA	AGAATAGGTT	TGTAATAATG	TTGCTACCGT	AAAGGTCTGT	575640
TGAGAGTTGA	GGATCAAGTG	ATGATGGCTC	GCTTAAGTTT	GATACTCTGA	AACTATTTT	575700
TTCTTTTTTA	GCATTACTAA	TACATGCTAT	TAAAGAAAAA	ATTATTAGCA	TTAAGGCTAT	575760
TTTTATATAT	TTCATGGGAT	TTTCCTTTTT	CAATATTTTA	TATATTTTTT	GTTCTCATTC	575820
TTTATTAATC	TTTTTTAATA	AATTTTAATA	AAGAATATTT	ATTTTGTTTT	AATTTTAAAT	575880
ATGTATGCCT	CCAGTACTTT	GATTTGTCTT	ACTTTGATTT	GTCTTGATT	TAAATTTTAC	575940
TTTAATTCTT	ATAATAAAAA	AAGTCTAATA	ATTTTAAATA	GTTTTTAGTA	TTATTTGTCT	576000
ATTGTTGCAA	GCCAAAATTT	TACTTTAATT	TGTATAGTAA	ATAAGGTATA	ATGGTGTGAA	576060
ATGTTTTTCA	AAATGTATGC	TTGTTTAATA	TTAGTTATTT	ATTGTTAGTC	TTATAGAGCT	576120
TTTTGTCTTT	AGTAAATAAA	ATAATATAAC	TAATGGTTAG	GTGGCAACAT	AGAATGCTTT	576180

AAAGGGTGCT	GGTTTTATGT	TTGTACAAAA	TGAAAGTTTT	GATAAATATT	TTAAAGACAT	576240
GGAAAGCGAC	TTTGTAAGTC	AATTTAAGTC	TGTTGAAAAT	GTTAATTATT	TGGATAAGTC	576300
TTATCGAAAT	GCAGATTCTA	AGAGTAGAAG	ATTGGCAGAT	AGAATGATAG	AGAGACTTCT	576360
TGAGAGTGGA	TCTACCATTG	TTGGCATACA	AAATATTTTA	GAACTTTACC	AAAAGACTAA	576420
ATCTGGCAAG	TCTTCAATTA	TATTAATGGA	GCATTATAGT	AATTTTGATT	TTCTTGTGTT	576480
CCAATTTTTA	CTTTACAAAA	TGGGTATCA	TGATATTGCA	GATCATATTA	TTCCAATAGC	576540
TGGAGTTAAG	CTTTTCAGAG	ATAATTTATT	TGTTAAGACC	CTTCTTTGG	GATACAATGC	576600
AATATTAGTG	TATCCACCGC	ACGCATTTGT	TGGGGTTGGT	TTAGAACATG	CTAGGCAAAG	576660
GCGTGTTTTT	AATACTAATT	CTATGAAGTA	TATTTATGAA	AAGAAAAATA	GTGGGTACAT	576720
TATACTTATT	TTTCCTACTG	CTACTAGGTA	TAGAAAAGGA	AGACCTGAAA	CAAAAAAAT	576780
AATTTTAGAA	ATTGGCAATT	ATTTTAAAAT	TTTTGATTAT	TATTTGATGA	TTGGAGTCAA	576840
TGGAAATGTT	TTAGAAGTTT	CTGAGGATGG	AGATATGTCT	CACGATGTTT	TTAAAAGAGA	576900
TTCACTTATA	TATAATGCTG	ACAAAGTTAT	AAGTATTGCT	GAGTATAGGG	ATGAAATTTT	576960
AAACACCTTG	AAAGATTCTC	AGACAGAGAT	TACAAAGGAA	GTTTTGGGTT	TAAAAATTGC	577020
TGAAGATTTA	GAAAATCGCT	TTAATGTTCT	TCATGCAAAA	GGTCATGAAT	TTTATAAAAA	577080
AAGCTTTTTA	TAAGCTAGGA	ACTTGATTAC	AATATGCCTG	ATGTAGATAA	GATAATACAG	577140
TTTAAAAGAG	AAATATTAGA	TAATCTTTCT	AATGAAAGAT	TATCTAAAGA	ATCTTTTGGC	577200
TTAAGTATGG	ATGTTAAGCT	TCCCGAGCCT	GGAGAGAGTA	TTGTTCCCTG	GATAGCGGAA	577260
GATCTTGCTT	TAGATGAAAC	TGATGATGAA	CTTGATTTAA	ATTTTATGCT	TGATGCTCTT	577320
GAGAATGAGG	ATAAATTATC	CTATTCTGAC	ATTTTAAATG	ACAATTTGCC	TTTAAGTGGT	577380
TCTAACTTAA	GGGTTGATGT	GGATTCAGAG	CTTTCAACTT	TAAATAATGA	TTTTGACGTT	577440
TCTTCTAGCG	ATTCTTTTGA	AAATAATATT	GACAAAGTTC	TTGATGATAA	TTCTATTGAT	577500
TTAGAAATTG	CTTCTAAGCT	TGATTTTGAC	AATTTAATCA	ATTCCCCAGA	ATTAAGTTCT	577560
GAGGAGTTGA	TTAACAATCA	AGGCAATAAT	AATTTTTTTG	AAGCCAATAA	TGATTCTTCT	577620
GTTTTAGGGG	ATAGTAATTT	TTTACAGTCT	AATGAATTTA	ATATTGATGA	TGCGGTAAAT	577680
GGCAAAAACC	AAACAGATGA	ACAATCAGAG	ATGTTTGTTG	GAGACAGTTT	AAATTTAAGT	577740
GCCGATGAGG	ATGATTTTGA	AAACGTTATA	GATGATTTTA	AATTTTTAGA	GTATGATCAA	577800
AATGCAAATT	TTAAACGTTT	TGAATTTAAG	GTTAATTATC	CATTATTTTT	AAAGCATTTA	577860
AATTCCTATC	CTAGAAATTT	AAGAATTGCA	ATTGCTGAGG	CTTAACTAA	GGAAAATGTT	577920
TCAAGGTTTA	AGCTTGAAGC	GCTAATTGAT	CTTGTTGAAA	AAAATAAAAA	AAGGTTGAAA	577980

TTTATTGCTA	AATTTGTAGG	AGATATTGTT	GGGCGATCTA	TTAAATTGCC	TGTAATTTAT	578040
TTCAAGGCGG	AAGAATTTAG	CAAGCTTCAG	CAAAAATTGA	GCTACAGGGT	TTCAAGGGCT	578100
TTGCTACCTT	TGATAAAAAT	AGCCTCTTTT	TTGTTGTTT	TAGTTTTAGT	TTCTTTGTAC	578160
CTTATAGTAG	ATGTAATATT	TTTTTATGTT	GCCTCTGAGA	GCAAGTATAA	AGAGGGCATA	578220
GAATCTATAT	ATGCAAATAA	AAGAGATCTT	GCCAAATCTA	TCTTTAGAGA	TGCTTACTAT	578280
ATTAGGCCTG	ATGATAAATG	GTTTATTAAT	TATGCTAAGG	CGTTTGAAGA	CGTTAGAGAT	578340
TTTGATAGTG	CTGAAGAGAA	GTATGAGGAA	TTGTTTACTA	TTGAGCCTTT	TTCTAAAAAT	578400
TCTACAAACA	GAAGACGAAA	AAAGTTTAAT	AAGGAAGGAT	ATATTTTCGT	TGCTTCCATG	578460
AAAATTGGTC	TTGGAGAGCA	CTCTGAGGCT	AATTCAATAC	TTGATGAGGT	TATATCTTAT	578520
GATCTTTACG	ATTATGATGC	TTTAGTATTA	AAGGGAGATA	ATTATTTTAA	ATGGGCTAAG	578580
ACAAATTCCA	ACTACTATAA	AGATAGTATT	AATAGCTATA	CGGTTGTGCT	TTCTAAATAT	578640
GGACAAAAAA	AGGAAATTTT	ATTTAAGCTT	TTCAATGCTT	ATATTGAAGC	TAATTTAGAT	578700
ACCGAGTCTG	ATAATGTCAA	TAATTTTATT	AAGTCAAATG	AAATTC TAGA	TATTGATGAA	578760
GTTGTTTACA	CAAAATATGC	TAAAAAGCTT	G TAGATAAGT	ATATTTCTTT	TGTGACTTAT	578820
AATCAAAGAG	CAAATAATCT	TGCTATAAAAT	TTAAATTATC	TTAATGGACA	AACAAATTTA	578880
TTGAATAAGG	AATTTTCTGA	TTTTAAAAAGA	AATGATGGCA	GA ACTATTTT	TAAGCTTGAC	578940
AATAATGTTA	ATATGAATTC	AGAGATTGAA	TACATTCTCA	GAAAAATATT	AAATAAAAAAT	579000
CCCAATTACG	ACAAGGCACT	TTTTGAAAGT	GGAAGATATT	CGTATTACAT	AGGAGATTTT	579060
AAGAAGGCCG	AAGTTTATTT	GCTTAAAGCA	TTAAATAGTT	TTAGGCATAA	AAATTCAATT	579120
GAAGATGCTG	GGGACAAGAT	ATTGGCTTAT	AAAATTTTAG	CAGACATTTA	TGAAAAAACT	579180
CGAGATTCTC	TTAGGGCTAG	TAATATTATT	GGTTTAGCCT	TGAGTGATTA	TTCTTTTTAT	579240
AAAAACACA	ATCTTATAAA	AGGATCTAAG	GAGATTTCTT	CAATTTATGA	AAAGCAAGGC	579300
GATATTCTTA	GATCTTTAAA	TGACTTTAAG	TCTGCGATAT	CTTCTTACAA	ATTGGCAATA	579360
AATGAGGGCG	TTGATTATCC	AGATGTTTAC	TATAAAGTTG	GA CTACTTAG	TTATAGAGAA	579420
AATAATTATG	ATGATGCATT	GAAATATTTA	TTTAAAGTAG	AGAGCATGGC	GGGGTTTTCA	579480
AGTAGTAACG	AAGTTTTTAAA	TACTATTGCC	CTAACTCTTT	ATAAAATAGG	CGATTTTTTTA	579540
GCTTCTAGGA	GCTATTATTT	AAGGGTTATG	CAAAATTTAG	AACTAGAGAA	GGCTAATGTT	579600
TTGAATTTTA	ACCCCAAAGA	AAATGATTAT	CATAAACTC	TTTTATTAAA	AGAAATTGAG	579660
ACTTATAATA	ATCTTGGGGT	TGTAGAAGTG	ATGGCTTCTT	TTTCATCTAT	AAGAGATACT	579720

AAACTTTTTTA	ATTCTGGAGT	TAGCAATTTA	AGCGAATCAG	CCAAGATTTT	TGATATATTA	579780
AATAGGGATG	AAGATATGGT	AAAAAGTGTT	AAAAAAGATC	TTGCTAGTTT	AAATCTCAGG	579840
AATATTTTTTA	AGAATAGTTT	TTCTAAATCT	AATGTTTTAT	TTTATGAAAA	TTTATCCGAA	579900
AAACTTTAAT	TATAGATCTT	ATTCATTGTT	TTTGAGTTAT	TTATGAGGGT	GGTTTCCTTA	579960
TGAAGAAAAT	TTTTTTATTT	CTTTTTATTA	GTTTTTATTT	GTTTGGATTT	GAAGATAGTT	580020
CTTTGAAAAT	AGGTATTGAT	GATGTTTATG	TTGAGGCTCA	TGAAGAGGGA	TTTCATCTTT	580080
TTATTAGAAA	AAAACCTGCA	ATCAAATCAG	TAATATTGAC	AGAGTCTTTT	GAAATTCCTG	580140
ATAAGAAAAA	AGATGTGGCT	ACTTATTCAT	TTCGTACATT	AAGTTATAAT	AAGGTTAATG	580200
GAGATGAAAT	TCGGATTTTA	AATGGAAGAG	TTATTAAGAA	TAAAGAACTT	TTATCATTGA	580260
CATCTTCCAC	CCCTGTTCCCT	AATAAAAAGT	TTGGAGAAGC	TTTTCATATA	TTGATTCCAA	580320
AAAAATTAAA	ATATGGATTT	CCAAATTTTT	CAACAAGAAG	TGGTGATATT	GACTTAGAAG	580380
TATTAAAAAG	TAAAAAAGAG	CCCTTTTGGT	TTTCTATAAG	ATCTTTTGAG	AAAAAATATA	580440
ATGATTATTT	GGGCAGATAT	CAAGACAATG	CTTATGAATT	GCTTTTCAAG	GATGATCAAA	580500
ATCAGGGAAA	AATTGAATTT	AATGAATTAA	AAGATACTTT	TACAAAATTT	TCAGATGAGG	580560
TTGTTATTGC	TAATAATGGC	ATTGATATTG	TTGATAAAAT	AAACAAAATT	TTAAAAAACT	580620
CAGAAGATTC	AGTTTATGAT	TTAGATTTAG	TGCTTGTTGT	TGATGTTACT	GATAGTATGA	580680
AAAGCAATAT	TGAGATTCTA	AAAGAGCATT	TGTTTTCAAT	AATAGAACCT	CAACTTCAAA	580740
AGTTTAAATC	CTACAGAATA	GGTCTTGTTT	TTTATAAAGA	CTATCTTGAA	GATTTTTTAA	580800
CCAAAGCTTT	TGATTTTAAT	ACTATTCCTT	ATTTAAATAA	TATTCTTAAG	TATGTTAATG	580860
TTGGTGCGCG	TGGGGATTAT	CCAGAAGCTG	TTTTTGAGGG	GATTGATGCT	GCTGTGACCC	580920
AATTTGATTG	GCGGGCAGAA	AGAAGGTTTA	TTATTGTTAT	AGGAGATGCA	CCTCCTCATG	580980
AGTATCCAAG	AGGGTCTATT	GTTTATAAAG	ATGTTATCAA	TTCTGCAAAG	GAAAAAGATA	581040
TTACAATTTA	TGGAATAATA	TTTCAGTAAA	AATTTTTTAT	TCTTAAATTA	TTATTTTTTA	581100
TTATTTTCTA	TTTTATTTAA	TATTTTTTTA	GCTAAAGGCT	TAATCCATTT	AGGCATTTCC	581160
ATATTATTTT	CTATTAATC	TTCAAAGATT	TTTTTTGCTT	TTTCTGTTTT	GTTTGTGTGA	581220
TAGTATATGA	ATGCAATTTT	ATATTTACCA	GTAGCAACTA	TATTTGAATT	GTGAGCGAAA	581280
TTTTGAATCA	TTTTTTTCGT	TGCTTTTAAA	GCCGAGTTAT	AATCATTGAC	ATTGACAGCT	581340
TTTTGAGCTT	CTCTAAGATA	AACTCCATAA	GGAGTTTCTT	TTGTTAATTT	TTCTAAGTTA	581400
ATCGTATAGC	AGGAAATAAA	TATTAAGTTT	AGTAATATTA	GCTTTTTTCAT	TTCTGCCTCT	581460
TTTAGAATGT	TTTTATTATT	TAATTTTATT	AGATATAAAA	TAAGAAAGCA	AGGCTTTTTTA	581520

AAGCCTTGCT	TTATGATTGT	TTTTGCTTAT	TTGGCAGGAA	TTATTATCTT	CCAGTTAGAA	581580
TGAATTAGAT	CCGGATTTTG	TATTTTTTGT	CTGTTGGCAA	ACCAAATTTT	TGGCCATAAG	581640
TAAGGATCGT	TGTATAAATT	TTTGGAATG	CCCCATAGGG	TATTGCCTAT	TTTTATTACG	581700
TAAAGCTCGC	TGCTTGCATT	GCTTTGATAA	GCTTCAAGGT	ATCTTGCAGA	TTCTAAAAAT	581760
AATTCATTGG	CAAGTCTAAA	GTTTTTTTACA	TTTTTAGCCT	CAACCCCTTT	TTCCCACAAT	581820
GTTCTAGATC	TTTCAATAAG	TTCTAGCGTT	TTGAATTGTT	CTTGAGGTTT	GGAGTTTTTTT	581880
GCTATTTCCA	CTTTTTCTTC	GTATGCGAGT	ACTATTGGAA	TTGAAATTTT	TGCTTCTCCA	581940
AGAAGATAAG	TGTCTTTATT	AGTATTTAAA	AGGTTTAAAGT	GACTGTTTCT	TTCTTTAATG	582000
AATGCTCTAC	CATTCCATGG	AGATGGCTTT	ATAAGCTTAT	TATTGCTATA	AATTGGTAAG	582060
TTGGAAGCCG	CTTCAAGTGC	TTTAAATTGT	TTGTACATTC	TCTCATCAGT	TTCTTTTAAA	582120
GCTTTAGCTT	CTTTGGCATT	TTTTGCTGCT	TGTTGTGCTC	TGTTAAAGGC	CTTGCTATAC	582180
ATGTCAAGGG	CATTATCAAG	ATCGTAATTT	TTATATTTTC	TTGTTGCTTC	AAAATATAAA	582240
TTATTTACTT	CGTCGATTTT	CAGCGGGATC	CATATGTATG	CTTCATTTGC	TTCTGCATCG	582300
TTTAGATACT	TTTCAATATT	TTCTTTAAGG	TAATTTGTTT	TTTCTTTTTT	TTCCCTCGTT	582360
TCTCTTATTA	TTGTTTTGTA	TCTTTCAAGT	ACTTTTAGAG	CAATTTCAAT	TCCTTCTATT	582420
GCTTTTTTTT	TGGAAAAACT	TTGTTTCATT	GCTTCTTCTA	ATCTTTCAGC	TTCATTAAC	582480
TCTTTGGAAT	AAAAAAGATG	TCCCCGTTCT	CTTATTAGTT	CATTTTAAAT	GTCTTTTATA	582540
TCTCTTAATT	GAAAATTTTT	ATTATCTGGT	TGTGCAATTT	TAGCATTTTT	ACTCTCTCTT	582600
GATTCTGGAG	GCGTTTTGCA	TGCGATAAAA	GAGATTGCTA	CTACAATTAG	CAGCGATATT	582660
AATTTATTCT	TTATATTCAT	AAATACACCC	TTCTAATAAC	TTGGCTTCTA	TTAATCTTTA	582720
AAGTAAGAAC	CTATAAATAT	TAAAGTTCTT	ACTTTTACTA	TTTTTATTAG	TATAGCAATT	582780
ATAGTATGTC	AATAAAAACT	TAATATTTTT	AATTCCTAAA	TTAAATTATA	CTTCTTTTTT	582840
ATCATTGTTC	AAAGTGTAAT	AAATTTATGT	AAAACAAGGT	ATAATTAAAT	TTATGAGTTT	582900
TTCAAAGATT	AGGAGAACTA	TATTTTTAGA	ATATATCAT	TTATCCTTTT	AATATTGCTT	582960
TCAAGTAGAA	CTTTATTTTC	TCAAGTGGCA	GTTGTAAAAG	AAATAGAAGG	TAGAGTTAGT	583020
GTTGTTAGAA	ATACATTTCC	CGTTAAGTTA	GATTTAGATG	ACGAAATTTT	TGAATATGAT	583080
TTTATTGAGG	TTGGAGAAAA	TTCAAAGCTT	AAAATAAATT	TATATGAAAT	AAATGGTATT	583140
TCTGTAGATT	TAATTTTTTA	TTCCAATACA	AATAGTTTTG	TGTTTTATT	TTCTCTTAAA	583200
GATTTGCAAG	ACGCAAAAAT	ATATTTATTT	AGAGGAAGTG	TTGATGCTAT	AATTCATAGC	583260

ATTGTTAAAG	GGTCTTCATT	TTCTGTTATA	ATAGATAATA	ACCTGTTTAA	AGCCGAAAAT	583320
ACTTCAAAAT	TTTATGTCAA	TAGCGATTAT	TTTAATAATT	GTTTTATTAA	TGTTTACAAG	583380
GGTAGCATCA	GACATATTAA	TAAAACCGAA	TATTTAATTT	TTCCCAATAC	CAGTCTTTTG	583440
CTTTTAAATG	GAAATTCCTT	TTTACACAAA	GTTAATGAAG	GCACTTTAAA	GGGTGTTAAT	583500
CAAAATTTTA	TAAGGATGGC	TAAAGATAAT	TTTATGTCTT	TAAATAAAAAG	GTTTTTATAT	583560
TTTTTTGTTT	TAAAATATAT	TGAGGATAGT	TTTAGATTCA	ACTTTATGTA	TAATTATTTA	583620
ATGAAAGATT	TTAAATTTAA	TTCTATATAT	TCAAAATGGA	GCCTGGAAGA	TAAAAATTAT	583680
AAATTTGGTA	ACAGGGTTGA	TATGATTAAA	AATGTTAATT	ATTTAAAGGG	TAGAATCGGA	583740
GTGCTTTTTTA	ATAATTTTGT	TGATTTGGCT	AATAGGTTTT	ATTTGTAGA	TGATGTTTTG	583800
AAATATTTTT	CTACTTTTTT	TGACAATTCA	ACAACTGTTA	ACGGGCCCAT	TTCAAAATTT	583860
TTAAAAGATT	ACAAAGCTAA	TAAAAATCTT	TTAAAAAATA	AGTTTTTTAA	AACAATCCAT	583920
TCTCTAAAGA	TGTATTTAAG	ACGCTCAAAT	GATGATATTA	CTAGTAATTT	AAATGTTAAT	583980
GAATTGTATT	TATTGCGCCC	TAGAGAGTTT	TGATTTTTAT	ATATTTAGCT	TTATGTTAAA	584040
GCTATTTGTT	AGATGGCATG	GTATATTCTT	TGAAAATTCA	AATTGAAGAA	GAAATTAACA	584100
TATTTGTTTT	TATCAGCTGT	TTGAACTAT	TAATATCAGC	CATTTTAAAA	AAAATGAAAA	584160
ATTTTCAAGT	TTTATTATAT	TATTCAACGA	AATTTAAAAT	TCACATTCAT	AATTTGCTTA	584220
ATATTTTATT	AAATTTGGGT	TGAGAATTTT	TTGCCAAAAT	TTTATCGTAA	GGGGGAAAAA	584280
TGCGCTCTTC	AGTTGATCGG	ATAATTAATT	TTTAAATTAG	TTTTGGCGGT	TTTATTTTTT	584340
ATAGCTTGTT	ATTGATTTTT	TATTTAACTT	TTATGGCATT	AAAGTGAATT	TAATAATAAT	584400
TAATAAAAGG	ATGTTTTTATT	TTTATGAGTA	AAAAGGTGTT	TTTTAAAGGG	TTTTGGATTT	584460
TATTTACGAT	ATTTCAATTA	TATTTATTTG	TTTATTTAAT	TTTTTTCAAG	AAGCGAAAGG	584520
TTGATATTTT	TAACAAAACC	AATATTGCTT	TATTTATTCC	CGGGGTATT	TCAGGATCTC	584580
CATCTTATAA	AGAAATGTAT	GATTCTTTGT	TTGAATTTAA	AAAAATCAT	GAAAATCTTG	584640
AAATTAAAGT	TTTAGAAGCT	GGATTTAATC	AAAGCGAGTG	GATAGAAATG	CTTGAAAAAC	584700
TATTAACCTC	AAAAAAATAT	GATTTTTTAA	TAACACAAA	TAATGCTATG	CAAGATATTG	584760
TTGACAGTGT	TTCAAGTAAT	TATCCTTATA	CTAAGTTTCT	CATTTTTGAT	TCTTTGGTTA	584820
AAAATACCAA	CAAGCAGGTT	TATTCAGTTT	CTTATAATGT	AGCAGAAGAG	GCATATATTT	584880
TAGGATATTA	TGTAGGTCTT	TTTTTAAAGG	AATTTATTAA	ATCTGGCTTT	GGAAATGCTG	584940
CTTTGATTGC	AGGTCAAAAT	TATCCCGTTA	TGAATGATTA	TATTTATCGT	TATTTCAAGA	585000
AAGGCATTCT	TGATACTGGT	ATGAGATCTG	AAGTTTATTA	TCGAGTTTTG	GGCAATTGGC	585060

ATGATAGCAA	TTTAGCTAAA	TTATTATCAG	ACTCTTTGAT	TAAGGATTCG	GGGGCTTTGG	585120
TAATACTTCC	TATTGTGGGG	CCTGCTGTTG	AAGGAGTGCT	TTCTTCTGTT	AGAGAGAATA	585180
ATATCTCTGC	AGTTCTTTTT	GATAGCGAAG	ATTATTTGGA	TAATAAAGAA	AATATTATTG	585240
G TTCAGGAAT	TACAAATCAA	AAATATTATG	TTTCACATAT	TTTAGATAAG	GCTCTTAAGT	585300
CAGAGATTAA	CTATGGAAAT	TCTGATATTT	TTGGCATAAA	ACATAAAGGA	GTTTTGTTTA	585360
ATGTTTCGAA	TGTTTTTTAT	TTAGAGCGAA	CCAGTCAAAA	GTTAAAAGAA	GATCTTTTAA	585420
AAAAAATAGA	AGAGGTTAGT	GCAAATGGTA	TAAAAATTAA	TTTGAACAA	AATTAATGGT	585480
AGAGTTTAAA	AACATAGTTA	AGTATTTTCC	AGATATTGAC	AAGCCTATTT	TGGATAGTAT	585540
TAATTTAAAA	ATTGGGGAAG	TTAAAATTTT	TACAGTAGTT	GGTAAAAATG	GAGAAGGAAA	585600
GAGCACTCTA	GCCAAGATTA	TTGCCGGACT	TATTGAATTT	GATGAGGGTG	AAATATTAGT	585660
AAATGGCATT	AAGCAAAAAA	ATTGGAATGT	AGATAAAGCT	AAAAATAATG	GTATTTATCT	585720
TGTTTCTCAA	GTTCTTAATT	TGAAAAATGAA	TTTAAGAGTA	TGGGAATATT	TGAGTATCTA	585780
TTGGTTTGGT	TATGAATTTT	TCATGCCGAT	GAATAAATCT	AAGACCTACA	AATATTATAG	585840
ATGGCTTATG	CAATTTTATA	AAATTTCTTT	TGATTTAGAT	AAGAAAATTA	AAGATTTAAA	585900
TATTAAAGAG	ATTTATTTTT	TACTTATTAT	TGCTGCTCTT	AAAGAGAATG	CAAAAATAAT	585960
TATTTTTGAT	GAGAGTGCTG	CTTATTTTTT	TCAAAAAGAA	GCACAAGCTT	TTATAAAATT	586020
GCTTGTATTG	CTTAAGAAAT	CGGGAGTTGC	GTCTCTTTTT	ATTACCCACA	GCGAGATTAC	586080
AGATGCTATA	AAATTTAGCG	ATGAGTTTAT	TATTTTAAAA	GATGGAAAGT	GTTTTAGAAC	586140
AGTAAACAAA	GAATCAATTT	TGAGCAAGCT	TGAATCCTCT	AGTGACAAAG	TATTTGTTGC	586200
AAATATTAAT	TGCAACAAAT	TTGAAAAAGA	TCCTATTAAA	TTTAATTTGT	TTTTTGAAGA	586260
TTTTTTGAAG	TATGATGTTA	GTTTTTCTTT	AAATAAAAGG	GGTGTTTTAG	GGATAATTGG	586320
CGAAGAAGCT	GTAATTAAAA	CTTGGGAAAA	ATTATTCCTA	GGAGAGCTTC	TTTTTGTTGG	586380
GTGCATAAAA	ATTGATGGCA	TTAGATATGA	GCGAATAAAT	ATTTTTGAGT	GTAAAGCGGG	586440
ATTTTTACCC	TTAGGTATTG	GTAATTTATT	CCCCGATAAT	AGCAGCATAT	TAGATAATTT	586500
TTTGGCCAAA	TTTATGAATT	TTGAAAATAA	AATTTTTATT	AGGCAATCTT	ACATTAATCA	586560
GATTAAAGAT	TTTTTTTAAA	AAAAAATGGA	ATTTTATAGC	GAAGAGAAAA	TATATAGAAT	586620
TCTTTATTCA	AAATCTTTGG	CATTTTCTGG	AGGAACTTTG	AAGAAATTTG	CTCTTTACAG	586680
AGAGATGTAT	ATTGCAAAAA	GTTTTTTAAT	TTGTTTTTCT	CCTTTGAGCA	ATTTAGATCA	586740
CAAAGCTTAT	AATGAAATGT	CTGTTGCTAT	TCGTAATTAT	TCAAAAGAAA	AGCCAGTTCT	586800

TTTGATTACT	TCCAATTTAG	ATGAATTGCT	TTTGCTCTCT	GATAACATTT	TGGCAATGAA	586860
AATGGGAGAA	GTTTTGTAA	ACGTATCTAG	AGAAAAGATT	AGTAAAGAAA	AATTAAAGGA	586920
ATTGCTATTT	TTATGATCTT	TTTtagAAAT	AGCTTTATGG	CATTAATTTT	TTCTTTTTCA	586980
ATATTAAAGTA	TTAGCTATTT	TTTCGGTGAT	TTTTTTCAAT	TTTCTTATAT	TAAAATGATA	587040
TCTTGGCGCT	TTATTTTATT	TTTAATTATG	GCTACGGGGA	TTGCTACTTG	TGCCAAGAGT	587100
AATTCATTAA	ATCTTGGGAA	TGAAGGTCAG	ATTTATTTTG	GGGCATTTTT	AGTTTATATA	587160
TTTTCAAGTT	TTTTTGGATT	AACCTATTTT	AATTTTGAT	TTTTGATACT	TTTAAGTTCT	587220
TTTTTTGTAG	GACTTTTGGG	GCTTATCCCC	TTTTTTATTA	CTTTTTTCTT	CGGATTAAAT	587280
AAAGCCTTAA	CAGGTCTTTT	AATATCTTAT	GGAAATCAAA	GATTGGTGGA	TGGATTTATT	587340
TTAAATATGT	TAAAAACAGG	TAGTTTTTCT	AATCAGACAA	AAAGGATTAA	TAGTTTGTTT	587400
GCTTTAGATT	CATCACTTAT	TTACTTGTTT	TTGCTTGGTG	TATCAGTTTG	GCTTTTTTAT	587460
GTTTTTATTC	ACAAAAAAC	TATTTATGGT	CTTCAGCTTG	AAATATTAAG	CAATAAAAAA	587520
AAGATAGACA	TTTTTTTCAA	TATAAATGAA	TTTAAATATA	AGTTTTTCGC	TGTATTTGGC	587580
AGTGCTTTTT	TAAATGGTCT	TGCAGGTTCT	ATGTTTGTAG	TGTTTTTTAG	ACCATATTTG	587640
GTTTTAGGGC	TAACCTCAGG	ACTTGGTTGG	AGTAGTCTAA	TTGTTGCTGT	AATTCAGGA	587700
TTTAATTATG	TTTATGTATT	ATTTTTTAGC	TTATTGTTTT	CAATATTAAT	TGAATTTAAT	587760
AATTTTCTTA	ATATAAATTA	TGACTTTAAG	TATGAATTTA	TTGGGCTTTG	TCAATCAATT	587820
GCTATTTTTA	TCTCTTTATT	TTTGATTAAA	GCTAGGAAAA	AGTAGATGTT	TAGTATTTTT	587880
GAGCAGGCTA	TTGTATTTTC	GTATTTAGCA	CTTGGAGTTC	TTTATACAGA	GAAAATAGGA	587940
TTTTTAAATG	TATCTATTGA	AGGCATTTTCG	TATCTTTCAA	TATTTTTAAC	ATCTTTTTTC	588000
ATCTATTTGG	GATATGGAAT	TTTTATGTCA	ACCATTTTTA	CCCTTTTTAT	TAGTTTTTTG	588060
TTTGGATTTT	TTTTATCTTT	TGTAGTAAAA	AAAAATTATG	ATATTTTTAT	AGCAGGAATA	588120
GGTATTAATA	TTTTTTGTTA	TTTTTTTGTT	GAWTATTTAA	TGAAGAGTAA	TTTTAATTTT	588180
ATTCCTGGTT	TTACTTTAAA	TTTATCTGGA	AATTTTGAGA	TTTTTGTTTT	TATTGCTGTT	588240
TTTTTCATTT	TTTTATTTAT	TACTGTTTAT	GTTATAAGTT	ATTCAAGAAT	TAGAGCAGTG	588300
TTTGAATTTA	TCTCTTCAGG	GAGTTATGAA	GACATTTTGG	GCGAGAAAAT	AAGCAGTCGT	588360
TTCAAATCTT	TTGCAATTTT	TGTATCAATT	TTACACAGCA	GTCTTGCTGG	CTCATTTATT	588420
GCGGTAAGTC	TTAATGCTTA	CTCTTATAAT	TTAGGATTAA	ACAATGGTTG	GCTTGCTATT	588480
TGCATTCTTT	ATATTGCATT	TTCAAATCCT	TTATTAATTT	TTCCAATTTT	TTTTTTGATA	588540
GTTTTTTTTG	AATATCAATT	TTTTCGCACT	CAAGAGTATG	TAAATTCTTA	TTTTTCTCTT	588600

TCTTTTCAAT	TTTATGTAGC	AATAATAATA	AATATATTGG	TTTCGTTGAT	TAAGAGAAAA	588660
GATAGATCTT	AGTTTAAGTT	CTGCACGTTG	TGTTTTGAAT	TGTTTTTAGA	GTGCTGATTT	588720
GTAGATATAA	TTCTTCTAAT	TTTTTTCTAT	TAAAATGATA	GAAGGGTATT	TGTTTTATTA	588780
TTTCTAAATT	ATTTAAAAAA	ATTATAAACA	ATGTGTCGTC	ATTGAGTGCT	AATTGAAACG	588840
TTGAAGATAA	TATTGCATTG	AATGCTGCAT	TTTCATTGTT	TGTAAAATGA	TAAATACTTT	588900
TTTTAAAAAG	GGCATCAATT	GCTATAAATA	TGTTTTCTCT	GAACAATTCT	TTACCGCTTT	588960
GGAAAAATTT	AATTATATAG	TCCATTGAAT	TTTTAACTTC	TCCTATTAAA	AAGTATGCCC	589020
AAGAGATATC	TAAAAAGTTC	TTTTTATCTT	TAAAGTCTAT	TATTTTAAAG	TAATCTTGAG	589080
ATTTAATAAT	TGCTTTTTTC	CAGTTTTTAT	TTAAATATTC	TAATCTGAG	AGCAAAAGAT	589140
GAGCATCAGC	TTGATTTTGA	TCCATGTAA	TTATTTTTGT	TAGACTTTCT	ATTGCTTTAT	589200
TATATTTTTT	TGAATCTTTT	AGTAACATTG	ATTTTTGGTA	AAGTTTTTCT	ATTGTATGk	589260
TGTTTGCTTT	TTTATTAAGT	TTTAATATTG	ATGTTGTTGT	AGTAGGGCAA	ACATTTATTA	589320
TCAAGCCATA	GAAAAGTATC	ATTATTGTTA	TTTTTCTCAT	TATATTCCTT	CTTTTATTTG	589380
CTCAATAGTA	TCTATTAGTA	GATTTTTATA	TCTATTTGTT	AGTGGGTATA	AATTGAGTTC	589440
GTTTTTAAAC	TCGTTTAAGT	ATTTTAAGGC	AACAATAGTT	GAATTTTTTA	TTGATTTTGA	589500
TGAGTTTATC	ATTTCTGTTa	GTTTAAATAT	TTCTTTTCTT	GCTTTGGTAG	TTTTGGTATT	589560
TTTTATTTGA	TTGAATTTTG	AAATAATTTT	TGGTTCAAAC	TTTTTTTCTT	GTAAAAATA	589620
AATTATTGGC	AAACTTTTTT	TCCCTTCGAG	TAAATCATCT	CCGAATTCTT	TACCATTAAT	589680
TTTATTTTTA	ATGTTTTTAA	TATCGTCTAT	TATTTGAAA	TAAACACCAA	GCTTTAAAAA	589740
TGTACTGTAA	ATTTTTTTAG	CTTTGTCTTC	ATTATTTGTG	AGTATTGCAG	CTAGAAAGCT	589800
GGCCATTCCA	AAAAGTGAAG	CTGTTTTTAA	TTCTACTAAA	GAGATGTATT	CTTTAATACT	589860
TGGGATGTAT	GACTCATTTG	GAAATTTAAT	ATCAATTCCT	TGTCCTAGGT	GGAGATTTGA	589920
AAGAGTTGTA	AAGAAATTTT	CATAAATTAA	TAATTTTTGA	TTTTCTTTTA	AATTTGATTT	589980
TTCTATTAAT	TTTGCAGGTA	AAAAATAAAT	TAAATTGCCA	GCATTTATAC	TGTTATCTAT	590040
TCCATAGATT	AAATGTATTG	CTGATGCACC	GCGTCTTTTT	AGTGAATTGT	CTTCAATGTC	590100
ATCAATAATC	AAGCTTCCAG	AATGAGGAAG	TTCAAGCAGC	AAGCTTAATT	TATATATTAG	590160
TTTGGTATTT	TTTTCTTTTA	AACCCAATGC	ATATGCTAAA	AGAATCATTA	TCATTGGTCT	590220
TATTCGTTTT	CCGCCCCAT	TAACAATTTT	AATTGCTGGT	GCTTTAATAT	AATCAAGGGT	590280
TTCTTTTTTT	ATTTTAAAAG	TAAATTTTAA	ATCGTTATCT	TTGAATAAAT	TTAGAAAATT	590340

AGTTGTTGAA	AAGATTTTAT	TAATATTTTT	TTCAATATTT	TTTAAAAATA	GTTTATTTTG	590400
CATAATAAGA	ATTATAATGA	AAAAGTATAA	TAAAGTGTAT	TAAAGGGATT	GATGTGTATC	590460
GCTTGGATGA	TGAATATTCT	AAAAAGCCA	AAAGAGAAGG	ATATTTGGCA	AGGTCTGTAT	590520
ATAAGTTGAT	AGAAATTAAT	GAAAAATTTT	CTTTATTTTC	TTCTGGCAAT	GTTTTAGATA	590580
TTGGCGCATC	ACCTGGCAGC	TTTTCTCAGT	ATGCTTATAA	AAAGCTTAAA	AGAGGAATTC	590640
TAGTATCTGT	TGATATTAAT	GATATTGGCC	TTAGATATGA	TGATAATTTT	TATTTTATAA	590700
AGGGAGATAT	CTTTTTAGAT	GATACAGTTT	TTAAAATTAA	TACGTTTAAA	CCTTATAGTC	590760
TTGTAATTAG	TGATGTGGCT	CCCAAGACTA	CTGGAAATAG	ACTTGTAGAT	ACCAGCAATT	590820
CTTTTAATTT	AAGCATGAGA	ATAATAGATT	TATCACTTGA	AGTTTTACTT	AAAAAAGGGA	590880
ATTTACTTGT	TAAAGTTTTT	CAGGGAGGAG	ACGAGATGCA	AATTTTTTAA	AAGTTTGAAA	590940
AATATTTTAA	ATTTGTAAAA	AAAATTAGAC	CCAAAGCTGT	AAGGAAAAAT	TCTTTTGAAA	591000
TTTATTTTTT	AGGCAAAAGT	TTTGCAAGT	AGCAAATTAA	TCAAATTGTT	ATAAACAGAT	591060
TTAAAGGTAT	AAAATATGTT	TAGAAAAGAA	AGTTCTAAAG	ACAGCAGATC	ACAGCTTCAA	591120
GTTGCAGGTT	TTAAAATAGG	AAAAGAAAGC	TATGGGGTGT	CAATAGAGCA	CATTAGAGAA	591180
ATTATTAAAG	TTCCATCAGA	AGGAGTTTAT	GCTATACCAA	ATGTTCCCGA	ATATATTATA	591240
GGTATTTATA	ATCTTAGAGG	CAGTATTATT	CCTTTAATTA	ATTTAAATAT	TAAATTTGGA	591300
GTTCTTCTA	TTTCGGTAAC	AGAAGAAGAC	ATGCTTTTAA	CAGGATACTT	AATAGTTAAG	591360
ATTAAAAATA	AGCTTTTAGG	CATTTTTGTT	GATAGAGTTC	TTAAAGTTAT	TAGCTTTGAT	591420
GATTCTAGGG	TTCAAGAACC	TCCCGCTACT	TTACAAACTT	TAGATAGAAA	ATATATATCT	591480
GGAGTTGTAA	AGCTTGACGA	GGCTGATAAT	CTTGAGAGTG	AATACTTAGT	ATTAATTGAT	591540
ATAGCAAAAA	TTTTTGATAA	ATGCGAATTT	GACGACATTC	CCTATAAAGA	TCAATATGAA	591600
GAATAAAGTT	CTTCTTTGCA	TTAATACTTT	AAAGTCGGGA	GCTAGTATTT	TAGGCAATGA	591660
TGTTAAAGTT	TATTTAGAAA	CCAAGTATTT	TGTTGAAGTA	GTGTTAATAG	ATGTTGGCAG	591720
ACCTTTATTT	TCTTTTCCAA	AAGAAAATTT	TCTTTTTTTG	ATAACTTTAG	GAGGAGATGG	591780
CACAGTTCTT	TTGGCTGTTA	ATTTGCTTCT	TGAAAATGAA	AACATTGATA	TTCCAATTAT	591840
TTCAATTAAT	ATGGGCAATG	TGGGATTTTT	AGCAGATATT	AAGATTGAAG	ATTTTAAAAA	591900
AGTCATAGAT	AGATTTTTTA	ACAATCTTTT	GTTATTAAAT	AAAAAATTTT	TGCTTCATGT	591960
AACAGTTTCT	CAACACGGTA	AAGATTTAAT	TTCTAAATAT	GCTTTAAACG	ATATTATTAT	592020
TCGCTCAAGC	GTTCTTAATA	AAATGATTTA	TGTAGATCTT	ATGGTTAATT	CTGAGAGTTT	592080
TTTATCATAC	AAAAGTGATG	GGATAATTGT	GTCTACTCCA	ACAGGCTCAA	CAGGATATTC	592140

TTTCTCAGCA	GGGGGTCCTA	TTTTAGAAGC	AGATCTTGAG	GGATTTTtYAC	TTACGCCTAT	592200
TTCTCCACAT	TCTGTTTATA	ATCGTTCCTT	TGTGTTCTCT	AAATTAAGTA	AACTTTCCAT	592260
TTCTTTTTCA	AAGGAATATT	TTATAGCAGC	AGCATCAATT	TTTTTAGATG	GAATTAATTT	592320
TGGTTCTTTC	GGAGTTGACG	TTGTTTTTGA	ATTTAAAATT	TCTTCTCAA	GCTTGAATTT	592380
TGTTTCATTT	TGTACGGATA	CTTTTGTTAA	GAGATTAAAA	AACAAATTAT	TGTAAGTTCA	592440
ATGTTTTTTT	AAACAGTGTT	CTTTTAAATA	AAAATTTTTC	TTGGTTGTTG	TTTGAATGTT	592500
TGGTTTAATC	TAATCTTTAA	TAAGGTTAGA	GGATTTTACA	TGTTTTATTA	TAAGGATTTT	592560
AATGTTTTGT	TTATTCGCAG	AGTTAATGTT	TAAAGGGTGT	TTTTTATAAA	TTTATAACTT	592620
GTTAAATAT	TTAATATATT	TTTGCTAAA	ATCAATATAT	TAGATAGCTG	ATAAATCACC	592680
CTTTTATGAG	TTTTAGGCAG	GTGTTTATGG	ATTTAATTGA	TAATGAAAAT	TATAAAAAAA	592740
TAGTGACAT	TAATAATCTT	GTTTAAAGGA	CTTTAAATGA	TATAGCAGCT	ATAAAAGAGA	592800
CTGGCGAATT	TACATCAAAT	GCTAAACTTT	CATTTAATCT	TATTGATTTC	AATTTAAATG	592860
TTTTAAGTTA	TATTTCTTCT	TTAAATTATT	TTTATACTAG	GCCTAGATTG	AAAGTAAATT	592920
ATTCTATAAA	AAAAATTTTG	TCTGGGTGA	TTTCTGATTT	TAGTTTAGTT	ATTAGCCCTG	592980
TTCTTAGTAT	TACTCCAAGA	GAGTTGATTG	AAATGCCTCA	GGCTCTTAAT	TTAAATCCAG	593040
AAGAGAGGTT	TTTAATTATT	AAAAAATTAG	GTTATTTAAT	TGATTTGGCT	AAAATTTTTA	593100
GCAAAAAAGA	TTCTAAAAACA	CTTGTTTTTC	TTGAGGATAT	GTATCTCAA	TTTATTGTTT	593160
TTTCTAAAAA	TATTATTGAT	TTTAGAGATT	TTTCTAAGAA	TTTAAACTT	GAGAGTCCTT	593220
ATTATAAATT	TCAATTTGAA	CACCTTATTA	AAGTGTGGGA	GCTTTTAGAA	GAAGGAGCTT	593280
TTATTTTAAG	GGGCAAATAT	GAGATTAGTG	GATCTCATGA	ATTTGGACTG	CATTCTCTTG	593340
GTTATCTTGA	AGCTGGAAGA	GCTTTGGCTA	CTATAGCCTC	TCAAAAAGAA	GCTGCTGAAA	593400
AATTTTCAAG	GTTTCATGGA	GTTTGGTCTT	CAAAGTTTAG	TTCAGATTTA	ATTAAAGTAA	593460
AATAGATAAA	TTAAGGTGGG	GAGAAAGTAG	TTATATTGAG	TTTTAATGTA	GAAGAGGGCA	593520
CTATTAAATT	CAAAAAATTA	AAATTTTTTT	TGATTCTAAG	CTTGTTTTTA	TTATTTATAA	593580
TTTTGATTGA	TTTTTTTATA	AGATCTACTA	TGAATGTATC	TAATTTTTAT	GATTTTAAGA	593640
ATTTTGAAAA	TAAATCTGAT	TGTAAAAATA	TAAATTTAAG	TAAGAATGTT	TTTGATCAA	593700
ATAAGGTTTT	AAGTCTTAAT	TTCGGGGAAT	CTTGTTATTC	TCTTTTAAGT	GATAACTTAA	593760
TAAGTTATTC	AGACTATTAT	TATGTGCTTT	TTAATCCGG	CGAAGATTAT	TCTGTTTTTT	593820
CTGTAAAAAA	CAATAAATTT	TTATTTACAC	TCAAGCTAAA	GGATTTTGTT	TTTGCAATAA	593880

ATAATTTAAT TTTTACTTTA AATAATTTAT ATAAAACTTT AGAAGTTTAT GATTCTAGCG 593940
GAAATAATAT ACTAATGCTC AATTTTTTTGT CCTCAATTTT AAGTGTGGAC TATAATAATG 594000
AAGTTTTGGT TTTGGGACTT TCTAATGGTG AGATTTATAT ATATAAACAG GGTAAGATAA 594060
TTTATATGGA AAATTTTTTA GAGAGAAAAAT TTCCAACATG TTTTGTAAAA TTAAGCTCCG 594120
ATAATAAATA TTTGGTTTCA CTAAAAGGCA GTTCTGAGTA TTTTTTAGAA ATAATTGATT 594180
TAGAGAATAA TTATAAAAAA ATTTTAGAAT TAAACAATTT AACCATTAAT AGTTTTGAGA 594240
CTTTTATAAA AATAGATGAT TATCATAATT TGTATTATTGA AGGCAAAAAT TCACTTGCGG 594300
TGATAAATAT TAAAAGTGGT AGAATATTTA AGGTTGAAAA TAAAAATTCT ATTTTAAGAG 594360
CGTCATATGA TTATTTTCAA AATATTTATA GAGTATATTT TTATTCTGAG AGTGAAAAAA 594420
TCATTAATAT AAAAAGTTAT TCTGCAAATT CTTTTAAATT GTTTGATAAT ATTTTTATTA 594480
AAGATGAAAT AAGCTCTTTT GTTGAATTTG GAAAGGGACT TTTGTATTTT AATAGTAATA 594540
ATGATTTAAA ATACTTGGA TTGGCTCAGT GATTTTAATT GTTTTATAT TTTTCTTTAA 594600
TATTTTAGAT TTATATTCAT TTTTGGAATT TAGAAATGAT GAAAAGTTTG CTTTAGTTAA 594660
AGATTTTGGT GTGTTGGATA ATAATAAGTT GAATATTAGC CTAAGGTTAA GGCCCTTGGA 594720
AAAAACCGTA TCTGTTTTTT CCAATAATTA TAAAATTTTA TATTCAAAAA ATAGTTTAAA 594780
TAGGGATGGT AGTATTTTAA TTATTTTGA TAATGATTTA AATCTAAATT TAGAGGTTTT 594840
TGGGGGATTT CTTTATAAGC TTGGA AAAAT TTTTTTAAAA GATGAAAAGA GTGTTATTGA 594900
TTTGGTAGTT AATGATCCTA GTGCTAAAAA AATTATCAAT CCTTGTTTA TTATCAAAAA 594960
TAGGAACAAT GTGGTTGCTG AGACAGTTTA TACATTGGGT AGGGTTTTTT TAAAAGGAAA 595020
GGGCGATGAT GAAAGATTGG AATTATCCAA AAATATAAAT TTAAATGTAG ATTCTGGTCA 595080
ATACAGTCTT TTGTTGTATT TTCATACTCA AAAAGTAGAA TCTTTTGAAA ATTCTCTTAA 595140
AGGAATTTAT TATTTTGAAG CTATTTTGAA TAATAAAAGT ATTCTTCGTT CAGATTTTCA 595200
AAATATTTTT TTGATTAATG ATACACATAC TTTAGCCCAA GAGAAAAATT ATGGGTTAGA 595260
TATTTTGAAC ATTAAAAAG ATGGGGGATG TCTTAAGATA AATGATCTTA ATTTTGTTAA 595320
GGTAAGAAT GAGCTTAAAA TAAAATATGG CGATGTTTAT GGAAATGAAA AAAAAATAAT 595380
TTATAGGTTT AAATTAAATG AATAATAATG CTTTTCATTT TCCAGTACTT CTTGATGCAA 595440
TTTGTAAGCT TATAGAAGAT TTGCCCCGTA AAAGTGACTT AATATACATT GATTCTACTC 595500
TTGGAGAAGG TGTTCATGCA AAGGCTATTC TTGAGAAATA TGACTTTTTTA AGTTTGGTTG 595560
GAATTGAAAG AGATCCTCAA ATTTTAGAAA GAGCAAGGCA GTTCTTTCT ATTTTGAAG 595620
AGAGAATTAC ATATTTTAAT GATTGGTTTG ATAATTTTTT CGTCAATTAT CCTTTAAATG 595680

TCAAAGCCAA TTTTATTTTA GTTGATCTTG GTATTTCTAT GTTTCATTAC AAGGGTAGTA 595740
AAAAAGGATT TTCTTTTCTT GAAGATGAGC CTTTAGATAT GAGGCTTTGT TCTTCTTCTT 595800
GCAAAATTAG TGCGGCTGAG ATTGTAAACA CTTATAGTAA ATATGACCTT GAAGCTTTAA 595860
TTTATGATTT AAGTAATGAA CATTATTCTA GAAGAATTC TAAGGCTATT GTAGAATATA 595920
GAAAAATTAA AAAAATAGAA ACCACAAAAG AGTTGCAATC CATAATAAGC AAAGTTTATC 595980
CTTTTTCAAA AGTTAAAATA AATCCAGCTA CAAAACTTT TCAAGCGTTA AGAATTTATG 596040
TAAATGATGA GCTTGCTCGG CTTAAAAGGA GCTTGCCTTT TTGGGTAGAA AATTTAGCTA 596100
AAGATGGAAT TTTAGCTATT ATTACGTTTC ATTCAATAGA GGACCGTATT GTAAAAGATT 596160
TTTTTAGAAG CTGAGCTGT GATTTGTATG CTAAGATCTC AAAAAGCCC ATTATGCCAA 596220
GTTTGTATGA GATTAAAAA AACAAACCTT CAAGGAGTGC AAAACTTAGA GTTGTA AAAA 596280
AATTATGAAC AGCATAAGTA AGATTGAATT TAAAGTTTAT TGTATTTTAG TTTTGATACT 596340
AACAGTTATA TTGTGTTTTA ATATTTATTT AAATTCAGA TATGTTGTAA AGCTTAGGGA 596400
ATTTAATCAC TTAGACAATG AACAGGAAAA TATTATTGAT GATAATTTAA GGTTACTGAC 596460
GGTAATATAT GAGCTTGAAA ATATTGATAG AATAGAGAGT TTTTGT TTTTG GAGAATTAAA 596520
TTTGGA AAAA AAAGCTAATG AAGATATAAA TATTTTGT GAGTAAAAGA TTTTAGAATG 596580
AGGTTTGAGT GCGTATAAAG ATTAAGGATA TTTTAATCTC TTCTAAAGAT GTGAAATTTG 596640
TGGGGAATAT AAAAATATT GAAAGAGTAG TGTCTTTTTA TTCGTTAGAT AGTCGCGAAA 596700
TAAAGGATGA CAATATCAAT GATAGTCTTT ATTTTGCGTA TAAGGGAAAT AAAGTAGATG 596760
GATTTTCTTT TGTAAATAT TTAATTGATC TGGGTGTAA ATGTTTGCA TGCTCAAGAG 596820
AGCATGAATC TGAGTGATT AAATATTTAA ATGACAATGA AGGGTTGGTT TTTTGCTTA 596880
CAAGCAATGT AATAAACTT CTTCAAGCTT TGGCATCGTT TTTAATTGAA AAAACAAGCT 596940
TTAAAAGAAT TGCTATTACG GGTAGCAATG GCAAACTAC AACTAAAGAG ATGCTTTACA 597000
GTATACTTTC AAAGAAATAC AAAACTTACA AAAGTTGGGG TAATTTAAAT TCTGATATTG 597060
GACTTCCTCT TAGTATTTTA AGGGTAGAGG GTAATGAAGA ATATGCTGTT TTTGAAGTTG 597120
GAGTTAGTTA TGTGAGAGAA ATGGATCTTT TATCTCAAAT TTTAAAACCA GAAATTGTTA 597180
TTATTACGAA TATAAGTTAT GCGCATATGC AAGCCTTCAA GGAGTTGCAA GCTATTGCTT 597240
TTGAAAAAAG CAAAATAATT GGCAAAAACA TTGAAATCTT TGTGTAAAT GAAATGAATG 597300
ATTATTGTGT TTATCTTGAA AAAAGAGCAA AAATCGCAA TCCAAATGTT AAAATCGTTT 597360
ATTTTGATTT TGAAAATCTT AGTATTAAGT CATTTCTTT TTTGGATGGG AAATTTCTT 597420

TTGATTTTGT TTACAAAGGG TTTGAATACT CTATTTTATT GCTGGGTCGG CATAATATTT 597480
TTAATGCAAT AGGGTGTATT AATTTGGCTT TATTTTATAGG AATGAGAGAA AAAGAAATAA 597540
AAGAGGGCCT TATTGAAACT GCTTTTCAAA AGGGTAGAGC AGAAATTTTG ACAAAAAATG 597600
GATATTTGAT TTAAACGAC TCTTATAATG GCAATATGGG TTCTTTTATG GCCTTAAAAA 597660
ATATGATTTT AGATCTTAAT ATCCAAAACA AAAAGTTTAT AGTTCTTGGG TCTTTTAAAG 597720
AGCTTGGGGA ATTGGCATAA AAAACTCACA AAGATTTAAT TCAAGAGGCT ATTTCAATGA 597780
ATTTTGATAA AATTTTCTTA ATTGGCGAAG AATTTTATAGA TGTTAGGGAT TCTGAGAATT 597840
TAGTTGAAAA GTGTTTATAT TACTTTAGCG AGTTTGATAA ATTTATTGAT TTTTTTTTAA 597900
AAAGCTTGGG ACCTTCAGTT TTTATTGTCA TTAAGGGCTC AAGGTTTAAAC AGGCTTGAGA 597960
GAATTTTAAA TATATTTAGA TGATAGTGGG GTTTTTATGT TTTACCTTTT AGGTTTGCCT 598020
TTGCTCAAAT ATATTACCTT TAGAATGGCT TATGCTACAA TTTTGCATT TTTACTTTCT 598080
TTGATTGTGG GCCCTTATAT TATTTTAAAG TTAAAAAAT TAAGAGCTGA TCAGATTTTA 598140
AGAGAAGATG GCCCTAAAAG ACATTTAAGT GAAAAAGCAG GAATTCCTAC CATGGGGGGC 598200
ATTCTTATTT TTTTTTGTGT TTTTATCTCT TTAGTATTTT GGAGCAACAT TTTAAATGTT 598260
TATTTTTTGA TTATGGTTTT TGTTATGCTG GGATTGCTT TTTTGGGCTT TATAGATGAT 598320
TTTTTAAAAA TAAAAAGAA AACCTCAGAT GGACTTAAAG CTCGATTAA GATTTATGGA 598380
CAAATAATAT TTTCTTTTTT TTCTGTTGGC ATTTTATATT ATTTTGGTGG TGAGCATGTT 598440
AGTGTAATCT ATTTTCCTTT TATTAAGTCT TTTCAAATAG ATTTGGGGTT ATTTTACATT 598500
CCTTTTGGCA TGTTTATTTT AATTTCTGCT TCTAATTCTT TCAATCTAAC AGATGGGCTT 598560
GATGGACTTG CAATTGGATT GAGTATAGTT ATAACAGGGG CTTTAATAAT AATAGCTTAC 598620
CTTACAAGTA GGGCTGATTT TGCAGCTTAT TTACATATTC CAAATATTAA AGGTTCTGAA 598680
GAGCTTGTA TATTTCTTGG GGCCTTGCTT GGGGGTAGTT TTGGATTTTT GTGGTTTAAT 598740
GCCTATCCTG CTAAAATTAT GATGGGAGAT ACAGGTAGTC TGGCTTTGGG GGCCATTCTT 598800
GGAATGGCAG CTTTGATTTT AAAAAGTGAA ATACTTTTTT CAATTCCTGC GGGTGTTTTT 598860
ATTATTGAAA CTATGTCTGT AATTATTCAA GTTTTGGTTT ACAAAAAAAC TAAAAAAGA 598920
GTATTTAAAA TGGCTCCACT TCATCATCAT TTTGAAGAAC TTGGGTGGTC TGAAATGCAA 598980
GTTGTTATTA GATTTTGGAT AATAGGGTTA ATATTTGCTA TAATTGCTTT AAGCACGATA 599040
AAAATCAGAT AATTTATTAT GGTGTAGAG ATAAATTCAC TTAGGACATG TTATTTGCTT 599100
GTTTTGCTGC TATTGGTAGC CTATGGCCTT GTAGTTTTTT ATACTTCTTC CTTTTTCTA 599160
AGCTTAGAAT TGACAGGTAA TCCAAATTTT TTATTTTCA CAAGACTTAA TTATCTTTTT 599220

TTAAGTTTTA TGGTTTTTCT TGTTTTTGAA AGGATTTCTT TAAATTTTTT AAAAAATCA	599280
ATATTTCTCG TATTGATTAT AACTCTTTTT TTAATTATGG CAACTTTTTT ATCTCCAAGT	599340
ATTTCTGGAG CAAAGAGATG GATATTCTTT CAAGGTGTTA GCATTCAACC TTCTGAGATT	599400
TTTAAAATAT CTTTTACTAT TTATCTTTCA GCTTATTTGA GCAAGTTTGA CCCAAGAAAA	599460
AACAATGGTA TTTCATACTG GATAAAGCCA ATGTTGATTT TTGCAATTTT TTGGGTGTTA	599520
ATAATTTTGC AAAACGATTA TTCAACAGCT ATTTATTTTG CCATTCTTTT TTTTATTGTT	599580
TTGTTTGTTT CTAATATGGC ATTTAGCTAT GTTTTTGCTA TTGTGGTTAC TTTTTTACCA	599640
GTTTCTGCTA TATTCTTGAT GCTTGAACCT TATAGGGTTT CTAGAATTTT TGCCTTTCTC	599700
AATCCTTACG ATGATCCTTC TGGCAAAGGT TACCAGATAA TAGCATCTCT TAATGCTTTA	599760
AAAAGTGGAG GAATTTTAGG TAAAGGGCTG GGAATGGGAG AGGTAAAACT TGGAAAATTA	599820
CCAGAGGCCA ATTCGGATTT TATTTTTTCA GTTCTTGGAG AAGAATTAGG ATTTTATAGG	599880
GTTTTGTTT CTATAAGCTT GTTTTTTTTG TTTTTTACT TTGGTTATTT TATAGCTATT	599940
CATTCTAATA GTAGGTTTAA ATTTTTTATT GCATTTATTT CAAGTCTTGC AATTTTTCTT	600000
CAAAGCATGA TGAATATTTT AATTGCAATC GGTCTTTTGC CTCCTACAGG GATAAATTTA	600060
CCATTTTTTT CATCTGGGGG ATCTTCTATT ATTGTTACCA TGGCATTGTC TGGCCTTATT	600120
TCAAATGTTT CAAAAAATTT AAGTAATAAT TGATTAGATT TTTCTAGTAG TGTAATTTGA	600180
GTTAGGTTAT GATTTTTGAG AGAAAATTTT TAATTAAGTA TATATATTTT TTGACGTCTT	600240
TAATTTTTTT TGAAATAATA ATTATTATTT TTGCATCTCC TTATTTTTTG ATTAGGTATA	600300
TTAGTATCAA TAATGATATT TCTCTTTCTA AAGAGGATAT AATCAAGATT TCAGGAATCA	600360
AGCCCAATAC GTATTATCAT AATGCTAATG TTAGAATATA TGAGGAGAAT CTTAAAAAAG	600420
ATTTAAGGGT AAAGAATGTT AAAGTTGATC TTAAGTTTCC CAATAAAATT AATATTAAAA	600480
TAGAAAAAAG AATACCGATT GCTGTTGCTT TAGAAAACGT AAATGGTAAT ATTACTTATT	600540
ATTGTATTGC ATCAGATGGT GTAATTTTGG AAAAAAGTAA GCATTTAATT TATGATTTGC	600600
CCGTAATTAG CGGATTAGTT TTGAATGACA ACAATGTAGG AGATTTTCTA GAGGATAGAA	600660
TGCTTAATAT TGTAAGAGGC CTTGATTATC TTAAAAATAA TCAAAAATAT TTGTATAATT	600720
TAATATCAGA GGTCAATTTT TTAAAATTGA ATTTCTATGA TTATAATGTA ATTTTGTATA	600780
TTAAAAGTAT ATATAATAAA ATATTGATAA CAGTTGATAT GAATTTAATG GATGTGATGC	600840
ATAAAGTGTT TCTTGCGGTT AATTTGCTTA AAGGAAAACC CGGCGTTATA GATTTAAGAA	600900
GTGGTGATAT CATTTTGTTA GGAGAAAGTT AGTGTCTAGG AATTTGATAG TAGGTTTAGA	600960

TGTTGGA	ACT	TCAAAA	ATTT	GTACTG	TTC	TGCCG	AGGTG	AATTTAA	ATG	ATCAAT	TAGA	601020
AATAGTT	GGA	ATAGGC	ACTA	GTATAT	CAAG	AGGAGT	TAGG	AAGGGAG	TTT	TAATAA	AATAT	601080
TGAGGCG	GCT	CTTGATT	CAA	TATCTA	AATC	TATTGAG	GCT	GCAGAG	CTCA	TCTCAG	GATG	601140
TGACATT	TACA	TCACTTT	CAG	TTTCTA	TGTC	TGGAAG	TAGT	GTTGAG	GGGA	CTAATTC	CACG	601200
CGGTGTT	GTT	GCAATA	AAAT	CAAAA	ACAAG	AGAGAT	TAAAC	GAAGA	AAGATG	TTGAA	AGGGT	601260
AATCGAA	GCG	GCAAAG	GCAA	TTGTTA	TATCC	AATGG	ATAGA	GAAATT	CCTC	ATGTTA	TATCC	601320
TCAAGA	ATTT	ATTGT	AGATG	GAATAC	CCCCA	TATAAAA	AAAT	CCAAT	AGATA	TGATG	GGGTAT	601380
TCGTCTT	GAA	GGAGAG	GTC	ACATT	TATAC	GGGCT	CTAGT	TCTTCT	AGTC	AGAATT	TAGT	601440
CAGATGC	GTA	AATCG	AGCTG	GCTTTG	CCGT	TGATG	AGGT	GTTCTT	GGAA	GTCTAG	CCTC	601500
ATCTTAT	GCA	ACTCTT	TCTA	AAGAAG	AGCG	TGAGAT	GGGG	GTTTTA	TTTA	TTGAT	ATGGG	601560
CAAAGGG	GACA	ACAGAT	ATTA	TTCTTT	TATAT	TGATG	GTTCT	CCTTAT	TATA	CGGGT	GTAAT	601620
TCCCATT	GGT	GTTAAT	AGAG	TGACTC	TGA	TATTGC	GCAA	GTTTG	GAAAG	TTCCT	GAGGA	601680
TGTTGCT	GAA	AATATT	AAAA	TAACAG	CTGG	CATTG	CTCAT	CCGTC	TATTC	TTGAG	AGTCA	601740
AATGGAA	ACT	GTAATT	TATTC	CAAATC	TGG	AACTCG	ACCC	CCTCA	AGAAA	AAAGT	AGAAA	601800
AGAGTTG	TCT	GTAATA	ATTA	ATTCA	AGACT	GAGAG	AAAT	TTTG	AAATGA	TGAA	AGCGGA	601860
AATACTT	AAG	CGCGG	ACTTT	ATAATA	AAAT	TAATGG	TGGA	ATAGT	TTTAA	CAGGC	GAGG	601920
AGCTTTA	TTC	CCAGG	CATTT	CTAATT	TAAT	AGAAG	AGGT	TTTA	ATTATC	CTGCA	AGAAT	601980
AGGTTTG	GCA	ATGAG	TATTA	ATGGA	ATTGG	AGAAG	AGCAT	ATAG	ACCCCA	AGTTT	TCTTC	602040
AGCTCTT	GGT	CTTGTT	CCTTT	ATAAG	CACGA	GCAAC	AAAAA	TTCA	ATAAAT	TAAAG	AAGGT	602100
AAGCAGT	AAA	GTTAAA	AGAA	AAAATA	AAAT	ATCTT	CAAAG	TTG	AAAGGT	GGT	TTTTTGAA	602160
AGAATGG	TTT	TGACCA	ATCA	TGGAG	GAAAGC	GTTAAT	GAAA	GATT	TATAATA	TGATT	GATAG	602220
CCATACA	AGA	AGATTT	GATT	CTACT	ACAAA	TCCTA	CAATT	CTTA	AGGTGA	TTGGT	GCGGG	602280
CGGAGG	AGGT	AGTAAT	GCTG	TTAAT	CGTAT	GATTG	AATAT	GGAG	TAAAG	ATGTT	GAATT	602340
TATTGTG	GCT	AATAC	GATC	TTCAG	GCTCT	CCAA	ACTTCT	ATTG	CTCCA	TAAAA	ATTGC	602400
CCTTG	GAGCA	AAAGT	TACAG	CAGGG	CTTGG	TGCTG	GGGGGA	AAGC	CTGAGA	TTGG	ACAAGC	602460
TGCAGC	AGAG	GAAG	ACATAG	ATGTT	TATACG	AAAT	CATCTT	TCTG	GTGCCG	ATATG	GGTGT	602520
TATTACT	GCT	GGTAT	GGGGG	GCGGG	ACAGG	AACCG	GAGCA	GCTC	CAGTTA	TTGCG	CAAGT	602580
TGCAAAA	AGAG	CTTGG	TATTT	TAAC	AGTTGG	AGTTG	TAAACA	AAGC	CTTTTA	AGTTT	GAAGG	602640
TCCTA	AGAAG	TTGAG	ACTTG	CTGAG	CAGGG	AATA	ATAAAC	TTA	AGAAAGT	CTG	TAGATAC	602700
ATTGAT	CATT	ATTCCA	AAATC	AAAAG	CTTTT	AACTG	TGTGT	GACAAA	AGAA	CCACC	ATTAA	602760

AGATGCTTTT AAGCGTGCAG ATGATGTTCT TAGAATGGGC GTTCAAGGTA TTGCAGGGCT	602820
TATTATTGAG CATGGAGAGG TTAATATTGA TTTTGCCGAT GTTAAAAGCA TTATGCAAGG	602880
CCAAGGAGAT GCTTTAATGG GAATAGGATA TGGCAAGGGC GAAAACAGAG CTGTTGATGC	602940
CGCAACTTCT GCTATTAGTA ATCCATTACT TGAGGAAGTT CGTATTGAAG GGTCTAAGGG	603000
GCTTCTTGTT AATGTTACTG GCGGAGATGA TTTTTCATTG CTTGAACTTG AAGAGATTAT	603060
GGGGATAATC ACGGTTAGTG TTGATGATGA GGCTACTGTA ATATATGGTC ATGCTATTAA	603120
TTCGAATCTT GAAGATGAAA TTTACGTTAC AGTTGTTGCT ACAGGTTTTG CATCTAAAAA	603180
GCAAAAAGAA ATATCTAGCA CACCAGAAAA TAATACTTTA AGTTCCAAAG AGTTTGATAC	603240
TTTAATGTCT GGCAATCAAA ATGCTCCTTC TGGATCTTAT GAGCAACAAG ATTCTTCTTT	603300
TGCGGCAAAG TCCAAAAATG TTAATTATTT TGATGATGAC ATTGATGTTT CAACATTTCT	603360
TAGAAATTTA AATAAAAAAA GTAGCGATGA TTAGATGAAA ATTTTGTGGT TAATAATTCT	603420
TGTTAATTTA TTTTATCTT GTGGCAATGA ATCTAAAGAA AAATCAAATC TTGGTCTTAG	603480
ATTAAGAGAA TTGGAAATTT CAGGTGGTGG ATCTGAATCT AAGATTGAAG TTTATAAAGA	603540
ATTTATTGAA AAAGAAGATA AGAATATTTT AAAGATAGTT AATTCATTG ATAAGAAAGC	603600
CAGATTTTTT AATTTAATTG GTCTTGAATT TTTTAAGCTT GGTCAGTACG GACCTGCTAT	603660
TGAATATTTT GCTAAAAATT TAGAAATCAA TCCCAATAAT TATTTATCTC ATTTTATAT	603720
AGGTGTTGCT TCTTATAATT TAGCTAAAAA TTTAAGAGTA AAAGATGAAG TTGAAAAATA	603780
CATAATCTT GCTGAAAATT CTTTTTTAAA ATCACTTTCA ATTAGAGATG ATTTTAAAGA	603840
TTCTCTTTTT GCCATTTCTA ATATGTACGT ATATGATCTT GATAAACAAC TTGAAGCTAA	603900
AAATTATTTA AATAAACTTG GTGATATGGG TGAGGACTAT TTTGAGTTTT TAATGTTAAG	603960
AGGTGCAAAT TATTATTCGC TGGGCGATCT TGGTAATGCT ATATTGTTTT ATGATAAAGC	604020
TAGTAAAAAG GCTTCAACTG AAGAGCAAAA AGAAGGTGTT TCTAGGATCA TGAGTAATTT	604080
GAAGTAATTA TTTATGATGA AATTGCTTTA TATTGATAAT TTGAAATTTT TAAAAGGCAA	604140
AGAAAAATTA AAACTTTTTA ATAATTTTGA TTTTAATAAT GTTATTAAAT TGACCCAGAA	604200
AGACATTGAG TCTTATTTTT TAAAATCATT TAGAAGATTG TTTAAGTTGC CCGATCTAAA	604260
ATTAGTAGAA TTACAAGAAA AAGTTATTCA AAGGACCAAA GCCAAAGTTG CTATTCTAGG	604320
GTCTAAGTCT TATCCTAATA AGCTTAAAAG AATTTATGAC CCTCCTTTTG CTATTTACTA	604380
CAAGGGCAAT TTACCAGATT GTTCTTTATT ATCTTGGGCT GTTGTGGTT CTAGAAAAAT	604440
TAGTAAACT CTGCTGAGA GAACAAGGGA ATTTTCTTCA CATCTTGCAA AGAATGGTGT	604500

AGAGATTATT	TCTGGATTTG	CAATTGGGGC	AGATATTGAG	GCTCATATAG	CAGCAATAAA	604560
TGAGAATAAG	AGAACATTTG	CTGTTATTCC	AACAGATATT	GACAATATTT	ATCCTAGGCA	604620
AAATCGAAAA	TATGTTTCCA	AGCTTTTAGA	ACAAGGTGGA	GGAATAATTA	CTGAGACTTT	604680
GCCATTTGAT	AAAATTCAAA	ATTATTTTTT	TGCCAAAAGA	AATAGATTGG	TATCAGGTCT	604740
GTCTGATGCT	ATTTTTATAA	CATATGCACC	CTTGAAATCA	GGAGCTTTAA	TTACAGCTGA	604800
GCTTGGTCTT	GACTTAGGAC	TTGATGTTTA	TGTTTATGAT	TTAGATTTTT	GTGGTGATGG	604860
AGCTGTAAAA	TTGCATGATT	TTGGTGCGCA	AGAAATAAAA	ACCGTTAAGG	ATCTTTATGC	604920
TTTATTAAAT	ATTAAATATG	TAGATTCCAA	TAATATTGAA	GATGATTCTA	AAGAGTGTG	604980
TAATTGTAAA	AATGTATCTG	ATGTTCTTAT	TGGGGAACCT	TTAAAAGAGG	TATGTAAATA	605040
GGGGGGTAAT	ATGAGCTTTA	AAGGAACCAC	AGTTATTGCA	ATAAAAAAAA	ATGGTAAGAC	605100
TGTGGTGGCA	GCAGATGGAC	AAGTAACTTT	TGGACATACT	GTTTTAAAGA	GTAATGCTAT	605160
TAAAAACGA	AAATTGCTTA	ATGGGAAAAT	TTTGGCAGGA	TTTGCAGGTT	CAACATCTGA	605220
TGCAATTACT	CTTTTTGAAA	AATTTGAAGA	AAAAATCAAA	GCAAAGGTG	ATGGCTTGAT	605280
TGACATTAAA	AGGGCGGCTG	TTGACCTTGC	AAAAGATTGG	CGTCTGACA	AAATACTGCA	605340
TAAGCTTGAG	GCTATGATGC	TTGTTGCTGA	TTCTAACAAT	ATTCTTTTGA	TTTCTGGTAC	605400
TGGTGATGTT	GTTGAGCCTG	AAGAGGATGT	TATTTGATT	GGCAGTGGTG	GTAATTATGC	605460
ATATTCAGCA	GCTCTTGCTT	ACATGGAGAA	CAAAAAATTA	AGCGCTTTTG	AGGTTGCACT	605520
TAGATCTTTA	AAAATAGCAG	CAAGAGTGTG	TATATATACT	AATTCTAATA	TTGTGCTTGA	605580
GGAGATTGAA	AATGAATAAA	TTAGAAGAGC	ACTATATAGT	TCCCAAAGAT	GTAGTTGCAG	605640
AACTTGATAA	ATATATAATA	GGTCAAGACG	AAGCTAAAAA	ATTAGTATCA	ATTGCTCTTG	605700
TTAATAGATA	TATAAGGTCT	AGGCTTCCAA	AAGAAATAAA	AGATGAGGTA	ATGCCTAAAA	605760
ACATTATTAT	GATTGGATCA	ACTGGCATTG	GGAAGACCGA	GATTGCAAGA	AGACTTTCTA	605820
AATTAATTAA	AGCTCCTTTT	ATTAAAGTTG	AGGCTACAAA	ATATACTGAG	GTTGGTTATG	605880
TTGGTCGTGA	TGTTGAATCT	ATGGTTAGAG	ATTTAATGAG	CATTGCAGTT	AATATGGTAA	605940
AAGAAGAGAT	GTATAGTACT	GTAAGAGATG	ATGCTTTAGT	AAGAACAGAG	GAGAGAATAG	606000
TTGATAGTCT	TTTAAAGGGA	TCTAGTAATT	CTGAGAATAT	GGATCCAAAT	GAAATAAAGG	606060
CGGAAGAAAA	GGTAAAAGAG	AAGCTTAGAA	AAAAGCTTAG	AGCAGGTGAG	CTTGATGATA	606120
CTACTATTGA	AATACAAATT	TCTAGTAAAA	TGCCATTTTC	TACAATAGAA	ATATTTACGG	606180
GTGGTAATTT	TGAAGAGATT	GATATGGGAA	TTGGCGGTTT	GCTGGGTAAT	ATATTTGATA	606240
GAAAAAGAA	AAGAGAATTG	AAGATTAAAA	AAGCAAAGGA	AATAATATTA	GCAGAAGAGC	606300